

R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A/Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen the
A/Reference number: A04626; MUID:76043692; PMID:126863
A/Accession: A04626
A/Molecule type: protein
A/Residues: 483-507; E'509-604 <W13>
R;Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A/Title: The primary structure of human plasminogen. II. The histidine loop of human pla
A/Reference number: A92125; MUID:73149248; PMID:4594729
A/Contents: annotation; active site
R;Groskopf, W.R.; Summaria, L.; Robbins, K.C.
J. Biol. Chem. 244, 3590-3597, 1969
A/Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A/Reference number: A92048; MUID:59234739; PMID:4240117
R;Trexler, M.; Vali, Z.; Patthy, L.
J. Biol. Chem. 257, 7401-7406, 1982
A/Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
A/Reference number: A92382; MUID:82213905; PMID:6919639
A/Contents: annotation; omega-aminocarboxylic acid binding sites
R;Vali, Z.; Patthy, L.
J. Biol. Chem. 259, 13690-13694, 1984
A/Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A/Reference number: A92458; MUID:85054794; PMID:6094526
A/Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Mari, D.; Soehndel, S.; McCance, S.G.;
J. Biol. Chem. 271, 29461-29467, 1996
A/Title: Kringle domains of human angiotensin. Characterization of the anti-proliferative
A/Reference number: A58811; MUID:97067211; PMID:8910613
A/Contents: annotation
R;Lijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A/Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M
A/Reference number: A58812; MUID:9548733; PMID:9548733
A/Contents: annotation
R;Tulinsky, A.; Mulichak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A/Reference number: A51341; PDB:1PK4
A/Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R;Tulinsky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A/Reference number: A51488; PDB:2PK4
A/Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R;Wu, T.P.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A/Reference number: A51911; PDB:1PKR
A/Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
R;Padmanabhan, K.; Tulinsky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A/Reference number: A52408; PDB:1PMK
A/Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A/Reference number: A65244; PDB:1CEA
A/Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Tulinsky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A/Reference number: A65245; PDB:1CEB
A/Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
Biochemistry 30, 10576-10588, 1991
A/Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å
A/Reference number: A58819; MUID:92031502; PMID:1657148
A/Contents: annotation
R;Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A/Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
A/Reference number: A58818; MUID:92031503; PMID:1657149
A/Contents: annotation
R;de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.
Biochemistry 31, 270-278, 1992

A/Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at
A/Reference number: A39483; MUID:92118803; PMID:1310033
A/Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Stec, B.; Tester, M.M.; Whitlow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A/Reference number: A65980; PDB:1KRN
A/Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-45
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A/Reference number: A65804; PDB:1HPK
A/Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 927-937, 1994
A/Title: (1)H-NMR assignments and secondary structure of human plasminogen kri
A/Reference number: 943645; MUID:94237157; PMID:8181475
A/Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
Eur. J. Biochem. 221, 939-949, 1994
A/Title: Solution structure of the epsilon-aminohexanoic acid complex of human
A/Reference number: A58817; MUID:94237158; PMID:8181476
A/Contents: annotation; conformation by (1)H-NMR
C/Comment: plasminogen is synthesized by the kidney and is present in plasma
d PIR:FGH383).
C/Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:IFHUA2) imme
rg-580, resulting in two chains connected by two disulfide bonds. Without the
C/Comment: Microplasmin is formed by autolytic cleavage of plasmin under artif
C/Comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angio
ting solid tumors.
C/Genetics:
A/Gene: GDB:PLG
A/Cross-references: GDB:119498; OMIM:173350
A/Map position: 6q26-6q27
A/Introns: 17/1; 52/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2;
C/Function:
A/Description: dissolves the fibrin of blood clots; acts as a proteolytic fact
ns the walls of the graafian follicle; also activates the urokinase-type plas
A/Pathway: fibrinolysis
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precurs
C/Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycopro
F1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F1-19/Domain: signal sequence #status predicted <SIG>
F20-810/Product: plasminogen #status experimental <PRO>
F79-466/Product: angiotensin #status experimental <APT>
F97-580/581-810/Product: plasmin #status experimental <MAT>
F97-580/Domain: plasmin chain A #status experimental <CHA>
F103-181/Domain: kringle homology <KR1>
F185-262/Domain: kringle homology <KR2>
F275-352/Domain: kringle homology <KR3>
F377-454/Domain: kringle homology <KR4>
F481-560/Domain: kringle homology <KR5>
F550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match

22.2%; Score 501; DB 1; Length 810;

Best Local Similarity 33.7%; Pred. No. 4.8e-31;

Matches 137; Conservative 45; Mismatches 169; Indels 56; Gaps 15

QY 10 NCDCCLNGTCVSNKYFNIHNCNPKFKGGQ-----HCEIDKSKTCYEGNGH 56

Db 428 NPDADKGPWCFTDPSVWVEYCNLKCSGTEASVAPPPVLLPNVETPSEDCMFGNGK 487

QY 57 FYRGKASTDTMGRCPLPWSATVLQTYHAHR----SDALQLGKGNKYNCPD-NRRRP 111

Db 488 GYRGKRAITVTGTPQDWAA-----QEPHRSITFTPETNPRAGLEK-NYCRNPDGVDGVP 541

QY 112 WCYVVGKLPVQECNCHDCKLKCQCKTKLRPR---FKIIGGFTTINQWPFAAI 168

Db 542 WCYT-TNPRKLYDCDVPQCA--APSPDCGPKQVSPKCKPGRVYVGGCVAPHSPWQVSL 598

RESULT 23

B61545
N;Accession: B61545
N;Alternate names: plasminogen
N;Contains: miniplasminogen
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 17-Mar-1999
C;Accession: B61545; MUID:89005015; PMID:3168975
R;Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A;Title: Structural aspects of the plasminogen of various species.
A;Reference number: A61545; MUID:89005015; PMID:3168975
A;Accession: B61545
A;Molecule type: protein
A;Residues: 1-37;38-117 <SCH>
R;Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 5, 21-25, 1992
A;Title: Complete amino acid sequence of ovine miniplasminogen.
A;Reference number: S28200; MUID:93149995; PMID:1492092
A;Accession: S28200
A;Molecule type: protein
A;Residues: 118-460 <SC2>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; 2
F:1-37/38-117/118-460/Product: plasminogen (fragments) #status experimental <PRO>
F:1-37/Domain: activation peptide (fragment) #status experimental <AP>
F:38-117,118-230,231-460/Product: plasmin (fragments) #status experimental <MAT>
F:41-118/Domain: kringle homology <KR4>
F:118-460/Product: miniplasminogen #status experimental <MIN>
F:132-211/Domain: kringle homology <KR5>
F:226-460/Domain: plasmin chain B #status experimental <BCH>
F:231-453/Domain: trypsin homology <TRV>
F:272,315,410/Active site: His, Asp, Ser #status predicted

Query Match 22.8; Score 502; DB 2; Length 460;

Best Local Similarity 34.7; Pred. No. 2.2e-31;

Matches 131; Conservative 43; Mismatches 158; Indels 46; Gaps 14;

QY 28 IHW--CNCPKKFGGCHCISDKTCYEGNGHFGYRGKASTDTMGSPCLPWNASATVLOQTYH 85
D 108 VRWFECNLKKAQAPSPVENPPEACDMLGIGKGYRGKATTVAGVPCQENAA-----QEPH 162
QY 86 AH----RSDALQLGLGKHNYCRNP--NRRPWCYVQVLKPLVQECMVHPCADGKUKQC 140
D 163 RHGIFTPTNPRAGLEK-NYCRNPDGVNGPWCT-TNPKLFYCDIPOC---ESSFDC 217
QY 141 GQKTLRPR--FKLIGFEFTIENQPFATYRRHGGSVTYVCGGLISPCWVISATHC 197
D 218 GKPVEPKKCPARVGGCVATPHSPWQVSRRSR-----EHFCGGTLISPEWLTAAHC 273
QY 198 FIDYPKKEDYTVYLGSRSLNNTQGMKFEYENILHKDYSADTFLAHNDIALIKRSKE 257
D 274 LDSILGPSFTYVILGAHYEMAREASVQEIPIVSRFLFEPRA-----DIALILKLSPP- 324
QY 258 GRCAQPSFTIOTICLPSPYNDPQF-----GTSCETITGKKNSTDTLYPEQLKMTVVKLIS 313
D 325 ---AVITDEVIPACLPSP-----PNYVADKTYCITIGMETQGT--FGVGRLEKARLPVIE 375
QY 314 HRECOQPHYGSEYVTKMLCAADPQWKTDSCQGGSGGPLVGLSLQGRMTLTGIVSWGRCGA 373
D 376 NKVCNRYEYLNGRVKSTELCAGDLAGGTDSCQGGSGGPLVCFKDKVILQGVTSWGLGCA 435
QY 374 LKDRGVYTRVSHFLPWI 391
D 436 RPNKPGVYRVSTVYPWI 453

RESULT 24

PLHU
N;Accession: A04625
N;Alternate names: plasminogen precursor [validated] - human

N;Contains: angiotatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C;Accession: A35229; I52242; A36646; I62738; I84609; S03735; A00929; A04627; A0
R;Peterson, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme in
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229
A;Molecule type: DNA
A;Residues: 1-810 <PET>
A;Cross-references: GB:J05286; GB:M34276; NID:9190064; PIDN:AAA60113.1; PID:938
A;Experimental source: leukocyte; lung fibroblast
R;Magaret, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolengh
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen S
A;Reference number: I52242; MUID:91097523; PMID:2268308
A;Accession: I52242
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-16 <MAL1>
A;Cross-references: GB:M62890; NID:9190092; PIDN:AAA36454.1; PID:G553613
R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for
A;Reference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
A;Molecule type: mRNA
A;Residues: 1-471, 'D', 473-810 <FOR>
A;Cross-references: GB:X05199; NID:935530; PIDN:CAA28931.1; PID:G35531
A;Experimental source: liver
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for h
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I62738
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 292-471, 'D', 473-810 <MAL2>
A;Cross-references: GB:K02922; NID:9190112; PIDN:AAA60124.1; PID:G387031
A;Accession: I84609
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 367-419 <MAL3>
A;Cross-references: GB:K02921; NID:9190110; PIDN:AAA60123.1; PID:9190111
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manne
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments o
A;Reference number: S03735; MUID:81212097; PMID:7239497
A;Accession: S03735
A;Molecule type: protein
A;Residues: 20-71, 'E', 73-76 <BRU>
R;Sottrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A;Reference number: A00929
A;Accession: A00929
A;Molecule type: protein
A;Residues: 20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>
R;Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:77225245; PMID:142009
A;Accession: A04627
A;Molecule type: protein
A;Residues: 581-810 <WIL>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid" and "lysine" forms of
A;Reference number: A04625; MUID:75093329; PMID:122932
A;Accession: A04625
A;Molecule type: protein
A;Residues: 20-50, 'Q', 51-71, 'E', 73-85, 87-100 <WIL2>

N:Alternate names: Hageman factor (activated)
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
C/Accession: S45281; #accession_revision 61329
R/Shibuya, Y.; Senba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biophys. Acta 1206, 63-70, 1994
A>Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison of the heavy chain of porcine plasmin. Comparison of the heavy chain of porcine plasmin. Comparison of the heavy chain of porcine plasmin.
A/Reference number: S45281; MUID:94242782; PMID:8186251
A/Accession: S45281
A/Molecule type: mkNA
A/Residues: 1-593 <SHR>
A/Cross-references: GB:S70164
A/Note: The authors translated the codon GAG for residue 23 as Val, GAG for residue 70 as Pro, CTC for residue 203 as Phe, GTG for residue 247 as Leu, CCG for residue 286 as Glu, and ATC for residue 505 as Leu
R/Fujikawa, K.; Walsh, K.A.; Davie, E.W.
Biochemistry 16, 2270-2278, 1977
A>Title: Isolation and characterization of bovine factor XII (Hageman factor).
A/Reference number: A61329; MUID:77182112; PMID:861210
A/Accession: A61329
A/Molecule type: protein
A/Residues: 10-16, 'X', 18-19, 525-550 <FUJ>
C/Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology; Fibrinolysis; blood coagulation; fibrinolysis; glycoprotein; hydrolase; monomer; plasma; F/37-78/Domain: fibronectin type II repeat homology <IF2>
F/88-120/Domain: EGF homology <EGF>
F/125-160/Domain: fibronectin type I repeat homology <FB1>
F/207-287/Domain: kringle homology <KR>
F/350-597/Domain: trypsin homology <TRY>
F/541/Active site: Ser #status predicted

Query Match 28.3%; Score 638; DB 2; Length 593;
Best Local Similarity 34.2%; Pred. No. 7.9e-42;
Matches 151; Conservative 59; Mismatches 164; Indels 68; Gaps 13;
DB 166 QVCTNPCLNGSDCLQAE---GHRLCRCAPSFAGRLCDVLDKASCVDVDRDRLGSLYRGMA 63
QY 64 TDTMGRCPLPWSATVLCQTY-NAHRSADALQGLGKINYCRNPDRRRPCVYQVGLKPL 122
DB 223 TLLSGAPCQSWAS---EATVNVVTAQVLNWLGDHAFCRPNPDNTRPCWFFWKGDRLS 278
QY 123 VQECWHDG--ADKLFQ-----CGQ 142
DB 279 WNYCLAPCAQAAGHEHFLPSPSALQPESTTQTPPLPSLTGWCSPFTPLASGGPGCGQ 338
QY 143 ---KTLRPRKIIIGGEFTTIENQFPAAIYRRHRGGSVTVVCGSLISPCWISATHCFI 199
DB 339 RLRLKWSLNLNVVGLVALPCAHPYIALYDQ-----HFCAGSLIAPCNVLTAAHCLQ 392
QY 200 DYPKEDYIYVLRSLNSNTQGMKFEVENLILHKDYSADTLAHNDIALKIR-SKEG 258
DB 393 NRPAKELTVLGDNRHNSCEOCQTLAVRDYELHEAFSPITYQH--DLALVRLQESADG 450
QY 259 RCAQPSRTIOTICLPMSVNDPQFQTS--CEITGFGKENSVDLYPEQLKMTVVKLISHRE 316
DB 451 CCAHPSFVQVCLPSTAAPASEAAVCAVAGHGFQEGE-YSSFQEAQVPLIDPQR 509
QY 317 CQPHYTGSEVTTKMLCAADPQWKTDSCQDGGGLVLC---SLQGRMTLFGIYVSWRGCA 373
DB 510 CSAFDVHGAAFTQMLCAGLEGGTACQDGGGLVLCEDTETPERQILIRGIYVSWGSGCG 569
QY 374 LKDKPGVTVRSHPLPIRSH 395
DB 570 NLRKPGVTVDVANLWIREHT 591

RESULT 22
PLPG
plasmin (EC 3.4.21.7) precursor - pig (fragment)
N:Alternate names: plasminogen
N:Contains: miniplasminogen

C/Species: Sus scrofa domestica (domestic pig)
C/Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C/Accession: S03733; #accession_revision 503737; A25834
R/Schaller, J.; Marti, T.; Roesselet, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A>Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the heavy chain of porcine plasmin. Comparison of the heavy chain of porcine plasmin.
A/Reference number: S03733
A/Accession: S03733
A/Molecule type: protein
A/Residues: 1-560 <SCH>
R/Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manuerg, A.
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of plasminogen and plasmin. Comparison of the primary structure of the N-terminal CNBr fragments of plasminogen and plasmin. Comparison of the primary structure of the N-terminal CNBr fragments of plasminogen and plasmin.
A/Reference number: S03735; MUID:81212097; PMID:7238497
A/Accession: S03737
A/Molecule type: protein
A/Residues: 1-57 <BRU>
R/Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A>Title: Determination of the complete amino-acid sequence of porcine miniplasminogen and plasminogen. Determination of the complete amino-acid sequence of porcine miniplasminogen and plasminogen. Determination of the complete amino-acid sequence of porcine miniplasminogen and plasminogen.
A/Reference number: A25834; MUID:85203907; PMID:3846533
A/Accession: A25834
A/Molecule type: protein
A/Residues: 450-790 <MAR>
C/Function:
A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in the walls of the graafian follicle; also activates the urokinase-type plasminogen activator; fibrinolysis
A/Pathway: fibrinolysis
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor; homol
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; s
F/1-730/Product: plasminogen-related protein precursor predicted <PRO>
F/1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLP>
F/78-560/Product: activation peptide #status predicted <APT>
F/84-162/Domain: kringle homology <KR1>
F/166-243/Domain: kringle homology <KR2>
F/256-333/Domain: kringle homology <KR3>
F/358-435/Domain: kringle homology <KR4>
F/450-790/Product: miniplasminogen #status experimental <MIN>
F/461-540/Domain: kringle homology <KR5>
F/561-790/Product: plasmin chain B #status experimental <BCH>
F/561-783/Domain: trypsin homology <TRY>
F/50-54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,2
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bonds: #status predicted
F/602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 22.5%; Score 508.5; DB 1; Length 790;
Best Local Similarity 36.2%; Pred. No. 1.2e-31;
Matches 130; Conservative 45; Mismatches 141; Indels 43; Gaps 14
QY 45 DKSKTCYEGNGHYGKASTDTMGRCPLPWSATVLCQTYHAHR---SDALQGLGKH 101
DB 456 DLSEDCMFGNGKRYRGKATTVAGVPCQEWAA---QEPHRHSITFTETNPRAGLEK-N 503
QY 101 YCRNPD-NRRSPCVQVGLKPLVQECWHDCAQGLKFCQGLRPR---FKLIGGEF 150
DB 510 YCRNPDGNDNGPWCT-TNPKLPDYCDVPCVTS--SFCGKPKVEPKKPARVVGCV 560
QY 157 TTENQPFATYRRHRGGSVTVVCGSLISPCWISATHCFIDYPKEDYIYVLRSL 214
DB 567 SIPHSWPQISLRVYRG---HFCGGTILSPWVLTAKHCKLEKSSSSPYKVLGAHEE 622
QY 217 NSNTQGMKFEVENLILHKDYSADTLAHNDIALKIRSKGRCAQPSRTIOTICLP 276
DB 623 YHLGEGVQEDVSKLF---KEPS-----EADIALKLKSSP---AVITDKVIPACLP 668
QY 277 NDPQF---GTSCEITGFGKENSVDLYPEQLKMTVVKLISHRECQPHYTGSEVTT 332
DB 669 --PNVVADRTACVITGWEKGT--YGAGLLKEARLPVLENKVCNRYELGKGVSPNEL 724
QY 333 CAADPQWKTDSCQDGGGLVLCISQGRMTLFGIYVSWRGCAKDKPGVTVRSHPLPI 391
DB 725 CAGHLAGIDSCQDGGGLVLCFEKDKYILQGVTSWGLGCALPNKPGVTVRSHPLPI 783

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Db 410 AAHCLQDRPAPEDTVVLGQRRNHSCEPOTLAVRSYRLHEAFS--PVSQYQHDALLRL 467
Qy 254 R-SKEGCAQPSRTIQTICLPSMYNDPQFGTSCBITGKENSNDYLYPQLKMTVVVKLI 312
Db 468 QEDADGSCALLSPVQVCLPSGAARPSSETTLQCVAGHGQFEGAEVASFLOBAQVPL 527
Qy 313 SHRECOQPHYGVSEVTTKMLCAADPOWKTDCQDGSGLPVCSLQG---RMTLTGIVSWG 369
Db 528 SLERCSAPDVHGSSILPMLCAGLEGGTDACQDGSGLPVCEQDAERRLTLQGTIISWG 587
Qy 370 RGCALKRDPGVVTVRSHPLWIRGHT 395
Db 588 SGQGRNPGVYTDVAVYLAMIREHT 613

RESULT 19
JC5878
plasma hyaluronan-binding protein precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999
C:Accession: JC5878
R:Hashimoto, K.; Tobe, T.; Sumiya, J.; Seguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, N.
  Biol. Pharm. Bull. 20, 1127-1130, 1997
A:Title: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyaluronan-bin
A:Reference number: JC5878; MUID:98065239; PMID:9401717
A:Accession: JC5878
A:Molecule type: mRNA
A:Residues: 1-558 <HAS>
C:Comment: This protein acts as serine protease.
C:Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsin
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-311/Product: plasma hyaluronan-binding protein large chain #status predicted <NATL>
F:725-106/Domain: EGF homology <EG1>
F:113-145/Domain: EGF homology <EG2>
F:152-185/Domain: EGF homology <EG3>
F:192-274/Domain: kringle homology <KRI>
F:312-558/Product: plasma hyaluronan-binding protein small chain #status predicted <NATL>
F:312-548/Domain: trypsin homology <TRY>

Query Match 29.4%; Score 664.5; DB 2; Length 558;
Best Local Similarity 36.9%; Pred. No. 6.5e-44;
Matches 154; Conservative 57; Mismatches 163; Indels 43; Gaps 14;

Qy 13 CLNGGTCVSNKYFNSIHWNCNCPKFGQHCIDSKTCYEGNGHFYRGKASTDTMGRPCL 72
Db 157 CQNGVCSSRRRRSRF--TCACPDQYKGFCEIGPD--DCYVGDGYSYRGKSKTYNQNPCL 214
Qy 73 PWSATVLOQTYHAHRS DALQLGLKHNCRPNRRPWCYVQVGLKPL-----VQBC 126
Db 215 YWNSHLLQETYNMFMEAEATHGIAEHNFNCPDGDHPCWFCVKNSEKVKWEYCDVTVC 274
Qy 127 MYHDCADGKLKPF-----CQGQKTLRPR--FKIIGGEFTTIENQPFPAIY---- 169
Db 275 PVPDTPNVPESLLEPVMELPQFESCGKTEVAHAKVIYGGFKSTAGKHPQVSLQSLP 334
Qy 170 ---RRHGGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGENK 226
Db 335 LTTSMPOG---HFCCGALIHPCWVLTAAHC--TDINTKLVV-LGDDQLKKTSHQOTF 389
Qy 227 EVENILHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDP--QFGTSC 285
Db 389 RVEKILKYSQYNERDEIPHNDIALKLPVGGHCALESRYKVTCLPS---DPPPSGTCE 445
Qy 286 EITGFGKENS TDLYPEQLKMTVVKLI SHRECOQPHYGVSEVTTKMLCAADPOWK--TDSC 344
Db 446 HISGGMVETG--GSRQLLDKAKVLIANPLNCSRLQYDHTIDDSMTCAGNLQKPGSDTC 503
Qy 345 QDSDGGLPVCSLQGRMTLTGIVSWGRCALKDKPGVTVRSHFLPWRSHRSTKEENG 401
Db 504 QDSDGGLTCERKDGTVYVYGVISWGQECG--KKPGVYTVTKFLNWKNTWHREAGL 558

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RESULT 20
JC4795
plasma hyaluronan-binding protein precursor - human
N:Alternate names: hepatocyte growth factor activator-like protein; PHBP
N:Contains: serine proteinase (EC 3.4.21.-)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002
C:Accession: JC4795
R:Choi-Miura, N.H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tomi, M.
  J. Biochem. 119, 1157-1165, 1996
A:Title: Purification and characterization of a novel hyaluronan-binding protei
A:Reference number: JC4795; MUID:96425001; PMID:8827452
A:Accession: JC4795
A:Molecule type: mRNA
A:Residues: 1-560 <CHO>
A:Cross-references: GB:S93182; MID:GL836158; PIDN:AAB45909.1; PID:gl836159
A:Experimental source: plasma
A:Note: parts of this sequence, including the amino ends of the mature chains,
C:Genetics:
A:Gene: GDB:HABP2; HABP; PHBP; HGFAI
A:Cross-references: GDB:457362
C:Complex: a disulfide-bonded heterodimer of chains produced from the same prec
C:Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology
C:Keywords: Chondroitin sulfate proteoglycan; Glycoprotein; Hyaluronic acid; Hy
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-313/Product: plasma hyaluronan-binding protein, 50K chain #status predicted
F:77-108/Domain: EGF homology <EG1>
F:115-147/Domain: EGF homology <EG2>
F:154-187/Domain: EGF homology <EG3>
F:194-276/Domain: trypsin homology <KRI>
F:314-550/Domain: kringle homology <KRI>
F:314-516/Product: plasma hyaluronan-binding protein, catalytic chain #status p
F:54-207/Binding site: carboxylate (Asn) (covalent) #status predicted
F:77-88,82-97,99-108,115-125,120-136,138-147,154-165,159-176,178-187,194-276,21
F:362,405,509/Active site: His, Asp, Ser #status predicted

Query Match 28.9%; Score 651.5; DB 1; Length 560;
Best Local Similarity 36.4%; Pred. No. 6.6e-43;
Matches 152; Conservative 58; Mismatches 161; Indels 47; Gaps 14;

Qy 13 CLNGGTCVSNKYFNSIHWNCNCPKFGQHCIDSKTCYEGNGHFYRGKASTDTMGRPCL 72
Db 159 CQNGATCSRHRRSKF--TCACPDQKGFCEIG--SDCCVGDGYSYRGGMNRTVNOHACL 216
Qy 73 PWSATVLOQTYHAHRS DALQLGLKHNCRPNRRPWCYVQVGLKPLVOE--CMWHDC 131
Db 217 YWNSHLLQETYNMFMEAEATHGIEHNFNCPDDEKPCWCFIKVTNDKVKWEYCDVSAC 276
Qy 132 ADGKLKPF-----CQGQKTLRPR--FKIIGGEFTTIENQPFPAIYRRHR 173
Db 277 SAQDVAYPESPTBSTKLPGPSGCKTEIAERKIKRIYGGFKSTAGKHPWQASLQ---- 332
Qy 174 GGSVT-----YVCGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGENK 225
Db 333 --SSLPLTISMPQGHFCGALIHPCWVLTAAHC-TDI-KTRHLKVLGDDQLKKEBFHEQS 389
Qy 226 FEVENILHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPQF--QT 283
Db 390 FRVEKIFKSHYNERDEIPHNDIALKLPVGGHCALESRYKVTCLP---DGSPPSSG 445
Qy 284 SCEITGFGKENS TDLYPEQLKMTVVKLI SHRECOQPHYGVSEVTTKMLCAADPOWK--TD 342
Db 446 ECHISGMVETGK--GSRQLLDKAKVLIANPLNCSRLQYDHTIDDSMTCAGNLQKPGQD 503
Qy 343 SCQDSDGGLPVCSLQGRMTLTGIVSWGRCALKDKPGVTVRSHFLPWRSHRSTKEENG 400
Db 504 TCQDSDGGLTCERKDGTVYVYGVISWGQECG--KKPGVYTVTKFLNWKNTWHREAGL 559

RESULT 21
S45281
coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)

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A:Accession: A25191
A:Molecule type: mRNA
A:Residues: 146-378, G', 380-615 <QUE>
A:Cross-references: GB:M13147; NID:G180360; PIDN:AAA70224.1; PID:G180361
E:McMullen, B.A.; Fujikawa, K.
J. Biol. Chem. 260, 5328-5341, 1985
A:Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (accessioned)
A:Reference number: A22248; MUID:85182674; PMID:3886654
A:Accession: A22248
A:Molecule type: protein
A:Residues: 20-379 <MC>
E:Fujikawa, K.; McMullen, B.A.
J. Biol. Chem. 258, 10924-10933, 1983
A:Title: Amino acid sequence of human beta-factor XIIa.
A:Reference number: A21037; MUID:83291041; PMID:6604055
A:Accession: A21037
A:Molecule type: protein
A:Residues: 354-362,373-615 <UJ>
E:Harris, R.J.; Ling, V.T.; Spellman, M.W.
J. Biol. Chem. 267, 5102-5107, 1992
A:Title: O-linked fucose is present in the first epidermal growth factor domain of factor XIIa.
A:Reference number: A44606; MUID:92184750; PMID:1544894
A:Contents: annotation; carbohydrate binding site
C:Genetics:
A:Gene: GDB:P12
A:Cross-references: GDB:1119892; OMIM:234000
A:Map position: 5q34-5qter
A:Mutons: 19/3; 39/1; 72/2; 96/1; 133/1; 177/1; 212/1; 267/2; 340/1; 417/2; 418/1; 515/1
C:Complex: factor XII, prekallikrein, and HMK kininogen form a complex bound to anion
C:Function:
A:Description: factor XIIa catalyzes the proteolytic activation of plasminogen; plasminogen
ikrein
A:Pathway: blood coagulation; fibrinolysis
C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat
C:Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolase; kringle
E:1-109/Domain: signal sequence #status predicted <SIG>
F:20-372/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:249,433/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:299,305,328,329,337/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:308/Binding site: carbohydrate (Ser) (covalent) #status predicted
F:412,461,563/Active site: His, Asp, Ser #status predicted
Query Match 30.2%; Score 681; DB 1; Length 615;
Best Local Similarity 34.1%; Pred.No.3.8e-45;
Matches 152; Conservative 58; Mismatches 158; Indels :78; Gaps 10
QY 13 CLNGGTCVSNKYFSNIHNCNPKFGQCEIDKSKTCYEGNGHFVRGKASDTMGRPLC 72
DB 183 CLHGRCLE---VEGRLCHCPGVYGPDCVDVTKASCYDGRGLSVRLARTLTSAPQC 235
QY 73 PMSATVLOQTY-HAHRSDALQLGKHNCRPNRRRPWCYVQGLKPLVQECNVHDC 131
DB 240 PWAS-----BATYRNVTAEQARWNLGGHAFCEKPNPDIRPWCFLNDRDLSEYCDLAQC 295
QY 132 -----ADGKL----- 136
DB 296 QITQTAAPTPVSPRLHVLMPAQAPAPKPPQPTTRTPPQSQTFGALPAKREQPPSLTRNG 355
QY 137 KFOCGQ---KTLRPRPKIIGBFTTIENOPWFAALYRRHRGGSVTVCGGSLISPCWVLS 192
DB 356 PLSCGQRLKSLSSMTYVGVGVALRGAPHYAALYWGHS-----FCAGSLIAPCWILT 405
QY 194 ATHCFIDYPKEDYIVLGRSLNSNTQCEMKFEVENLLHKDYSADTLAHNDIALLKI 253

F1-34/Domain: signal sequence #status predicted <SIG>
F108-148/Domain: fibronectin type II repeat homology <IF2>
F164-197/Domain: EGF homology <EG1>
F202-237/Domain: fibronectin type I repeat homology <IF1>
F245-278/Domain: EGF homology <EG2>
F286-367/Domain: kringle homology <KG>
F373-437/Product: hepatocyte growth factor activator light chain #status exper ntal
F408-655/Product: hepatocyte growth factor activator heavy chain #status exper ntal
F408-641/Domain: trypsin homology <TRY>
F408-481,290,468,494,546/Binding site: Carbohydrate (Asn) (covalent) #status predicted
F164-175,169-186,188-197,202-230,228-237,245-256,250-267,269-278,286-367,307-338-447,497,538/Active site: His. Asp. Ser #status predicted

Query Match	32.2%;	Score	726.5;	DB 1;	Length	655;			
Best Local Similarity	37.2%;	Pred. No.	1.2e-48;						
Matches	158;	Conservative	53;	Mismatches	161;	Indels	53;	Gaps	9;

QY	5	HQVFNCLNGGTCVSNKYFSNTHW-----CNCPKFGGOHCEIDKSKTCYEGNGH	56
Db	242	HTACUSSPCLNGGTC-----HLIVATTTWCACPPGFAGRLCNIEDPERCFLNGT	292
QY	57	FYRGKASTDTMGRPCLPNSATVLCQTVHAHRSDALQLGLGKHNYCRNPDNRNRPWCVV-	115
Db	293	GVRGVASTSAGSLCLANNSDLLYQELHVDVSGAALLGLGPHAYCRNPDNDRPWCYVV	352
QY	116	-----QVGLPXLPOEVMHDCAGKLKFCQGOK-----TURPRFKI	151
Db	353	KDSALSWBYCRLEACESITRVQLSPDLLATLPEPASGRQ--ACGRHKKTFLRPR--I	408
QY	152	IGCBFTTIENQSFWAAIYVRHRGGSVTYVCGSLISPCWISATHCFIDYKPKEDYIVYL	211
Db	409	IGGSSLPGSHPLWLAALY---IGDS---FCAGSLVHTCWWVSAAHCFSSHSPRDSVVL	462
QY	212	GSRLNSNTQGMKEFEVENLIHKDYSADTLAHNDIALIKRSKGBCAQPSRTIQTC	271
Db	463	GQHFFNRRTDVTQTGIEKYPITLYSVFNESDH-DLVLI RLKKKGDRCATRSQFVQPIC	521
QY	272	LPSMYNDQFGTSCBITFGKENSSTDYLPQLKMTVVKLI SHRECQOPHYVYGVSEVTKM	331
Db	522	LPEGSTTPAGHKCIAGWHLDENVSGYSSSLREALVPLVADHKCSSPFEVYGADISNM	581
QY	332	LCAADPQWKTSDSCQDSDGGLVCSLQGRMTITGVSWRGCGCALDKPQVYTRVSHFLPMI	391
Db	582	LCAGVPDCKSIACQDSDGGLACENGVAVLVGII SMGDGCGRLHKPQVYTRVANYVDWI	641

QY 392 RSHTK 396
Db 642 NDRIR 646

RESULT 17
S28941
coagulation factor XIa (BC 3.4.21.38) - guinea pig (fragment)
N:Alternate names: Hageman factor
C:Species: Cavia porcellus (guinea pig)
C:Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S28941
R:Semba, U.; Yamamoto, T.; Kuniisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Abe, R.; Biochim. Biophys. Acta 1159, 113-121, 1992
A:Title: Primary structure of Guinea-pig Hageman factor: sequence around the cleavage site
A:Reference number: S28941; MUID:93003367; PMID:1390917
A:Accession: S28941
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-603 <SEM>
A:Cross-references: EMBL:X68615; NID:G49578; PIDN:CAA48600.1; PID:G49579
C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat
C:Keywords: hydrolase; serine proteinase
F:46-87/Domain: fibronectin type II repeat homology <FBI>
F:134-169/Domain: fibronectin type I repeat homology <FBI>
F:177-208/Domain: EGF homology <EGF>
F:216-294/Domain: kringle homology <KRG>
F:359-597/Domain: trypsin homology <TRY>

C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-36/Domain: propeptide #status predicted <PRO>
F;37-47/Domain: plasminogen activator alpha-1 #status predicted <PLA>
F;42-79/Domain: fibronectin type I repeat homology <1FA>
F;87-120/Domain: EGF homology <EGF>
F;128-209/Domain: kringle homology <KR>
F;226-471/Domain: trypsin homology <TRY>
F;42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-438,441-457,461-477,481-497,501-517,521-537,541-557,561-577,581-597,601-617,621-637,641-657,661-677,681-697,701-717,721-737,741-757,761-777,781-797,801-817,821-837,841-857,861-877,881-897,901-917,921-937,941-957,961-977,981-997,1001-1017,1021-1037,1041-1057,1061-1077,1081-1097,1101-1117,1121-1137,1141-1157,1161-1177,1181-1197,1201-1217,1221-1237,1241-1257,1261-1277,1281-1297,1301-1317,1321-1337,1341-1357,1361-1377,1381-1397,1401-1417,1421-1437,1441-1457,1461-1477,1481-1497,1501-1517,1521-1537,1541-1557,1561-1577,1581-1597,1601-1617,1621-1637,1641-1657,1661-1677,1681-1697,1701-1717,1721-1737,1741-1757,1761-1777,1781-1797,1801-1817,1821-1837,1841-1857,1861-1877,1881-1897,1901-1917,1921-1937,1941-1957,1961-1977,1981-1997,2001-2017,2021-2037,2041-2057,2061-2077,2081-2097,2101-2117,2121-2137,2141-2157,2161-2177,2181-2197,2201-2217,2221-2237,2241-2257,2261-2277,2281-2297,2301-2317,2321-2337,2341-2357,2361-2377,2381-2397,2401-2417,2421-2437,2441-2457,2461-2477,2481-2497,2501-2517,2521-2537,2541-2557,2561-2577,2581-2597,2601-2617,2621-2637,2641-2657,2661-2677,2681-2697,2701-2717,2721-2737,2741-2757,2761-2777,2781-2797,2801-2817,2821-2837,2841-2857,2861-2877,2881-2897,2901-2917,2921-2937,2941-2957,2961-2977,2981-2997,3001-3017,3021-3037,3041-3057,3061-3077,3081-3097,3101-3117,3121-3137,3141-3157,3161-3177,3181-3197,3201-3217,3221-3237,3241-3257,3261-3277,3281-3297,3301-3317,3321-3337,3341-3357,3361-3377,3381-3397,3401-3417,3421-3437,3441-3457,3461-3477,3481-3497,3501-3517,3521-3537,3541-3557,3561-3577,3581-3597,3601-3617,3621-3637,3641-3657,3661-3677,3681-3697,3701-3717,3721-3737,3741-3757,3761-3777,3781-3797,3801-3817,3821-3837,3841-3857,3861-3877,3881-3897,3901-3917,3921-3937,3941-3957,3961-3977,3981-3997,4001-4017,4021-4037,4041-4057,4061-4077,4081-4097,4101-4117,4121-4137,4141-4157,4161-4177,4181-4197,4201-4217,4221-4237,4241-4257,4261-4277,4281-4297,4301-4317,4321-4337,4341-4357,4361-4377,4381-4397,4401-4417,4421-4437,4441-4457,4461-4477,4481-4497,4501-4517,4521-4537,4541-4557,4561-4577,4581-4597,4601-4617,4621-4637,4641-4657,4661-4677,4681-4697,4701-4717,4721-4737,4741-4757,4761-4777,4781-4797,4801-4817,4821-4837,4841-4857,4861-4877,4881-4897,4901-4917,4921-4937,4941-4957,4961-4977,4981-4997,5001-5017,5021-5037,5041-5057,5061-5077,5081-5097,5101-5117,5121-5137,5141-5157,5161-5177,5181-5197,5201-5217,5221-5237,5241-5257,5261-5277,5281-5297,5301-5317,5321-5337,5341-5357,5361-5377,5381-5397,5401-5417,5421-5437,5441-5457,5461-5477,5481-5497,5501-5517,5521-5537,5541-5557,5561-5577,5581-5597,5601-5617,5621-5637,5641-5657,5661-5677,5681-5697,5701-5717,5721-5737,5741-5757,5761-5777,5781-5797,5801-5817,5821-5837,5841-5857,5861-5877,5881-5897,5901-5917,5921-5937,5941-5957,5961-5977,5981-5997,6001-6017,6021-6037,6041-6057,6061-6077,6081-6097,6101-6117,6121-6137,6141-6157,6161-6177,6181-6197,6201-6217,6221-6237,6241-6257,6261-6277,6281-6297,6301-6317,6321-6337,6341-6357,6361-6377,6381-6397,6401-6417,6421-6437,6441-6457,6461-6477,6481-6497,6501-6517,6521-6537,6541-6557,6561-6577,6581-6597,6601-6617,6621-6637,6641-6657,6661-6677,6681-6697,6701-6717,6721-6737,6741-6757,6761-6777,6781-6797,6801-6817,6821-6837,6841-6857,6861-6877,6881-6897,6901-6917,6921-6937,6941-6957,6961-6977,6981-6997,7001-7017,7021-7037,7041-7057,7061-7077,7081-7097,7101-7117,7121-7137,7141-7157,7161-7177,7181-7197,7201-7217,7221-7237,7241-7257,7261-7277,7281-7297,7301-7317,7321-7337,7341-7357,7361-7377,7381-7397,7401-7417,7421-7437,7441-7457,7461-7477,7481-7497,7501-7517,7521-7537,7541-7557,7561-7577,7581-7597,7601-7617,7621-7637,7641-7657,7661-7677,7681-7697,7701-7717,7721-7737,7741-7757,7761-7777,7781-7797,7801-7817,7821-7837,7841-7857,7861-7877,7881-7897,7901-7917,7921-7937,7941-7957,7961-7977,7981-7997,8001-8017,8021-8037,8041-8057,8061-8077,8081-8097,8101-8117,8121-8137,8141-8157,8161-8177,8181-8197,8201-8217,8221-8237,8241-8257,8261-8277,8281-8297,8301-8317,8321-8337,8341-8357,8361-8377,8381-8397,8401-8417,8421-8437,8441-8457,8461-8477,8481-8497,8501-8517,8521-8537,8541-8557,8561-8577,8581-8597,8601-8617,8621-8637,8641-8657,8661-8677,8681-8697,8701-8717,8721-8737,8741-8757,8761-8777,8781-8797,8801-8817,8821-8837,8841-8857,8861-8877,8881-8897,8901-8917,8921-8937,8941-8957,8961-8977,8981-8997,9001-9017,9021-9037,9041-9057,9061-9077,9081-9097,9101-9117,9121-9137,9141-9157,9161-9177,9181-9197,9201-9217,9221-9237,9241-9257,9261-9277,9281-9297,9301-9317,9321-9337,9341-9357,9361-9377,9381-9397,9401-9417,9421-9437,9441-9457,9461-9477,9481-9497,9501-9517,9521-9537,9541-9557,9561-9577,9581-9597,9601-9617,9621-9637,9641-9657,9661-9677,9681-9697,9701-9717,9721-9737,9741-9757,9761-9777,9781-9797,9801-9817,9821-9837,9841-9857,9861-9877,9881-9897,9901-9917,9921-9937,9941-9957,9961-9977,9981-9997,10001-10017,10021-10037,10041-10057,10061-10077,10081-10097,10101-10117,10121-10137,10141-10157,10161-10177,10181-10197,10201-10217,10221-10237,10241-10257,10261-10277,10281-10297,10301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Qy 59 RGKASTDTMGPRCLPWN SATVLQOYTHAHRSDALQGLGKHNYCRNPDRRRPWCYVQG 118
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Db 316 PADTASHPWQAIAFKRRSPGERFLCGGILISSCWLSAAHCQEPFPFHITVILGRT 375
Qy 215 RLNSNTQCEMKFEVENILHXYDADTLAHNDIALKIRSKGRCACQAPRTIQTICLPS 274
Db 376 YRVVPGEEQKFEYKIVHKEFDDT--YNDIALQLKSDSSRCAQESSVVRVTCCLPP 433
Qy 275 MYNDPQFTSCIEITGFKENSTDIYPEQLKMTVKLISHRECQPHYSEVTTMLCA 334
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Db 554 DWIRDNR 561

RESULT 12
A35029
t-plasminogen activator (EC 3.4.21.68) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A35029; A31597
R:Peng, P.; Ohlsson, M.; Ny, T.
J. Biol. Chem. 265, 2022-2027, 1990
A:Title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec
A:Reference number: A35029; MUID:90130448; PMID:2105315
A:Accession: A35029
A:Status: preliminary
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R:Ny, T.; Leonardsson, G.; Heueh, A.J.W.
DNA 7, 671-677, 1988
A:Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activat
A:Reference number: A31597; MUID:89170114; PMID:3148445
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C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
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Query Match 37.3%; Score 841.5; DB 1; Length 559;
Best Local Similarity 36.5%; Pred. No. 1.2e-57;
Matches 180; Conservative 65; Mismatches 143; Indels 105; Gaps 12;
Qy 3 ELHVP-----SNCDLNGGTCVSNKYSNIHWCNCPKFGGQCEIDKSKTCYEGNGHFY 58
Db 74 QHSVPKSCSEPCFCNGTCQOALYFSDP-VCQCPGPGAGKCEIDTRATCEDQGISY 132
Qy 59 RGKASTDTMGPRCLPWN SATVLQOYTHAHRSDALQGLGKHNYCRNPDRRRPWCYV-QV 117
Db 133 RGTWSTAEGAEACTNWS SALLAQPKYSGRRPDAIRLGLGNHNYCRNPDRDRSKPCYVFA 192
Qy 118 GL-----KPLVQECMV----- 128
Db 193 GKYTEFCSTPACPKPTEDCYVGKGYRGTHSITSGASCLPWNMILGKYVTAQNP 252
Qy 129 -----HDCADGKLKFO-----CGOKTLR-PRFKIIGG 154
Db 253 NSQAALGLGKHNYCRNP DGDGAKPWCHVKNRLTWECYDVPSCSTCGLRQYQPOFRIKGG 312
Qy 155 ETTIENQWPAIY-RHRRGSGTVVCGGSLISPCWISATHCFIDYPKKEDIYVILGR 213
Db 313 LFTDITSHPWQAIAFVKRRSPGERFLCGGVLISCWLSAAHCQEPFPFHLLKVLGR 372
Qy 214 RLNSNTQCEMKFEVENILHXYDADTLAHNDIALKIRSKGRCACQAPRTIQTICLPS 273
Db 373 YRVVPGEEQKFEYKIVHKEFDDT--YNDIALQLKSDSSRCAQESSVVRVTCCLP 430
Qy 274 SMYNDPQF-----GTSCIEITGFKENSTDIYPEQLKMTVKLISHRECQPHYSEVTT 329
Db 431 ----DPDVLQPDWTECELSGYGKHEALSPFYSERLEAHVRLYPSRSTQSHLLFNKTITS 486
Qy 330 KMLCAADP-----QWKTDSCQDSSGGLVCSLQGRMTLTGVSMGRGKALCKDKPGVYTRV 384
Db 487 NMLCAGDTRTGGNQDVHDACQDSSGGLVCLNDGRMTLVGLIISWGLGCGQKDVFGVYTKV 546
Qy 385 SHFLPWIRSHTK 397
Db 547 TNYLAWIQDNMKQ 559

RESULT 13
JS0597
t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat
N:Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: JS0597
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampir
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0597
A:Molecule type: mRNA
A:Residues: 1-477 <KRA>
A:Cross-references: GB:M63987; NID:gl66070; PIDN:AAA31591.1; PID:gl66071
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I r

RESULT 11

UKHT

t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human
 N/Alternate names: t-PA; tissue plasminogen activator
 C/Species: Homo sapiens (man)
 C/Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000
 C/Accession: A94004; A23529; J0562; A93293; S02125; A91343; A93951; A91322; A54645; 160
 R/RY, T.; Elgin, F.; Lund, B.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984
 A/Title: The structure of the human tissue-type plasminogen activator gene: correlation
 A/Reference number: A94004; MUID:84298137; PMID:6089198
 A/Accession: A94004
 A/Molecule type: DNA
 A/Residues: 1-562 <NYT>
 A/Cross-references: GB:U00141
 A/Note: The codon given for residue 93 (ACC) is inconsistent with the authors' translation
 R/Friener Degen, S.J.; Rajput, B.; Reich, E.
 J. Biol. Chem. 261, 6972-6985, 1986
 A/Title: The human tissue plasminogen activator gene.
 A/Reference number: A23529; MUID:86196143; PMID:3009482
 A/Accession: A23529
 A/Molecule type: DNA
 A/Residues: 1-562 <DEG>
 A/Cross-references: GB:K03021; NID:G339817; PIDN:AAA98809.1; PID:G339818
 R/Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuoka, S.; Higashio, K.
 Agric. Biol. Chem. 55, 1225-1232, 1991
 A/Title: Purification and characterization of tissue plasminogen activator secreted by H
 A/Reference number: J0562; MUID:91291340; PMID:1368681
 A/Accession: J0562
 A/Molecule type: mRNA
 A/Residues: 31-562 <ITA>
 A/Cross-references: DDBJ:D01096; NID:G220128; PIDN:BAA00881.1; PID:G441174
 A/Experimental source: embryonic lung fibroblast IMR-90 cells
 A/Note: part of this sequence, including the amino end of the mature protein, was confir
 R/Pennica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vohar, G.A.; Ward, C.A.; Bennett
 Nature 301, 214-221, 1993
 A/Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche
 A/Reference number: A93293; MUID:83115262; PMID:6337343
 A/Accession: A93293
 A/Molecule type: mRNA
 A/Residues: 1-562 <PEN>
 A/Cross-references: GB:U00141
 A/Experimental source: melanoma cells
 R/Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.
 Nucleic Acids Res. 16, 5695, 1988
 A/Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe
 A/Reference number: S02125; MUID:88262579; PMID:3133640
 A/Accession: S02125
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-562 <SAS>
 A/Cross-references: EMBL:X07393; NID:G37243; PIDN:CAA30302.1; PID:G37244
 R/Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma
 FEBS Lett. 199, 145-149, 1985
 A/Title: Expression in *Escherichia coli* of finger-domain lacking tissue-type plasminogen
 A/Reference number: A91343; MUID:85285620; PMID:3896853
 A/Accession: A91343
 A/Molecule type: mRNA
 A/Residues: 1-38, 'G', 435-562 <KAG>
 A/Experimental source: Detroit 562 cells; ATCC 138
 R/Selund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
 Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
 A/Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ
 A/Reference number: A93951; MUID:83169656; PMID:6572897
 A/Accession: A93951
 A/Molecule type: mRNA
 A/Residues: 251-358 <EDL>
 A/Experimental source: melanoma cells
 R/Fohl, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.
 Biochemistry 23, 3701-3707, 1984

A/Title: Tissue plasminogen activator: peptide analyses confirm an indirectly
 differences.
 A/Reference number: A90488; MUID:85000468; PMID:6433976
 A/Contents: annotation; melanoma cells, partial sequence of residues 36-562, a
 R/Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.
 FEBS Lett. 168, 29-32, 1984
 A/Title: Differences between uterine and melanoma forms of tissue plasminogen
 A/Reference number: A91322; MUID:84158956; PMID:6538514
 A/Accession: A91322
 A/Molecule type: protein
 A/Residues: 33-45,311-320 <POH>
 A/Experimental source: uterus
 A/Note: in the uterus, cleavage of the activation peptide may also occur after
 R/van Zonneveld, A.J.; Veerman, H.; Pannecoek, H.
 J. Biol. Chem. 261, 14214-14218, 1986
 A/Reference number: A37567; MUID:87033611; PMID:3021732
 A/Contents: annotation; fibrin binding site
 R/Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, F.
 EMBO J. 5, 3525-3530, 1986
 A/Title: Involvement of finger domain and kringle 2 domain of tissue-type plas
 A/Reference number: A37568; MUID:87161761; PMID:3030730
 A/Contents: annotation; fibrin binding site
 R/Dodd, I.; Nunn, B.; Robinson, J.H.
 Thromb. Haemost. 59, 523-528, 1988
 A/Title: Isolation, identification and pharmacokinetic properties of human tis
 A/Reference number: A60902; MUID:89044681; PMID:3142086
 A/Contents: annotation: novel forms of expressed recombinant t-PA
 R/Harris, T.J.R.; Patel, T.; Marsden, F.A.O.; Little, S.; Emrage, J.S.; Opdena
 Mol. Biol. Med. 3, 279-292, 1986
 A/Title: Cloning of cDNA coding for human tissue-type plasminogen activator at
 A/Reference number: A54645; MUID:86284200; PMID:3090401
 A/Accession: A54645
 A/Molecule type: mRNA
 A/Residues: 1-562 <HAR>
 A/Cross-references: GB:M15518; NID:G190031; PIDN:AAA60111.1; PID:G190032
 A/Note: parts of this sequence were confirmed by peptide sequencing
 R/Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
 DNA 6, 461-472, 1987
 A/Title: Expression of human uterine tissue-type plasminogen activator in mous
 A/Reference number: I60110; MUID:88054470; PMID:2824147
 A/Accession: I60110
 A/Status: translated from GB/EMBL/DDBJ
 A/Molecule type: mRNA
 A/Residues: 1-562 <RES>
 A/Cross-references: GB:M18182; NID:G340176; PIDN:AAA36800.1; PID:G340177
 R/Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, D.
 J. Biol. Chem. 260, 11223-11230, 1985
 A/Title: Isolation and characterization of the human tissue-type plasminogen a
 A/Reference number: I55232; MUID:85289338; PMID:3161893
 A/Accession: I55232
 A/Status: preliminary; translated from GB/EMBL/DDBJ
 A/Molecule type: DNA
 A/Residues: 1-36 <RE2>
 A/Cross-references: GB:M11890; NID:G339837; PIDN:AAA61213.1; PID:G339839
 C/Comment: Cleavage by plasmin or trypsin produces two chains held together by
 C/Comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val
 C/Comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type
 C/Genetics:
 A/Gene: GDB:PLAT
 A/Cross-references: GDB:119496; OMIM:173370
 A/Map position: 8p12-8p12
 A/Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1;
 C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I
 C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine pr
 F/1-33/Domain: signal sequence #status predicted <SIG>
 F/24-32/Domain: propeptide #status predicted <PRO>
 F/33-562/Product: t-plasminogen activator #status experimental <MAT>
 F/33-310/Product: t-plasminogen activator chain A #status experimental <ACH>
 F/41-78/Domain: fibronectin type I repeat homology <1F1>
 F/86-119/Domain: EGF homology <EGF>
 F/127-208/Domain: kringle homology <KR1>
 F/215-236/Domain: kringle homology <KR2>
 F/311-562/Product: t-plasminogen activator chain B #status experimental <BCH>

A:Accession: A24615
A:Molecule type: mRNA
A:Residues: 1-433 <BBL>
A:Cross-references: GB:J02389; NID:g55127; PIDN:CAA26231.1; PID:g55128
C:Genetics:
C:Introns: 19/3; 30/1; 66/1; 124/2; 155/1; 229/2; 279/1; 326/1; 375/3
C:Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C:Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-178/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F:32-63/Domain: kringle homology <EGF>
F:71-152/Domain: kringle homology <KRG>
F:180-431/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
F:190-421/Domain: trypsin homology <TRY>
F:193-301,211-227,219-230,315-384,347-363,374-402/Disulfide bonds: #status predicted
F:226,277,378/Active site: His, Asp, Ser #status predicted

Query Match 72.1%; Score 1626.5; DB 1; Length 433;
Best Local Similarity 70.2%; Pred. No.1e-118;
Matches 283; Conservative 50; Mismatches 61; Indels 9; Gaps 2;

QY 9 SNCDCLNGTCVSNKYFSNIHWNCPCPKFGQHCHEIDKSKTCYEGNGHGYRGAASDTMG 68
DB 30 SNGCGQNGVGVSYKYFSRIKRCSPKRFQGEHCHEIDASKTCYHNGDSYRGRANTDTKG 89
QY 69 RPLCPWNSATVLOOTYHAHRSDALQGLGKHNYCRNPDRRPPWCYVQVGLKPLVQECMV 128
DB 90 RPLANNAPAVLQXPYNAHNPDAISLGLGKHNYCRNPDRKRPWCYVQIGLRQFVQECMV 149
QY 129 HDCADGKJK-----FQCGQKTLRPRFKIIGCEFTTIENQPMFAAIYRHRGGS-VTY 179
DB 150 HDCSLSKPKSSVDDQGFQCGQKALRPRFKIVGGEFTVENQPMFAAIYKNGGSPPSF 209
QY 180 VCGSLLSPCWVISATHCFFDYPKKEYIVYVGLGRSLNSNTQGEKPEVENLILHKDYSA 239
DB 210 KCGSLLSPCWVAAAHCFQLPKENYVVLGOSKESSYNPGEMKFEVQLILHEYRE 269
QY 240 DTLAHNDIALLKIRSEKRCACQPSRTIQTICLPSMYNDPQFGTSCITIGFKENSTDYL 299
DB 270 DSLAYHNDIALLKIRTSGCAQPSRSIQITCLPPRTDAPFGSDCIITIGFKESSESYL 329
QY 300 YPEQLKMTVVKVLSHRSCQPHYTGSEVTHKVLCAADPQWKTDSCQDSSGGLVCSIQGR 359
DB 330 YPKNLKMSVVKVLSHEQCMQPHYTGSEINYMKLCAADPEWKTDSCKDGSGGLICNIEGR 389
QY 360 MTLTGIVSWGRGCKALDKPGVYTVSHFLPWIRSHTKXENGLA 402
DB 390 PTLSGIVSWGRGCKAKKPGVYTVSHFLDWIQSHIGEEKGLA 432

RESULT 7
A35005
U-plasminogen activator (EC 3.4.21.73) precursor - chicken
N:Alternate names: uPA
C:Species: Gallus gallus (chicken)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
C:Accession: A35005
R:Leslie, N.D.; Kessler, C.A.; Bell, S.M.; Degen, J.L.
J. Biol. Chem. 265, 1339-1344, 1990
A:Title: The chicken urokinase-type plasminogen activator gene.
A:Reference number: A35005; MUID:90110185; PMID:2295632
A:Accession: A35005
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-434 <LRS>
A:Cross-references: GB:J05187; NID:g212858; PIDN:AAA49131.1; PID:g212859
C:Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C:Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-171/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F:40-71/Domain: EGF homology <EGF>
F:79-158/Domain: kringle homology <KRG>
F:173-428/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>

```
F;173-416/Domain: trypsin homology <TRY>
F;162-296,202-218,210-285,310-379,342-358,369-397/Dissulfide bonds: #status predicted
F;217,272,373/Active site: His, Asp, Ser #status predicted

Query Match      44.2%; Score 997; DB 1; Length 434;
Best Local Similarity 47.8%; Pred. No. 7.6e-70;
Matches 187; Conservative 64; Mismatches 122; Indels 18; Gaps 7

Qy    11 CDCINGGTCVSNKYFNSIHWCNCPKPGFGQHCHSIDSKCTCYEGNGHFYRGKASDTWTGRP 70
       |||||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    40 CQCINGGTCITYRFFSGIKECCLPEGVGGHLHCEIDTNSICYSGNGEDYRGWAEDP---G 95

Qy    71 CLFPWASATVLQ-QTYHAHRSDALQLGLGKNYCRNPDRRRPCWCVGVGLKPLVQE--CM 127
       :::::||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    96 CLYNDFPSVIRWDGYHADLKNALQLGLGKNYCRNPGRSRPWCYTK--RRYSIQETPCS 153

Qy    128 VHCADGKLKFQCGQKTLPFRFKIIEGEFTTIENQPFAAIYRRHRGGSVTVVCGGSLIS 187
       |||||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    154 TIE----KCERTCGQRSPSKYFKIVGSQAQEVETQPIAGIFQNIM-GTQOFLCGGSLID 208

Qy    188 PCWVISATHCFID-----YPKEBYYIVLGSRRLNSNTQGEMKTEVENLLIHKDYSADTLA 243
       :::::||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    209 FCWVLTAAACHFYNPFTKKQPNKSVYKVFGLGSIILTNDEHQEVFMVDRIISHPDFTHTGG 268

Qy    244 HHNDIALLKTRSKXEGRCAPQSRITQITCLPSMTYNDPOFGTSCEITGFGKNSSTDLYLPEQ 303
       |||||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    269 NDNDIALIRITASGCQAVESNVYVCLPEKLNLYDNVTWEIAGVGKNSDYIIYAOR 328

Qy    304 LKMTVKYLISHRECQQPHYYGSVTTKMLCAADPMQMKTDSCQGDGSGPLVCLOGRMILT 363
       |||||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    329 LMSATVNLSIQDDCKNKYIDSTRVDNMVACADPLMETDACKGDSGGPFVCEHNRMRTLY 388

Qy    364 GIYSWGSGCALDKDPGVYTVSHFLPWIRSH 394
       |||||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    389 GIYSWGSGCACAKNKPGVYTVRYLNWIDSN 419

RESULT 8
t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat
N/Alternate names: tissue plasminogen activator
C/Species: Desmodus rotundus (common vampire bat)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C/Accession: J0598
R/Kcaetzschar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagac
Gene 105, 229-237, 1991
A/Title: The plasminogen activator family from the salivary gland of the vampi
A/Reference number: J05097; MUID:92039036; PMID:1937019
A/Accession: J05098
A/Molecule type: mRNA
A/Residues: 1-477 <KRA>
A/Cross-references: GB:M63988; NID:g166074; PID:AAA31593.1; PID:g166075
C/Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-36/Domain: propeptide #status predicted <PRO>
F;37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
F;42-79/Domain: fibronectin type I repeat homology <1FA>
F;87-120/Domain: EGF homology <EGF>
F;128-209/Domain: kringle homology <KR>
F;226-471/Domain: trypsin homology <TRY>
F;442-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265
F;185,398/Binding site: carboxylate (Asn) (covalent) #status predicted
F;225-226/cleavage site: His-Ser (plasmin) #status predicted
F;272,321,428/Active site: His, Asp, Ser #status predicted

Query Match      38.5%; Score 868.5; DB 2; Length 477;
Best Local Similarity 43.7%; Pred. No. 8e-60;
Matches 178; Conservative 60; Mismatches 148; Indels 21; Gaps 5

Qy    3 ELHQV-----SNCDLNGGTCSVSNKYSFNTHWCNPKPKFGQHCHCEIDKSTCYEGNHGFY 58
Db    78 OCHTVPVKSCSELRCFNGGTCWOAASFDF-VCCPRKGYTGKCEVTHATCYAQGVTV 136
```

A;Molecule type: mRNA
A;Residues: 1-433 <KRA>
A;Cross-references: GB:L03546; NID:G163800; PIDN:AA51419.1; PID:G163801
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-179/Product: plasminogen activator chain A #status predicted <MA1>
F;21-179/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F;23-64/Domain: EGF homology <EGF>
F;72-153/Domain: kringle homology <KRG>
F;181-433/Product: plasminogen activator chain B #status predicted <MA2>
F;181-433/Domain: trypsin homology <TRY>
F;170-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
F;226,277,378/Active site: His, Asp, Ser #status predicted

Query Match 76.6%; Score 1728; DB 1; Length 433;
Best Local Similarity 73.8%; Pred. No. 1.4e-126;
Matches 305; Conservative 44; Mismatches 54; Indels 10; Gaps 2;

QY 1 SNEHQV--PNCDCNLNGTCTVSNKYFSNIHWCNPKKFGQHQCEIDKSKTCYEGNGHFY 58
DB 21 SNEVKEGSEGCNCGCLNGKCVTKYFSNIQRCSCPKKFGQHQCEIDKSKTCYEGNGHVS 80

QY 59 RGKASTDTMGPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDRRRPWCYVOVG 118
DB 81 RGNANRDLGRPCLANSDPTVLLKMYHAHRSDALQLGLGKHNYCRNPDRRRPWCYVOIG 140

QY 119 LKPLVQECMVHDCADGKL-----XPCQCKTLRPRFKIIGFEFTTIENQWFAAIYR 170
DB 141 LKQFVQCVQDCSVGKSPSPSPREKEBFQCCQKALRPRFKIIGFEFTTIENQWFAAIYR 200

QY 171 RHRGGSVTVYCGSLISPCWVISATHCFIDYPKKEDYIVLGRSLNSNTQGMKPEVEN 230
DB 201 RHRGGSITVYCGSLISPCWVVSATHCFIDHFKXENIVVIGQRLNSDTRGEMQFEVK 260

QY 231 LILHKDYSADTLAHHNDIALKIRSKGRCAQPSRTIOTICLPSMYNDPQFGTSCEITGF 290
DB 261 LILHEDYSAESLAHHNDIALKIRTSRGCAQPSRSIOTICLPRPEHDAHSRTRCEITGF 320

QY 291 GKENSTVLYPEQLKMTVVKLISHRECOOPHYGSEVTTKMLCAADPQWKTDCQGDSSG 350
DB 321 GKENPSDVRYSDELKMTFVLSVSEVCCQPHYGAETVTKMLCAADPQWETDSCQGDSSG 380

QY 351 PLVSLQGRMTLTGIVSGRCALKDKPGVTVTRVSHFELPWIRSHRTEENGLAL 403
DB 381 PLVCTIQGRLLTLTGIVSGRCACAKYKPGVTVTRVSKFLPWINTHTRGEINLVL 433

RESULT 5
S18932
u-plasminogen activator (EC 3.4.21.73) precursor - rat
N;Alternate names: plasminogen activator, urokinase-type, urinary plasminogen activator
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence revision 10-Feb-1995 #text_change 18-Jun-1999
C;Accession: S24604; I60186; I53472; S18932
R;Rabbani, S.A.
submitted to the EMBL Data Library, April 1992
A;Reference number: S24604
A;Accession: S24604
A;Molecule type: mRNA
A;Residues: 1-15,'H',17-23,'G',25-331,'N',333-432 <RAB>
A;Cross-references: EMBL:X65651; NID:G57456; PIDN:CAA46601.1; PID:G57457
A;Experimental source: tissue kidney
R;Henderson, B.R.; Tansey, W.P.; Phillips, S.M.; Ramshaw, I.A.; Kefford, R.F.
Cancer Res. 52, 2489-2496, 1992
A;Title: Transcriptional and posttranscriptional activation of urokinase plasminogen act
A;Reference number: I60186; MUID:92233409; PMID:1568219
A;Accession: I60186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-432 <RES>
A;Cross-references: EMBL:X63434; NID:G57465; PIDN:CAA45028.1; PID:G57466
A;Experimental source: strain Fischer 344; tissue mammary

R;Ragno, P.; Cassano, S.; Degen, J.; Kessler, C.; Biasi, F.; Rossi, G.
FEBS Lett. 306, 193-198, 1992
A;Title: The receptor for the plasminogen activator of urokinase type is up-reg
A;Reference number: I53472; MUID:92339549; PMID:I321734
A;Accession: I53472
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 31-62 <RE2>
A;Cross-references: EMBL:X66907; NID:G396200; PIDN:CAA47356.1; PID:G938279
C;Genetics:
A;Gene: uPA
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homo
C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-177/Product: urokinase-type plasminogen activator chain A #status predicte
F;31-62/Domain: EGF homology <EGF>
F;70-151/Domain: kringle homology <KRG>
F;179-432/Product: urokinase-type plasminogen activator chain B #status predict
F;179-420/Domain: trypsin homology <TRY>
F;168-300,210-226,218-289,314-383,346-362,373-401/Disulfide bonds: #status pred
F;225,276,377/Active site: His, Asp, Ser #status predicted

Query Match 73.4%; Score 1656.5; DB 1; Length 432;
Best Local Similarity 72.2%; Pred. No. 4.8e-121;
Matches 291; Conservative 45; Mismatches 58; Indels 9; Gaps 2;

QY 9 SNDCCLNGTCTVSNKYFSNIHWCNPKKFGQHQCEIDKSKTCYEGNGHFYRGKASTDTMG 68
DB 29 SNCGCQNGCVSVYKFSIRRCSCPKKFGQHQCEIDKSKTCYEGNGOSYRGKANTDTKG 88

QY 69 RCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPDRRRPWCYVOVGLKPLVQECMV 128
DB 89 RCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPDRRRPWCYVOVGLKPLVQECMV 148

QY 129 HDCADGKL-----FQCQCKTLRPRFKIIGFEFTTIENQWFAAIYRHRGGS-VTY 179
DB 149 QCCLSKKSPSSVTDQCCQKALRPRFKIIGFEFTTIENQWFAAIYRKNKGSPSPF 208

QY 180 VCGSLISPCWVISATHCFIDYPKKEDYIVLGRSLNSNTQGMKPEVENLILHKDYS 239
DB 209 KCGSLISPCWVASATHCFVNPQKKEVYVILGQSKNSYNPGENKFEVQLIHEDFSD 268

QY 240 DTLAHHNDIALKIRSKGRCAQPSRTIOTICLPSMYNDPQFGTSCEITGFGENSTLYL 299
DB 269 ETAFHNDIALKIRTSRGCAQPSRTIOTICLPRPEHDAHSRTRCEITGFQESATDYF 328

QY 300 YPEQLKMTVVKLISHRECOOPHYGSEVTTKMLCAADPQWKTDCQGDSSGGLVCSLOGR 359
DB 329 YPKDLKMSVVTKIISHQCKQPHYGEINYNKMLCAADPEWKTDCSGDGGGLICNIDGR 388

QY 360 MTLTGIVSGRCALKDKPGVTVTRVSHFELPWIRSHRTEENGLA 402
DB 389 PTLGIVSGSCAEKNKPGVTVTRVSYFLNWIQSHIGEENGLA 431

RESULT 6
UKMS
u-plasminogen activator (EC 3.4.21.73) precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A29420; A24615
R;Degen, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
Biochemistry 26, 8270-8279, 1987
A;Title: The murine urokinase-type plasminogen activator gene.
A;Reference number: A29420; MUID:88163489; PMID:2831940
A;Accession: A29420
A;Molecule type: DNA
A;Residues: 1-433 <DEG>
A;Cross-references: GB:M17922; NID:G202296; PIDN:AAA40539.1; PID:G202297
R;Belin, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.
Eur. J. Biochem. 148, 225-232, 1985
A;Title: Cloning, nucleotide sequencing and expression of cDNAs encoding mouse
A;Reference number: A24615; MUID:85179474; PMID:2985383

QY 353 VCSLOGRMTLTGIVSWGRCALCKDQGVYTRVSHFLPWIRSHTKENGGLAL 403
Db 381 VCSLOGRMTLTGIVSWGRCALCKDQGVYTRVSHFLPWIRSHTKENGGLAL 431

RESULT 2

UKBAY
u-plasminogen activator (EC 3.4.21.73) precursor - yellow baboon
C:Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C:Accession: S14687; S08651
R:AU, Y.P.T.; Wang, T.W.; Clowes, A.W.
Nucleic Acids Res. 18, 3411, 1990
A:Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasminogen
A:Reference number: S14687; MUID:90287734; PMID:2113276
A:Accession: S14687
A:Molecule type: mRNA
A:Residues: 1-433 <AUY>
A:Cross-references: EMBL:X51935; NID:g38130; PID:g38131
C:Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C:Keywords: Glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-176/Product: plasminogen activator chain A #status predicted <ACH>
F:30-61/Domain: EGF homology <EGF>
F:69-150/Domain: kringle homology <KRG>
F:178-433/Product: plasminogen activator chain B #status predicted <BCH>
F:178-433/Domain: trypsin homology <TRY>
F:167-298-208-224-216-287,315-384,347-363,374-402/Disulfide bonds: #status predicted
F:223,274,378/Active site: His, Asp, Ser #status predicted
F:324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.6%; Score 2090; DB 1; Length 433;
Best Local Similarity 90.6%; Pred. No. 1.1e-154;
Matches 375; Conservative 17; Mismatches 10; Indels 12; Gaps 3;

QY 1 SNEHQVPSNCDCLNGTGVSNKYFSNIHNCNPKFGGQHCIDKSKTCYEGNGHYRG 60
Db 21 SREL-QVPSDCGLNGTGVSNKYFSNIHNCNPKFGGQHCIDKSKTCYEGNGHYRG 79
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHCYCRNPDRRPPWCYVQVGLK 120
Db 80 KASTDTMGRSCLAWNSATVLOQTYHAHRSALQGLGKHCYCRNPDRRPPWCYVQVGLK 139
QY 121 PLVQECVHDCADGK-----LKFCGQKTLRPRFKIIGGFTTIENOPWFAAIYRRH 172
Db 140 QRVOECVHNCADGKFPSPPELQFCQGTURPRFKIIGGFTTIENOPWFAAIYRRH 199
QY 173 RGGSVTVYCGGSLISPCWVISATHCFIDYPKKEDIYVILGRSLNSNTQGMKFEVENLI 232
Db 200 RGGSVTVYCGGSLISPCWVISATHCFINYPKKEDIYVILGRSLNSNTQGMKFEVENLI 259
QY 233 LHKDYSADTLAHNDIALKIRSEKGRCAOPSRITQICLPSMYNDPQ---FGTSCEITG 289
Db 260 LHEDYSADTLAHNDIALKIRSEKGRCAOPSRITQICLPSMYNDPDPFPFGTSCEITG 319
QY 290 FGKNSDLYPEQLKMTVVKLIASHRECOQPHYYGSEVTTKMLCAADPQWTKDSCQDSG 349
Db 320 FGKNSDLYPEQLKMTVVKLVSHQKCOQPHYYGSEVTTKMLCAADPQWTKDSCQDSG 379
QY 350 GPLVCSIOGRMTLTGIVSWGRCALCKDQGVYTRVSHFLPWIRSHTKENGGLAL 403
Db 380 GPLVCSIOGRMTLTGIVSWGRCALCKDQGVYTRVSHFLPWIRSHTKENGGLAL 433

RESULT 3

UKRG
u-plasminogen activator (EC 3.4.21.73) precursor - pig
N:Alternate names: uPA
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
C:Accession: A00932
R:Nagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 9525-9541, 1984

A:Title: cDNA and gene nucleotide sequence of porcine plasminogen activator.
A:Reference number: A00932; MUID:85087954; PMID:6096832
A:Accession: A00932
A:Molecule type: DNA
A:Residues: 1-240, 'H', 242-442 <NAG1>
A:Experimental source: kidney cell line LLC-PK1
R:Nagamine, Y.
submitted to the Protein Sequence Database, December 1986
A:Reference number: A37566
A:Contents: annotation; correction to residue 241
C:Genetics:
C:Introns: 19/3; 31/1; 67/1; 125/2; 165/1; 238/2; 288/1; 335/1; 384/3
C:Superfamily: urokinase-type plasminogen activator; EGF homology; kringle hom
C:Keywords: Glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-189/Product: urokinase-type plasminogen activator chain A #status predict
F:33-64/Domain: EGF homology <EGF>
F:72-153/Domain: kringle homology <KRG>
F:190-442/Product: urokinase-type plasminogen activator chain B #status predic
F:190-430/Domain: trypsin homology <TRY>
F:152/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:179-310,220-236,228-299,324-393,356-372,383-411/Disulfide bonds: #status pre
F:235,286,387/Active site: His, Asp, Ser #status predicted

Query Match 81.0%; Score 1827.5; DB 1; Length 442;
Best Local Similarity 78.1%; Pred. No. 2.6e-134;
Matches 329; Conservative 32; Mismatches 41; Indels 19; Gaps 2;

QY 1 SNEHQV--PSNCDCLNGTGVSNKYFSNIHNCNPKFGGQHCIDKSKTCYEGNGHY 58
Db 21 SHELHQSASNCGLNGKVCYKFSNIQRCSCPKKFGQHCIDKSKTCYEGNGHSY 80
QY 59 RKGASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHCYCRNPDRRPPWCYVQV 110
Db 81 RKGANTNTGGRPCLPWNSATVLLNTYHAHRPDALQGLGKHCYCRNPDRRPPWCYVQV 140
QY 119 LKPLVQECVHDCADG-----LKFCGQKTLRPRFKIIGGFTTIEN 161
Db 141 LKQLVQECVWPCNCSGSHREPAYDCKNFFPEKVFQCGQKALRPRFKIIGGKSTTIEN 200
QY 162 QPWFAAIYRRHGGSVTVYCGGSLISPCWVISATHCFIDYPKKEDIYVILGRSLNSNTQ 221
Db 201 QPWFAAIYRRHGGSVTVYCGGSLISPCWVISATHCFINYPKKEDIYVILGRSLNSNTQ 260
QY 222 GSKFEVENLIHDKDYSADTLAHNDIALKIRSEKGRCAOPSRITQICLPSMYNDPQF 281
Db 261 GSKFEVEKLILHEDYSADSLAHNDIALKIRTDKGGCAOPSRITQICLPPVNGDAHF 320
QY 282 GTSCEITGFGKNSDLYPEQLKMTVVKLIASHRECOQPHYYGSEVTTKMLCAADPQWTK 343
Db 321 GASCEIVGFGKEDPSDLYPEQLKMTVVKLVSHRECOQPHYYGSEVTTKMLCAADPQWTK 380
QY 342 DSCQDSGGLVCSIOGRMTLTGIVSWGRCALCKDQGVYTRVSHFLPWIRSHTKENGGL 401
Db 381 DSCQDSGGLVCSIOGRMTLTGIVSWGRCALCKDQGVYTRVSHFLPWIRSHTKENGGL 440
QY 402 A 402
Db 441 A 441

RESULT 4

JN0560
u-plasminogen activator (EC 3.4.21.73) precursor - bovine
N:Alternate names: uPA
C:Species: Bos primigenius taurus (cattle)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C:Accession: JN0560
R:Kraetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
Gene 125, 177-183, 1993
A:Title: Bovine urokinase-type plasminogen activator and its receptor: cloning
A:Reference number: JN0560; MUID:93216119; PMID:8385052
A:Accession: JN0560

A;Accession: I52209
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 145-161 <NAGI>
A;Cross-references: GB:K03027; NID:g340174; PIDN:AAA61257.1; PID:g340175
A;Note: Nagai, M.; Hiratsuka, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama,
Gene 36, 183-188, 1985
A;Title: Molecular cloning of cDNA coding for human preprourokinase.
A;Reference number: JTC0102; PMID:86056954; PMID:2415429
A;Accession: JTC0102
A;Molecule type: mRNA
A;Residues: 1-213, 'I', 215-431 <NAG2>
A;Cross-references: GB:K03226; NID:g340155; PIDN:AAC97138.1; PID:g340158; GB:D00244; NID:
A;Note: Verde, P.; Stopponelli, M.P.; Galeffi, P.; Di Nocera, P.; Blasi, F.
Nat'l. Acad. Sci. U.S.A. 81, 4727-4731, 1984
A;Title: Identification and primary sequence of an unspliced human urokinase poly(A) + RN
A;Reference number: A37561; MUID:84272706; PMID:6589620
A;Accession: A37561
A;Molecule type: mRNA
A;Residues: 66-431 <VER>
A;Cross-references: GB:D00244; NID:g220138
A;Note: Jacobs, P.; Cravador, A.; Lortau, R.; Brockly, F.; Coliau, B.; Chuchana, P.; van Elsen,
DNA 4, 139-146, 1985
A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of human prep
A;Reference number: A38102; MUID:85203359; PMID:3888571
A;Accession: I38102
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-150, 'W', 152-213, 'I', 215-385, 'C', 387-429, 'V', 431 <JAC>
A;Cross-references: EMBL:X02760; NID:G35297; PIDN:CAA26535.1; PID:g35298
A;Note: Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki,
Biochim. Biophys. Acta 1293, 83-89, 1996
A;Title: Characterization of single chain urokinase-type plasminogen activator with a no
A;Reference number: S65783; MUID:96186279; PMID:8652631
A;Accession: S65783
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 21-140, 'L', 142-213, 'I', 215-431 <YOS>
A;Cross-references: EMBL:D11143; NID:g311467; PIDN:BAAO1919.1; PID:g1199928
A;Note: Gunzler, W.A.; Steffens, G.J.; Otting, F.; Kim, S.M.A.; Frankus, E.; Flohe, L.
Eur. J. Biochem. 125, 251-257, 1982
A;Title: Human low-molecular-weight urinary urokinase. Partial characterization and prel
A;Reference number: A37563; MUID:83003608; PMID:6749491
A;Accession: A37563
A;Molecule type: protein
A;Residues: 156-176/179-193, 'T', 195, 'T', 197-224 <SCH>
A;Cross-references: GUNZLER, W.A.; OTTING, F.; FRANKUS, E.; FLOHE, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
A;Title: The complete amino acid sequence of low molecular mass urokinase from human uri
A;Reference number: A37564; MUID:83055099; PMID:6754572
A;Accession: A37564
A;Molecule type: protein
A;Residues: 158-410 <STE>
A;Note: Kentzer, E.J.; Buko, A.; Menon, G.; Sarin, V.K.
Biochem. Biophys. Res. Commun. 171, 401-406, 1990
A;Title: Carbohydrate composition and presence of a fucose-protein linkage in recombinan
A;Reference number: A35689; MUID:90365737; PMID:2393398
A;Accession: A35689
A;Molecule type: protein
A;Residues: 21-30, 'X', 32, 'X', 34-38, 'X', 40-43 <KEN>
A;Note: Identification of a fucose and attempt to determine its attachment site
R;Rabbani, S.A.; Desjardins, J.; Bell, A.W.; Banville, D.; Mazur, A.; Henkin, J.; Goltz
Biochem. Biophys. Res. Commun. 173, 1058-1064, 1990
A;Title: An amino-terminal fragment of urokinase isolated from a prostate cancer cell li
A;Reference number: A36697; MUID:91097529; PMID:2125213
A;Accession: A36697

A:Molecule type: protein
A:Residues: 21-34 <RAB>
R:Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.
submitted to the Brookhaven Protein Data Bank, July 1993
A:Reference number: A51255; PDB:1KDU
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
R:Li, X.; Smith, R.A.G.; Dobson, C.M.
Biochemistry 31, 9569-9571, 1992
A:Title: Sequential (1)H NMR assignments and secondary structure of the kringle
A:Reference number: A4375; MUID:93003110; PMID:1327118
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
R:Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettesheim, D.G.; Mazar, A.P.; Ole
submitted to the Brookhaven Protein Data Bank, January 1994
A:Reference number: A66922; PDB:1URK
A:Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
R:Sraggon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson
submitted to the Brookhaven Protein Data Bank, July 1995
A:Reference number: A6058; PDB:1LMW
A:Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 168-175;
C:Comment: This enzyme is found in urine in a high molecular mass form, consist
C:Comment: Urokinase-type plasminogen activator proteolytically activates plasmin
C:Genetics:
A:Gene: GDB:PLAU
A:Cross-references: GDB:119497; OMIM:191840
A:Map position: 10q24-10q24
A:Introns: 19/3; 29/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
C:Function:
A:Description: proteolytically activates plasminogen
A:Pathway: fibrinolysis
C:Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homo
C:Keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; kringle; serine
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-431/Product: urokinase-type plasminogen activator, single chain form #stat
F:21-177/Product: urokinase-type plasminogen activator chain A #status experime
F:31-62/Domain: EGF homology <EGF>
F:70-151/Domain: kringle homology <KR>
F:156-177/Product: urokinase-type plasminogen activator chain A1 #status experi
F:179-431/Product: urokinase-type plasminogen activator chain B #status experim
F:179-439/Domain: trypsin homology <TRY>
F:31-39,33-51,53-62,70-151,91-133,122-146,168-299,209-225,217-288,313-382,345-3
F:38/Binding site: carboxylate (Thr) (covalent) #status predicted
F:178-179/Cleavage site: Lys-Ile (plasmin) #status experimental
F:224,275,376/Active site: His, Asp, Ser #status experimental
F:322/Binding site: carboxylate (Asn) (covalent) #status experimental

Query Match	99.2%	Score	2240;	DB 1;	Length	431;			
Best Local Similarity	97.8%	Pred No	2	4e-166;					
Matches	402;	Conservative	1;	Mismatches	0;	Indels	8;	Gaps	1;
QY	1	SNELHQVPSNCDLNGGTCVSNKYFSNIHWNCNPKFKGGQCHCIDKSKTCYEGNGHFYRG	60						
DB	21	SNELHQVPSNCDLNGGTCVSNKYFSNIHWNCNPKFKGGQCHCIDKSKTCYEGNGHFYRG	80						
QY	61	KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKKNYCRNPDRRPPWCVVQVGLK	120						
DB	81	KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKKNYCRNPDRRPPWCVVQVGLK	140						
QY	121	PLVQECMWHDCADGK-----LKPQCQCKTLRPFRKLIIGSEFTTIENQWPFAAIYRRH	172						
DB	141	PLVQECMWHDCADGKPPSPBELFKQCQCKTLRPFRKLIIGSEFTTIENQWPFAAIYRRH	200						
QY	173	RGGSVTVYCGGSI..SPCWVISATHCFIDPKEDYIVLGRSLNSNTQCEMKFEVENLI	232						
DB	201	RGGSVTVYCGGSLSPCWVISATHCFIDPKEDYIVLGRSLNSNTQCEMKFEVENLI	260						
QY	233	LHKDYSDTLAHHNDIALKIRSKGRCQAQPSRTIQTICLPMSYNDPQFGTSCBITGFGK	292						
DB	261	LHKDYSDTLAHHNDIALKIRSKGRCQAQPSRTIQTICLPMSYNDPQFGTSCBITGFGK	320						
QY	293	ENSTDLYLPEQLKMTYVKLISHRECCQPHYVGSVTTKMLCAADPQNKTTSCQSDSGPL	352						
DB	321	ENSTDLYLPEQLKMTYVKLISHRECCQPHYVGSVTTKMLCAADPQNKTTSCQSDSGPL	380						

417 SRCQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRC 476
191 QOPHYGSEVTTKMLCAAD-----POMKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRC 244
477 TSQHLNRTVTDNMLCAGDTRSGGPGQANLHDACQDGGPLVCLNDGRMTLVGLIISWGLG 536
245 CALKDKPGVYTRVSHFLPWIRSHTK 269
537 CGQKDPVPGVYTKVTNYLDWIRDNR 561

Search completed: May 25, 2004, 15:00:03
Job time : 21.1096 secs

Query Match 39.7%; Score 583; DB 6; Length 562;
Best Local Similarity 44.9%; Pred. No. 6.1e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;
13 CG-QKTLRPRFKIIGGFTTIENQWPFAAIYRRH-RGGSVTVYCGGSLISPCWVISATHC 70
299 CGLRQYSQOPFRKGGFLADIASHPWQAIFAKHRRSPGERFLCGGILISSCWILSAHC 358
71 FIDYPKKEDYIVLGRSLNSNTQGENKFEVENILHKDYSADTLAHNDIALKIRSK 130
359 FOERFPPHLLTVILGRYRVVPGEEQKFEVEKYIVHKEFDDT--YDNDIALQLKSDS 416
131 GRCAQPSRTIQTICLPSMYNDPQGTSCITGCKENSTDYLYPEOLKMTVVKLIHSHREC 190
417 SRCQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRC 476
191 QOPHYGSEVTTKMLCAAD-----POMKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRC 244
477 TSQHLNRTVTDNMLCAGDTRSGGPGQANLHDACQDGGPLVCLNDGRMTLVGLIISWGLG 536
245 CALKDKPGVYTRVSHFLPWIRSHTK 269
537 CGQKDPVPGVYTKVTNYLDWIRDNR 561

RESULT 50
5200340-2
Patent No. 5200340
APPLICANT: POSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
ACTIVATORS
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
SEQ ID NO:2:
LENGTH: 562
5200340-2

Query Match 38.7%; Score 583; DB 6; Length 562;
Best Local Similarity 44.9%; Pred. No. 6.1e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;
13 CG-QKTLRPRFKIIGGFTTIENQWPFAAIYRRH-RGGSVTVYCGGSLISPCWVISATHC 70
299 CGLRQYSQOPFRKGGFLADIASHPWQAIFAKHRRSPGERFLCGGILISSCWILSAHC 358
71 FIDYPKKEDYIVLGRSLNSNTQGENKFEVENILHKDYSADTLAHNDIALKIRSK 130
359 FOERFPPHLLTVILGRYRVVPGEEQKFEVEKYIVHKEFDDT--YDNDIALQLKSDS 416
131 GRCAQPSRTIQTICLPSMYNDPQGTSCITGCKENSTDYLYPEOLKMTVVKLIHSHREC 190


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/ FILING DATE: 09-FEB-1987
/ APPLICATION NUMBER: 483,052
/ FILING DATE: 07-APR-1983
/ APPLICATION NUMBER: 398,003
/ FILING DATE: 14-JUL-1982
/ APPLICATION NUMBER: 374,860
/ FILING DATE: 05-MAY-1982
/ SEQ ID NO: 8
/ LENGTH: 527
/ 5185259-8

Query Match      38.7%; Score 583; DB 6; Length 527;
Best Local Similarity 44.9%; Pred. No. 5.6e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPFKIIIGGFTTIENQWFAAIYRRH-RGGSVTVYVCGSLISPCWVISATHC 70
Db 264 CGLRQYSQPFRIKGGFLADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAHC 323
QY 71 FIDYPKKEDYIVYGRSRLNSNTQGEWKPEVENLILHKDYSADTLAHNDIALKIRSK 130
Db 324 FQERFPPHLLTVILGRTYRVVPGEEQKFEVEKIYVHKFDDDT--YDNDIALQLKSDS 381
QY 131 GRCAQPSRTITICLPMSYNDPQGTSCITGFGKENSTDYLYPEQLKMTVVKLIHSHREC 190
Db 382 SRCQESSVVRTVCLPADLQLPDWTECELSGVYKHEALSPFYSERLKEAHRVLYPSSRC 441
QY 191 QQPHYGSEVTTKMLCAAD-----PQWKT-DSQCGSDGGPLVCSLQGRMTLTGIVSWG 244
Db 442 TSQHLNRTVTDNMLCAGDTRSGGPQANLHDACQSDGGPLVCLNDGRMTLVGIISWGLG 501
QY 245 CALKDKPGVTVRVSHFLPWIRSHTK 269
Db 502 CGQKDPGVTVTKVNYLDWIRDNR 526

RESULT 45
US-08-811-949-43
; Sequence 43, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NINA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORVAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-966-0
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-811-949-43

Query Match      38.7%; Score 583; DB 2; Length 562;
Best Local Similarity 44.9%; Pred. No. 6.1e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPFKIIIGGFTTIENQWFAAIYRRH-RGGSVTVYVCGSLISPCWVISATHC 70
Db 299 CGLRQYSQPFRIKGGFLADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAHC 358
QY 71 FIDYPKKEDYIVYGRSRLNSNTQGEWKPEVENLILHKDYSADTLAHNDIALKIRSK 130
Db 359 FQERFPPHLLTVILGRTYRVVPGEEQKFEVEKIYVHKFDDDT--YDNDIALQLKSDS 416
QY 131 GRCAQPSRTITICLPMSYNDPQGTSCITGFGKENSTDYLYPEQLKMTVVKLIHSHREC 190
Db 417 SRCQESSVVRTVCLPADLQLPDWTECELSGVYKHEALSPFYSERLKEAHRVLYPSSRC 476
QY 191 QQPHYGSEVTTKMLCAAD-----PQWKT-DSQCGSDGGPLVCSLQGRMTLTGIVSWG 244
Db 477 TSQHLNRTVTDNMLCAGDTRSGGPQANLHDACQSDGGPLVCLNDGRMTLVGIISWGLG 536
QY 245 CALKDKPGVTVRVSHFLPWIRSHTK 269
Db 537 CGQKDPGVTVTKVNYLDWIRDNR 561

RESULT 46
US-08-560-098A-50
; Sequence 50, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WNEB, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
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Db 387 TSQHLLNRTVTDNMLCAGDTRSGGPOANLHDACQSDGGLVCLNDGRMTLVGIISWGLG 446
Qy 245 CALKDKPGVYTVRSHFLPWIRSHTK 269
Db 447 CGQKDPGVYTKVTNYLDWIRDNR 471

RESULT 42

US-07-609-510B-16
; Sequence 16, Application US/07609510B
; Patent No. 5326700
; GENERAL INFORMATION:
; APPLICANT: Berg et al.
; TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue PI
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN.
; COUNTRY: U.S.A.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/609,510B
; FILING DATE: 19901106
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-609-510B-16

Query Match 38.7%; Score 583; DB 1; Length 527;

Best Local Similarity 44.9%; Pred. No. 5.6e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

Qy 13 CG-QKTLPRFKIIGGEFTTIENQWFAAIYRRH-RGGSVTVYVCGGSLISPCWVISATHC 70
Db 264 CGLRQYSQPFRIKGLFADIAHPQAAIFAKHRSFGERFLCGGILISSCWILSAHC 323
Qy 71 FIDYPKKEDYIYVLRSLNNTQGMKFEVENLILHKDYSADTLAHNDIALKIRSK 130
Db 324 FQERFPPHLLTVILGRTYRVVPGEBEQFEVEKYIVHKEFDDT--YNDNDIALQLKSDS 381
Qy 131 GRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDVLYPEOLKMTVVKLISHREC 190
Db 382 SRCQAGSSVVRVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSRC 441
Qy 191 QQPHYYGSEVTTMLCAAD-----PQWKT-DSCQDGGGGLVCSLQGRMTLTGVISWGRG 244
Db 442 TSQHLNRTVTDNMLCAGDTRSGGPOANLHDACQSDGGLVCLNDGRMTLVGIISWGLG 501
Qy 245 CALKDKPGVYTVRSHFLPWIRSHTK 269
Db 502 CGQKDPGVYTKVTNYLDWIRDNR 526

RESULT 43

PCT-US91-01025A-2
; Sequence 2, Application PC/TUS9101025A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin
; TITLE OF INVENTION: Specific Properties

; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01025A
; FILING DATE: 19910214
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/486,657
; FILING DATE: 1 March 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 454P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/352-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US91-01025A-2

Query Match 38.7%; Score 583; DB 5; Length 527;

Best Local Similarity 44.9%; Pred. No. 5.6e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

Qy 13 CG-QKTLPRFKIIGGEFTTIENQWFAAIYRRH-RGGSVTVYVCGGSLISPCWVISATHC 70
Db 264 CGLRQYSQPFRIKGLFADIAHPQAAIFAKHRSFGERFLCGGILISSCWILSAHC 323
Qy 71 FIDYPKKEDYIYVLRSLNNTQGMKFEVENLILHKDYSADTLAHNDIALKIRSK 130
Db 324 FQERFPPHLLTVILGRTYRVVPGEBEQFEVEKYIVHKEFDDT--YNDNDIALQLKSDS 381
Qy 131 GRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGKENSTDVLYPEOLKMTVVKLISHREC 190
Db 382 SRCQAGSSVVRVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSRC 441
Qy 191 QQPHYYGSEVTTMLCAAD-----PQWKT-DSCQDGGGGLVCSLQGRMTLTGVISWGRG 244
Db 442 TSQHLNRTVTDNMLCAGDTRSGGPOANLHDACQSDGGLVCLNDGRMTLVGIISWGLG 501
Qy 245 CALKDKPGVYTVRSHFLPWIRSHTK 269
Db 502 CGQKDPGVYTKVTNYLDWIRDNR 526

RESULT 44

5185259-8
; Patent No. 5185259
; APPLICANT: GOEDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
; VEHAR, GORDON A.
; TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
; ACTIVATOR
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/489,855
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 12,694

Patent No. 6309861
GENERAL INFORMATION:
APPLICANT: Ambrosius, Dorothee
APPLICANT: Rudolph, Rainer
APPLICANT: Schaeffner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production of naturally folded and secreted proteins
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 10
LENGTH: 378
TYPE: PRT
ORGANISM: E. coli
US-09-553-498-10

Query Match 38.7%; Score 583; DB 4; Length 378;
Best Local Similarity 44.9%; Pred. No. 3.5e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPRFKIIGGEFTTIENQWFAAIYRRH-RGGSVTVVCGGSLISPCWVISATHC 70
DB 115 CGLRQYSQPFRIKGLFADIASHPWQAAIFAKHRSRSPGERFLCGGILISSCWILSAHC 174
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSK 130
DB 175 FQERPPPHLTVILGRYRVVPGGEEQKFEVEKIVHKEFDDT--YNDIALIQLKSDS 232
QY 131 GRCAQPSRTIOTICLPMSYNDPQFCTSCIEITGFGKENSVDLYPEQLKMTVVKLISHREC 190
DB 233 SRCAQESSVWTVCLPPADLQLPDWTCELSYGKHEALSPFYSERLKEAHRVLYPSRRC 292
QY 191 QOPHYGSEVTTKMLCAAD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRG 244
DB 293 TSQHLLNRTVDNMLCAGDTRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLG 352
QY 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
DB 353 CGQKDVPGVYTKVNYLDWIRDNR 377

RESULT 38
US-09-618-869-10
Sequence 10, Application US/09618869
Patent No. 6455279
GENERAL INFORMATION:
APPLICANT: Ambrosius, Dorothee
APPLICANT: Rudolph, Rainer
APPLICANT: Schaeffner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
TITLE OF INVENTION: CHAPERONES
FILE REFERENCE: 20381
CURRENT APPLICATION NUMBER: US/09/618,869
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR FILING DATE: 1999-07-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 378
TYPE: PRT
ORGANISM: Escherichia coli
US-09-618-869-10

Query Match 38.7%; Score 583; DB 4; Length 378;
Best Local Similarity 44.9%; Pred. No. 3.5e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPRFKIIGGEFTTIENQWFAAIYRRH-RGGSVTVVCGGSLISPCWVISATHC 70
DB 115 CGLRQYSQPFRIKGLFADIASHPWQAAIFAKHRSRSPGERFLCGGILISSCWILSAHC 174
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSK 130
DB 175 FQERPPPHLTVILGRYRVVPGGEEQKFEVEKIVHKEFDDT--YNDIALIQLKSDS 232
QY 131 GRCAQPSRTIOTICLPMSYNDPQFCTSCIEITGFGKENSVDLYPEQLKMTVVKLISHREC 190
DB 233 SRCAQESSVWTVCLPPADLQLPDWTCELSYGKHEALSPFYSERLKEAHRVLYPSRRC 292
QY 191 QOPHYGSEVTTKMLCAAD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRG 244
DB 293 TSQHLLNRTVDNMLCAGDTRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLG 352
QY 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
DB 353 CGQKDVPGVYTKVNYLDWIRDNR 377

RESULT 39
US-08-558-269-6
Sequence 6, Application US/08558269
Patent No. 5961973
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/558,269
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,800
FILING DATE: 08-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: CRI-001CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-558-269-6

Query Match 38.7%; Score 583; DB 2; Length 383;
Best Local Similarity 44.9%; Pred. No. 3.6e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPRFKIIGGEFTTIENQWFAAIYRRH-RGGSVTVVCGGSLISPCWVISATHC 70
DB 120 CGLRQYSQPFRIKGLFADIASHPWQAAIFAKHRSRSPGERFLCGGILISSCWILSAHC 179
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSK 130

13	CG-OKTURPRFKLIGEBFTIENOPWFAALYERH-RGGSVTVVCCGSLISPCWLSATHC	70
Ddb	:::::	
92	CGLFQYSQPQFRKIGULFADIAHPQMAIFAKHRSPGERFLCGILISICWLSAHC	151
Ddb	:::::	
71	FIDYPKEDIVYLGRSRLNSNTQGEMKEFEVENLIHKDYSADTAAHNDAALKIRSKZ	130
Ddb	:::::	
152	PQERPPHHUTVLIGRTYRVVPGBEQKEVEKYLVHKEFDODT--YNDNALQLQKS	209
Ddb	:::::	
131	GRCAQPERTQTICLPSMYNDPFGTSCHITGFGENSTDYLYPQLKWTVKLISHREC	190
Ddb	:::::	
210	SRCAGESVVRTVCLPADLQLPDWTECLSGLVGHEALSPTYSERLKEAHVRUYPSRRC	269
Ddb	:::::	
191	QQPHYSGEVTTKMLCAAD-----PWKT-DSQCQSDGGPLVCYSIQGMTITGVSMRG	244
Ddb	:::::	
270	TSQHLLARTVTDNNLCAGDTRSGGPQANLHDACQSDGGPLVCLNDGRMTLVGIISWL	329
Ddb	:::::	
245	CALKDKDPGVTRYSHFLEWIRSHTK	269
Ddb	:::::	
330	CGQRDVGYTKVTNYLDNR	354
Ddb	:::::	

[illegible]

Db 270 TSQHLLNRTVTDNMLCAGDTRSGGPQANLHDAQCQDSGGPLVCLNDGRMTLVGIISWGLG 329
QY 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
Db 330 CGQKDVPGVYTKVTNYLDWIRDNR 354

RESULT 30

US-08-217-617A-1
; Sequence 1, Application US/08217617A
; Patent No. 5676947
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich
; APPLICANT: Fischer, Stephan
; TITLE OF INVENTION: METHOD FOR TREATING THROMBOEMBOLIC
; TITLE OF INVENTION: CONDITIONS USING THROMBOLYTICALLY ACTIVE PROTEINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,617A
; FILING DATE: 25-MARCH-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5676947man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1030.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
US-08-217-617A-1

Query Match 38.7%; Score 583; DB 1; Length 355;
Best Local Similarity 44.9%; Pred. No. 3.2e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;
QY 13 CG-OKTLRPRFKIIGGFTTIENOPWFAAIYRRH-RGGSVTVYVCGGLISPCWVISATHC 70
Db 92 CGLRQYQOPQFRIGKGLFADIASHPWQAAIFAKHRRSPGPFGLCGGILISSCWILSAHC 151
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFVEVNIILHKOYSADTLAHNDIALLKIRSK 130
Db 152 FQERFPPPHLTVILGRYRVVPGEEQKFEVEKYIVHKEFDDT--YDNDIALQLKSDS 209
QY 131 GRCAQPSRTIQTICLPSMYNDPQGTSCETITGFGKENS TDLYPEQLKMTVVKLISHREC 190
Db 210 SRCAQESSVVRTVCLPADLQLPDWTCELSGKGHEALSPFYSERLKEAHVLYPSSRC 269
QY 191 QQPHYGSEVTTKMLCAAD-----POWKT-DSOQDSSGGPLVCSLQGRMTLTGIVSWGRG 244
Db 270 TSQHLLNRTVTDNMLCAGDTRSGGPQANLHDAQCQDSGGPLVCLNDGRMTLVGIISWGLG 329
QY 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
Db 330 CGQKDVPGVYTKVTNYLDWIRDNR 354

RESULT 31

US-08-217-616-1
; Sequence 1, Application US/08217616
; Patent No. 5690931
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich
; APPLICANT: Fischer, Stephan
; TITLE OF INVENTION: METHOD FOR TREATING THROMBOEMBOLIC CONDITIONS
; TITLE OF INVENTION: BY INHIBITING REOCLUSION VIA THE USE OF
; TITLE OF INVENTION: MULTIPLE BOLUS ADMINISTRATION OF
; TITLE OF INVENTION: THROMBOLYTICALLY ACTIVE PROTEINS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,616
; FILING DATE: 25-MARCH-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5690931man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1026.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
US-08-217-616-1

Query Match 38.7%; Score 583; DB 1; Length 355;
Best Local Similarity 44.9%; Pred. No. 3.2e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;
QY 13 CG-OKTLRPRFKIIGGFTTIENOPWFAAIYRRH-RGGSVTVYVCGGLISPCWVISATHC 70
Db 92 CGLRQYQOPQFRIGKGLFADIASHPWQAAIFAKHRRSPGPFGLCGGILISSCWILSAHC 151
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFVEVNIILHKOYSADTLAHNDIALLKIRSK 130
Db 152 FQERFPPPHLTVILGRYRVVPGEEQKFEVEKYIVHKEFDDT--YDNDIALQLKSDS 209
QY 131 GRCAQPSRTIQTICLPSMYNDPQGTSCETITGFGKENS TDLYPEQLKMTVVKLISHREC 190
Db 210 SRCAQESSVVRTVCLPADLQLPDWTCELSGKGHEALSPFYSERLKEAHVLYPSSRC 269
QY 191 QQPHYGSEVTTKMLCAAD-----POWKT-DSOQDSSGGPLVCSLQGRMTLTGIVSWGRG 244
Db 270 TSQHLLNRTVTDNMLCAGDTRSGGPQANLHDAQCQDSGGPLVCLNDGRMTLVGIISWGLG 329
QY 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
Db 330 CGQKDVPGVYTKVTNYLDWIRDNR 354

RESULT 32

US-08-811-949-45
; Sequence 45, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA

```

; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
US-08-217-618-1

Query Match 38.7%; Score 583; DB 1; Length 355;
Best Local Similarity 44.9%; Pred. No. 3.2e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPRKIIIGGEFTTIENQWFAAIVRRH-RGGSVTVVCGGSLISPCWVISATHC 70
DB 92 CGLRQVSPQPRFKIGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAHC 151
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSK 130
DB 152 FOERPPPHLTVILGRTRVVPGESEQFEVEKIVHKEFDDT--YNDIALQLKSDS 209
QY 131 GRCAQPSRTIOTICLPMSYNDPQFCTSCITGFGKENSTDYLYPEQLKMTVVKLISHREC 190
DB 210 SRCQESSVVRTVCLPPADLPDWTCELSGYKHEALSPFYSERLKEAHVRLYPSRC 269
QY 191 QQPHYGVSEVTMKLCAAD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWG 244
DB 270 TSOHLNRTVDNMLCAGDTRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLG 329
QY 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
DB 330 CGQKDVPGVYTKVNYLDWIRDNR 354

RESULT 28
US-08-427-640-2
; Sequence 2, Application US/08427640
; Patent No. 5658788
; GENERAL INFORMATION:
; APPLICANT: Berg et al.
; TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN.
; COUNTRY: U.S.A.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,640
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/689,410
; FILING DATE: 22 APRIL 1991
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
US-08-427-640-2

Query Match 38.7%; Score 583; DB 1; Length 355;
Best Local Similarity 44.9%; Pred. No. 3.2e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPRKIIIGGEFTTIENQWFAAIVRRH-RGGSVTVVCGGSLISPCWVISATHC 70
DB 92 CGLRQVSPQPRFKIGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAHC 151
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSK 130
DB 152 FOERPPPHLTVILGRTRVVPGESEQFEVEKIVHKEFDDT--YNDIALQLKSDS 209
QY 131 GRCAQPSRTIOTICLPMSYNDPQFCTSCITGFGKENSTDYLYPEQLKMTVVKLISHREC 190
DB 210 SRCQESSVVRTVCLPPADLPDWTCELSGYKHEALSPFYSERLKEAHVRLYPSRC 269
QY 191 QQPHYGVSEVTMKLCAAD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWG 244

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DB 92 CGLRQVSPQPRFKIGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAHC 151
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSK 130
DB 152 FOERPPPHLTVILGRTRVVPGESEQFEVEKIVHKEFDDT--YNDIALQLKSDS 209
QY 131 GRCAQPSRTIOTICLPMSYNDPQFCTSCITGFGKENSTDYLYPEQLKMTVVKLISHREC 190
DB 210 SRCQESSVVRTVCLPPADLPDWTCELSGYKHEALSPFYSERLKEAHVRLYPSRC 269
QY 191 QQPHYGVSEVTMKLCAAD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWG 244
DB 270 TSOHLNRTVDNMLCAGDTRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLG 329
QY 245 CALKDKPGVYTRVSHFLPWIRSHTK 269
DB 330 CGQKDVPGVYTKVNYLDWIRDNR 354

RESULT 29
US-08-427-640-6
; Sequence 6, Application US/08427640
; Patent No. 5658788
; GENERAL INFORMATION:
; APPLICANT: Berg et al.
; TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic isor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN.
; COUNTRY: U.S.A.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,640
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/689,410
; FILING DATE: 22 APRIL 1991
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-427-640-6

Query Match 38.7%; Score 583; DB 1; Length 355;
Best Local Similarity 44.9%; Pred. No. 3.2e-52;
Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5;

QY 13 CG-QKTLRPRKIIIGGEFTTIENQWFAAIVRRH-RGGSVTVVCGGSLISPCWVISATHC 70
DB 92 CGLRQVSPQPRFKIGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAHC 151
QY 71 FIDYPKEDYIVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSK 130
DB 152 FOERPPPHLTVILGRTRVVPGESEQFEVEKIVHKEFDDT--YNDIALQLKSDS 209
QY 131 GRCAQPSRTIOTICLPMSYNDPQFCTSCITGFGKENSTDYLYPEQLKMTVVKLISHREC 190
DB 210 SRCQESSVVRTVCLPPADLPDWTCELSGYKHEALSPFYSERLKEAHVRLYPSRC 269
QY 191 QQPHYGVSEVTMKLCAAD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWG 244

```


REFERENCE/DOCKET NUMBER: 18-966-0
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-57

Query Match 38.9%; Score 587; DB 2; Length 437;
Best Local Similarity 45.3%; Pred. No. 1.6e-52;
Matches 120; Conservative 38; Mismatches 97; Indels 10; Gaps 5;
QY 13 CG-QKTRPRFKIIGGFTTIENQWFAALYRRH-RGGSVTVYVCGSLSPCWVISATHC 70
DB 174 CGLRQVSPQDFIIGLFDIASHPWQAALFAKHRRSPGGRFLCGGILISSCWILSAHC 233
QY 71 FIDYPKEDYVYVGRSLNSNTQGMKFEVENLILHKDYSADTLAHNDIALKIRSK 130
DB 234 FQRRFPFPHLTVLGRYRVVPGEEQKFEVEKYIVHKEFDDDT--YDNDIALQLKSDS 291
QY 131 GRCAQPSRTIOTICLPSMYNDPQGTSCITGFGKENSTDYLYPEOLKMTVVKLISHREC 190
DB 292 SRCQAESVVRVCLPPADLQLPDWTCELSGKGHEALSPFYSERLKEAHRVLPSSRC 351
QY 191 QPHYGVSEVTTKMLCAAD-----PQWKT-DSQGDGGPLVCSLQGRMTLGTIVSWG 244
DB 352 TSQHLNRTVTDNMLCAGDTRSGGPQANLHDAQCQDGGPLVCLNDGRMTLVGIISWGLG 411
QY 245 CALKDKGVYTRVSHFLPWIRSHTK 269
DB 412 CGQKDPGVYTKVNYLDWIRDNMR 436

RESULT 26

US-08-137-116-1

Sequence 1, Application US/08137116

Patent No. 5500411

GENERAL INFORMATION:

APPLICANT: Martin, Ulrich

APPLICANT: Koenig, Reinhard

TITLE OF INVENTION: METHOD FOR TREATING THROMBOEMBOLIC

TITLE OF INVENTION: CONDITIONS BY INHIBITING REOCCCLUSION

TITLE OF INVENTION: VIA THE USE OF MULTIPLE BODIES

TITLE OF INVENTION: ADMINISTRATION OF THROMBOLYTICALLY

TITLE OF INVENTION: ACTIVE PROTEINS

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/137,116

FILING DATE: June 30, 1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP92/00851

FILING DATE: 15 April 1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 41 12 398

FILING DATE: 16 April 1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 41 23 845
FILING DATE: 18 July 1991
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 550041man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acids
TOPOLOGY: linear
US-08-137-116-1

Query Match 38.7%; Score 583; DB 1; Length 355;

Best Local Similarity 44.9%; Pred. No. 3.2e-52;

Matches 119; Conservative 39; Mismatches 97; Indels 10; Gaps 5

QY 13 CG-QKTRPRFKIIGGFTTIENQWFAALYRRH-RGGSVTVYVCGSLSPCWVISATHC 70
DB 92 CGLRQVSPQDFIIGLFDIASHPWQAALFAKHRRSPGGRFLCGGILISSCWILSAHC 151
QY 71 FIDYPKEDYVYVGRSLNSNTQGMKFEVENLILHKDYSADTLAHNDIALKIRSK 130
DB 152 FQRRFPFPHLTVLGRYRVVPGEEQKFEVEKYIVHKEFDDDT--YDNDIALQLKSDS 209
QY 131 GRCAQPSRTIOTICLPSMYNDPQGTSCITGFGKENSTDYLYPEOLKMTVVKLISHREC 190
DB 210 SRCQAESVVRVCLPPADLQLPDWTCELSGKGHEALSPFYSERLKEAHRVLPSSRC 269
QY 191 QPHYGVSEVTTKMLCAAD-----PQWKT-DSQGDGGPLVCSLQGRMTLGTIVSWG 244
DB 270 TSQHLNRTVTDNMLCAGDTRSGGPQANLHDAQCQDGGPLVCLNDGRMTLVGIISWGLG 329
QY 245 CALKDKGVYTRVSHFLPWIRSHTK 269
DB 330 CGQKDPGVYTKVNYLDWIRDNMR 354

RESULT 27

US-08-217-618-1

Sequence 1, Application US/08217618

Patent No. 5510330

GENERAL INFORMATION:

APPLICANT: Martin, Ulrich

APPLICANT: Fischer, Stephan

TITLE OF INVENTION: COMBINATIONS OF THROMBOLYTICALLY ACTIVE

TITLE OF INVENTION: PROTEINS AND NON-HEPARIN ANTICOAGULANTS, AND USES THEREOF

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/217,618

FILING DATE: 25-MARCH-1994

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5510330man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1032

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

```

; APPLICATION NUMBER: US/08/811,949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-9666-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-811-949-51

Query Match 39.1%; Score 590; DB 2; Length 437;
Best Local Similarity 45.3%; Pred. No. 8e-53;
Matches 120; Conservative 39; Mismatches 96; Indels 10; Gaps 5;

QY 13 CG-QKTLRPKRIIGBEFTTIENQFWPAAIYRRH-RGGSVTVYVCGGSLSPQWVISATHC 70
DB 174 CGLRQVSQPFALITGLFADTASHFWQAAIFAKHRRSPGFRFCGGLISLSCWILSAHC 233
QY 71 FIDYPKEDYIVYLGSRSLNNTGEMKFVEVENILHKDYSATLAHNDIALLKIRSK 130
DB 234 FQERFPFHLTVILGRTVVYPGEBEQFVEKYIVHKEFDDDT--YDNDIALQLKSDS 291
QY 131 GRCAQPSRTIQICLPMSVNDPQFGTSCETIGFKENSTDYLYPEQLKMTVVKLISHREC 190
DB 292 SRCAGESSVVRTVCLPPADQLQPDWTECLSGYKHEALSFYSERLKEARVLYPSSRC 351
QY 191 QQPHYVGSVTTKMLCAAD-----PWKMT-DSCCGDSGGPLVCSLQGRMTLTGIVSWGSG 244
DB 352 TSOHLNRTVTDNMLCAGDTRSGGPQANLHACQGDGGPLVCLNDGEMTLVGIISWGLG 411
QY 245 CALKDXPGVYTVSHFLPWIRSHTK 269
DB 412 CGOKDYEGVYTKVNYLDWIRNMR 436

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RESULT 24
US-08-811-949-39
Sequence 39, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SAKAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: P.C. C. JEFFERSON DAVIS HIGHWAY, SUITE 400
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-966-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-811-949-39
;
; Query Match 39.1%; Score 590; DB 2; Length 527;
; Best Local Similarity 45.3%; Pred. No. 1e-52;
; Matches 120; Conservative 39; Mismatches 96; Indels 10; Gaps 5;
;
Qy 13 CG-QKTLAPRKLTGGSEFTIENQNPFAALYRHH-RGGSVTVVCGSLISPCWVLISATHC 70
Db 264 CGLRQYSQFRII-GGFAFIASHPQWAAIFAKHRSRPGERFLCGGILISSCWIIISAHC 323
Qy 71 FIDYPKKEDYIVLGRSRLNSNTQGENMKFEVENLILHKDYSADTLAHNDIALLKIRSK 130
Db 324 FQERFPPLHLTVILGRIVRVVPGEEQKFEVKYIVHKEPDDDT--YNDNDIALQLKSDS 381
Qy 131 GRCAQPSRTIQTICLPMSYNDPQGTSCETITGSKENSTDYLYPEOLKMTVVKLISHREC 190
Db 382 SRCQAQESSVTVVCLFPADQLQPDWTECELSGKGKHEALSPFFSEKLEAHVRLVPSRRC 441
Qy 191 QQPHYVYGEVTTKMLCAAD-----PWKTT-DSQCGSDGGPLVCSLQGRMTLTGIVSWGRG 244
Db 442 TSCHLLNRTVTDNMLCAGDTRSGGFQANLHDAQCQSDGGGPLVCLNDRMTLVGIISWGLG 501
Qy 245 CALKDKPGVYTVSHFLPWIRSHTK 269
Db 502 CGQKDPGVYTKVTNILDNRDNMR 526
;
; RESULT 25
; US-08-811-949-57
; Sequence 57, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHIMA
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSER: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
;

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-59

Query Match 40.3%; Score 607; DB 2; Length 355;
Best Local Similarity 46.8%; Pred. No.1e-54;
Matches 124; Conservative 36; Mismatches 95; Indels 10; Gaps 5

QY 13 CG-QXTLRRPKLTCGETTITENPWAAYRRH-RGGSVTVYCGSLSPCWVISAHC 70
DB 92 CGLRQTLRPFKIKGLFADIASHPQQAIFAKHRRSPGFRFLCGGILSSCWILSAHC 151
QY 71 FIDYPKEDYIVLGRSLNENTQEMKFVENLILHKDYSADTLAHHNDIALLKIRSK 130
DB 152 FQERPPPHLTVLGRTVVPGEQKFEVKIVHKEFDDT--YDNDIALQLKSDS 209
QY 131 GRCAQPSRTIQTICLPSMYNDPQGTSCITGPKENSTDYLYPEQLKMTVVKLISHREC 190
DB 210 SRCQAESSVVRTVCLPPADLQLPDWTCELSGCGKEALSPFYSERLKEARVLYPSSRC 269
QY 191 QCPHYGYSVTTKMLCAAD----PWKNT--DSCQDSDGGPLVCSLOGRWTLTGIVSWGRC 244
DB 270 TSQLLRNRTVNMLCAGDTRSGGPGQANLHDACQDSDGGPVLCLNDGRWTLVGLISWGLG 329
QY 245 CALKQKPGVYTRVSHFLPWIRSHTK 269
DB 330 CGQKQVGYVTKVTVYLDWIRDNR 354

RESULT 22
US-08-811-949-47
Sequence 47, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8900
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-560-098A-49

Query Match 91.1%; Score 1374; DB 2; Length 254;
Best Local Similarity 99.2%; Pred. No. 1.5e-134;
Matches 252; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 23 KIIGFETIENQPFPAIYRRHGGSVTVYCGGSLISPCWVISATHCFIDYPKEDIVY 82
DB 1 KIIGFETIENQPFPAIYRRHGGSVTVYCGGSLISPCWVISATHCFIDYPKEDIVY 60
QY 83 YLGRSLNNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIQT 142
DB 61 YLGRSLNNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIQT 120
QY 143 ICLPSMYNDPQFTSCETITGFGKENSTDYLYPEQLKMTVVKLIISHRECCQPHYGVSEVTT 202
DB 121 ICLPSMYNDPQFTSCETITGFGKENSTDYLYPEQLKMTVVKLIISHRECCQPHYGVSEVTT 180
QY 203 KMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRGKALKDKPGVTVRVSHFLP 262
DB 181 KMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRGKALKDKPGVTVRVSHFLP 240
QY 263 WIRSHTKENGLAL 276
DB 241 WIRSHTKENGLVL 254

RESULT 21
US-08-811-949-59
; Sequence 59, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202

; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,483
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6193.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 253 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6232456e
; US-08-944-483-73

Query Match 91.6%; Score 1382; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 2.2e-135;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LIIGFETIENQPFPAIYRRHGGSVTVYCGGSLISPCWVISATHCFIDYPKEDIVY 83
DB 1 LIIGFETIENQPFPAIYRRHGGSVTVYCGGSLISPCWVISATHCFIDYPKEDIVY 60
QY 84 LGRSLNNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIQT 143
DB 61 LGRSLNNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIQT 120
QY 144 ICLPSMYNDPQFTSCETITGFGKENSTDYLYPEQLKMTVVKLIISHRECCQPHYGVSEVTTK 203
DB 121 ICLPSMYNDPQFTSCETITGFGKENSTDYLYPEQLKMTVVKLIISHRECCQPHYGVSEVTTK 180
QY 204 MLCADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRGKALKDKPGVTVRVSHFLP 263
DB 181 MLCADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRGKALKDKPGVTVRVSHFLP 240
QY 264 IRSHTKENGLAL 276
DB 241 IRSHTKENGLAL 253

RESULT 20
US-08-560-098A-49
; Sequence 49, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WENDT, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
```

```

; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; APPLICATION NUMBER: 148/42448
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-560-098A-46

Query Match 99.2%; Score 1496; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.6e-147;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SSPPEELKFCQGKTLRPRFKIIGGFTTIENQPFALYRHRGGSVTVYCGSLISPC 62
Db 33 SSPPEELKFCQGKTLRPRFKIIGGFTTIENQPFALYRHRGGSVTVYCGSLISPC 92

Qy 63 WVTSAHCFIDYPKKEDIYVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIA 122
Db 93 WVTSAHCFIDYPKKEDIYVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHNDIA 152

Qy 123 LLKIRSKGRCQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSVDLYPEQLKMTVV 182
Db 153 LLKIRSKGRCQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSVDLYPEQLKMTVV 212

Qy 183 KLISHRECCQPHYGYSEVITKMLCAADPQKMTDSCQDGGPLVCSLQGRMTLTGIVSWG 242
Db 213 KLISHRECCQPHYGYSEVITKMLCAADPQKMTDSCQDGGPLVCSLQGRMTLTGIVSWG 272

Qy 243 RGCALKDKPGYTVRSHFLPWIRSHTKKEENGLAL 276
Db 273 RGCALKDKPGYTVRSHFLPWIRSHTKKEENGLAL 306

RESULT 18
US-08-560-098A-48
; Sequence 48, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WENNDT, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEPFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; MEDIUM TYPE: Floppy disk
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; APPLICATION NUMBER: 148/42448
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-560-098A-48

Query Match 99.1%; Score 1495; DB 2; Length 411;
Best Local Similarity 99.3%; Pred. No. 8e-147;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPEELKFCQGKTLRPRFKIIGGFTTIENQPFALYRHRGGSVTVYCGSLIS 60
Db 136 KPSSPPEELKFCQGKTLRPRFKIIGGFTTIENQPFALYRHRGGSVTVYCGSLIS 191

Qy 61 PCWVISATHCFIDYPKKEDIYVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHND 120
Db 196 PCWVISATHCFIDYPKKEDIYVYLGSRSLNSNTQGMKFEVENILHKDYSADTLAHND 251

Qy 121 IALLKIRSKGRCQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSVDLYPEQLKMT 180
Db 256 IALLKIRSKGRCQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSVDLYPEQLKMT 319

Qy 181 VKLISHRECCQPHYGYSEVITKMLCAADPQKMTDSCQDGGPLVCSLQGRMTLTGIVS 240
Db 316 VKLISHRECCQPHYGYSEVITKMLCAADPQKMTDSCQDGGPLVCSLQGRMTLTGIVS 379

Qy 241 WGRGCALKDKPGYTVRSHFLPWIRSHTKKEENGLAL 276
Db 376 WGRGCALKDKPGYTVRSHFLPWIRSHTKKEENGLAL 411

RESULT 19
US-08-944-483-73
; Sequence 73, Application US/08944483
; Patent No. 6232456
; GENERAL INFORMATION:
; APPLICANT: COHEN, MAURICE
; APPLICANT: COLPITTS, TRACEY L.
; APPLICANT: FRIEDMAN, PAULA N.
; APPLICANT: GRANADOS, EDWARD N.
; APPLICANT: KLASS, MICHAEL R.
; APPLICANT: RUSSELL, JOHN C.
; APPLICANT: STEWART, KENT D.
; APPLICANT: STROUPE, STEVEN D.
; TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
; TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
; TITLE OF INVENTION: OF THE PROSTATE
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA

```

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/942,157A
FILING DATE: 19920908
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631,673
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TS1108Cont.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)815-6508
TELEFAX: (404)815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..19
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "WAP signal"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 198..203
OTHER INFORMATION: /label= modified
OTHER INFORMATION: /note= "six amino acids deleted in mutant"
US-07-942-157A-3

Query Match 99.8%; Score 1505; DB 1; Length 430;
Best Local Similarity 99.6%; Pred. No. 7.8e-148;
Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSPPEELKFCQCKQLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVYVCGSLIS 60
DB 155 KPSPPEELKFCQCKQLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVYVCGSLMS 214
QY 61 PCWISATHCFIDYPKKEDYVILGRSLNSNTQGMKFEVENILHKDYSADTLAHND 120
DB 215 PCWISATHCFIDYPKKEDYVILGRSLNSNTQGMKFEVENILHKDYSADTLAHND 274
QY 121 IALLKIRSGRCQAPSTTIQICLPSMYNDPQGTSCITGFKENSTDYLYPEQLKMT 180
DB 275 IALLKIRSGRCQAPSTTIQICLPSMYNDPQGTSCITGFKENSTDYLYPEQLKMT 334
QY 181 VVKLSHRECOQPHYGSEVTTKMLCAADPWKTDSCQDGGPLVCSLQGRMTLTGIVS 240
DB 335 VVKLSHRECOQPHYGSEVTTKMLCAADPWKTDSCQDGGPLVCSLQGRMTLTGIVS 394
QY 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
DB 395 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 430

RESULT 16
US-08-560-098A-45
Sequence 45, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WENNDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700

CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 306 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-098A-45

Query Match 99.2%; Score 1496; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 4.1e-147; Indels 0; Gaps 0;
Matches 274; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 SSPPEELKFCQCKQLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVYVCGSLISPC 62
DB 33 SSPPEELKFCQCKQLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVYVCGSLISPC 92
QY 63 WVISATHCFIDYPKKEDYVILGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIA 122
DB 93 WVISATHCFIDYPKKEDYVILGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIA 152
QY 123 LKIRSGRCQAPSTTIQICLPSMYNDPQGTSCITGFKENSTDYLYPEQLKMTV 182
DB 153 LKIRSGRCQAPSTTIQICLPSMYNDPQGTSCITGFKENSTDYLYPEQLKMTV 212
QY 183 KLSHRECOQPHYGSEVTTKMLCAADPWKTDSCQDGGPLVCSLQGRMTLTGIVSWG 242
DB 213 KLSHRECOQPHYGSEVTTKMLCAADPWKTDSCQDGGPLVCSLQGRMTLTGIVSWG 272
QY 243 RGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
DB 273 RGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 306

RESULT 17
US-08-560-098A-46
Sequence 46, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WENNDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA

; Sequence 47, Application US/08560098A

; Patent No. 5976841

; GENERAL INFORMATION:

; APPLICANT: WENDET, Stephan

; APPLICANT: HEINZEL-WIELAND, Regina

; APPLICANT: STEFFENS, Gerd Josef

; TITLE OF INVENTION: Proteins having Fibrinolytic and

; TITLE OF INVENTION: Coagulation-inhibiting Properties

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan

; STREET: 1200 G Street, N.W., Suite 700

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/560,098A

; FILING DATE: 17-NOV-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: P 44 40 892.7

; FILING DATE: 17-NOV-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: EVANS, Joseph D.

; REGISTRATION NUMBER: 26,269

; REFERENCE/DOCKET NUMBER: 148/42448

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 628-8800

; TELEFAX: (202) 628-8844

; INFORMATION FOR SEQ ID NO: 47:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 432 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-560-098A-47

Query Match 100.0%; Score 1508; DB 2; Length 432;

Best Local Similarity 100.0%; Pred. No. 3.8e-148;

Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPSSPPELKFQCGQKTLRPFKLIIGGEFTTIENQPFPAIYRRHGGSVTVYCGGSLIS 60

Db 157 KPSSPPELKFQCGQKTLRPFKLIIGGEFTTIENQPFPAIYRRHGGSVTVYCGGSLIS 216

Qy 61 PCWISATHCFIDYPKKEDYIVLGRSLNSNTQGENKFEVENLILHKDYSADTLAHND 120

Db 217 PCWISATHCFIDYPKKEDYIVLGRSLNSNTQGENKFEVENLILHKDYSADTLAHND 276

Qy 121 IALLKIRSGRCQAQPSRTIOTICLPMSYNDPFGTSCETITGFGKENSTDYLYPEQLKMT 180

Db 277 IALLKIRSGRCQAQPSRTIOTICLPMSYNDPFGTSCETITGFGKENSTDYLYPEQLKMT 336

Qy 181 VVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPLVCSLQGRMTLTGIVS 240

Db 337 VVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPLVCSLQGRMTLTGIVS 396

Qy 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276

Db 397 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 432

RESULT 14

US-09-403-736-2

; Sequence 2, Application US/09403736

; Patent No. 6638502

; GENERAL INFORMATION:

; APPLICANT: Aventis S.A.

; APPLICANT: LI, Hong

; APPLICANT: LU, He

; APPLICANT: GRISCELLI, Frank

; APPLICANT: OPOLON, Paule

; APPLICANT: SORIA, Claudine

; APPLICANT: RAGOT, Thierry

; APPLICANT: LEGRAND, Yves

; APPLICANT: SORIA, Jeanette

; APPLICANT: MABILAT, Christelle

; APPLICANT: PERRICAUDET, Michel

; APPLICANT: YEH, Patrice

; TITLE OF INVENTION: Adenovirus-Mediated Intratumoral Delivery Of An Angioge

; TITLE OF INVENTION: For The Treatment of Tumors

; FILE REFERENCE: A2778A-US

; CURRENT APPLICATION NUMBER: US/09/403,736

; CURRENT FILING DATE: 1999-10-26

; PRIOR APPLICATION NUMBER: PCT/EP98/02491

; PRIOR FILING DATE: 1998-11-05

; PRIOR APPLICATION NUMBER: 60/044,980

; PRIOR FILING DATE: 1997-04-28

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 2

; LENGTH: 411

; TYPE: PRT

; ORGANISM: humanurokinase

; US-09-403-736-2

Query Match 99.8%; Score 1505; DB 4; Length 411;

Best Local Similarity 99.6%; Pred. No. 7.3e-148;

Matches 275; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 1 KPSSPPELKFQCGQKTLRPFKLIIGGEFTTIENQPFPAIYRRHGGSVTVYCGGSLIS 60

Db 136 KPSSPPELKFQCGQKTLRPFKLIIGGEFTTIENQPFPAIYRRHGGSVTVYCGGSLIS 19

Qy 61 PCWISATHCFIDYPKKEDYIVLGRSLNSNTQGENKFEVENLILHKDYSADTLAHND 120

Db 196 PCWISATHCFIDYPKKEDYIVLGRSLNSNTQGENKFEVENLILHKDYSADTLAHND 25

Qy 121 IALLKIRSGRCQAQPSRTIOTICLPMSYNDPFGTSCETITGFGKENSTDYLYPEQLKMT 180

Db 256 IALLKIRSGRCQAQPSRTIOTICLPMSYNDPFGTSCETITGFGKENSTDYLYPEQLKMT 31

Qy 181 VVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPLVCSLQGRMTLTGIVS 24

Db 316 VVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPLVCSLQGRMTLTGIVS 37

Qy 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276

Db 376 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

RESULT 15

US-07-942-157A-3

; Sequence 3, Application US/07942157A

; Patent No. 5648253

; GENERAL INFORMATION:

; APPLICANT: Wei, Cha-Mer

; TITLE OF INVENTION: Inhibitor-Resistant Urokinase

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kilpatrick & Cody

; STREET: 1100 Peachtree Street Suite 2800

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-4530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

Db 256 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCETITGFGKENSIDLYPEQLKMT 315
Qy 181 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 240
Db 316 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 375
Qy 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
Db 376 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

RESULT 10
5219569-2
; Patent No. 5219569
; APPLICANT: BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
; GORDON A.
; TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,858
; FILING DATE: 16-AUG-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 725,468
; FILING DATE: 22-APR-1985
; SEQ ID NO:2
; LENGTH: 430
5219569-2

Query Match 100.0%; Score 1508; DB 6; Length 430;
Best Local Similarity 100.0%; Pred. No. 3.8e-148; Indels 0; Gaps 0;
Matches 276; Conservative 0; Mismatches 0;
Qy 1 KPSSPPEELKFCQGGKTLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVTVVCGSLIS 60
Db 155 KPSSPPEELKFCQGGKTLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVTVVCGSLIS 214
Qy 61 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
Db 215 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 274
Qy 121 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCETITGFGKENSIDLYPEQLKMT 180
Db 275 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCETITGFGKENSIDLYPEQLKMT 334
Qy 181 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 240
Db 335 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 394
Qy 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
Db 395 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 430

RESULT 11
US-09-101-272G-1
; Sequence 1, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: mat_peptide
; LOCATION: (21)-()
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (20)-()
; OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)
US-09-101-272G-1

Query Match 100.0%; Score 1508; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.8e-148; Indels 0; Gaps 0;
Matches 276; Conservative 0; Mismatches 0;
Qy 1 KPSSPPEELKFCQGGKTLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVTVVCGSLIS 60
Db 156 KPSSPPEELKFCQGGKTLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVTVVCGSLIS 215
Qy 61 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
Db 216 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 275
Qy 121 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCETITGFGKENSIDLYPEQLKMT 180
Db 276 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCETITGFGKENSIDLYPEQLKMT 335
Qy 181 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 240
Db 336 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 395
Qy 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
Db 396 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431

RESULT 12
5188829-1
; Patent No. 5188829
; APPLICANT: KOBAYASHI, YO-ICHI; OMORI, MUNEKI; YAMADA, CHIKAKO
; TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/340,007
; FILING DATE: 18-AUG-1998
; SEQ ID NO:1
; LENGTH: 431
5188829-1

Query Match 100.0%; Score 1508; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 3.8e-148; Indels 0; Gaps 0;
Matches 276; Conservative 0; Mismatches 0;
Qy 1 KPSSPPEELKFCQGGKTLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVTVVCGSLIS 60
Db 156 KPSSPPEELKFCQGGKTLRPRFKIIGGFTTIENQWPFAAIYRRHGGSVTVVCGSLIS 215
Qy 61 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
Db 216 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 275
Qy 121 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCETITGFGKENSIDLYPEQLKMT 180
Db 276 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCETITGFGKENSIDLYPEQLKMT 335
Qy 181 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 240
Db 336 VVKLISHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 395
Qy 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
Db 396 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431

RESULT 13
US-08-560-098A-47

NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-799-18

Query Match 100.0%; Score 1508; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.6e-148;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 KPSSPPEELKFCQCGKTLRPRFKIIGGEFTTIENQPFPAALYRRHRGGSVTVVCGGSLIS 60
DB 136 KPSSPPEELKFCQCGKTLRPRFKIIGGEFTTIENQPFPAALYRRHRGGSVTVVCGGSLIS 195
QY 61 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
DB 196 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 255
QY 121 IALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSTDYLYPEQLKMT 180
DB 256 IALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSTDYLYPEQLKMT 315
QY 181 VVKLISHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 240
DB 316 VVKLISHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 375
QY 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
DB 376 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

RESULT 9

US-09-181-816-1
Sequence 1, Application US/09181816
Patent No. 6277818
GENERAL INFORMATION:
APPLICANT: MAZAR, Andrew P.
APPLICANT: JONES, Terence R.
TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR
FILE REFERENCE: 329042000300 SIDN 1-7
CURRENT APPLICATION NUMBER: US/09/181,816
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 411
TYPE: PRI
ORGANISM: Homo sapiens
US-09-181-816-1

Query Match 100.0%; Score 1508; DB 3; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.6e-148;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 KPSSPPEELKFCQCGKTLRPRFKIIGGEFTTIENQPFPAALYRRHRGGSVTVVCGGSLIS 60
DB 136 KPSSPPEELKFCQCGKTLRPRFKIIGGEFTTIENQPFPAALYRRHRGGSVTVVCGGSLIS 195
QY 61 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
DB 196 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 255
QY 121 IALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSTDYLYPEQLKMT 180

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-286-748B-18

Query Match 100.0%; Score 1508; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.6e-148;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 KPSSPPEELKFCQCGKTLRPRFKIIGGEFTTIENQPFPAALYRRHRGGSVTVVCGGSLIS 60
DB 136 KPSSPPEELKFCQCGKTLRPRFKIIGGEFTTIENQPFPAALYRRHRGGSVTVVCGGSLIS 195
QY 61 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
DB 196 PCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 255
QY 121 IALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSTDYLYPEQLKMT 180
DB 256 IALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQGTSCETITGFGKENSTDYLYPEQLKMT 315
QY 181 VVKLISHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 240
DB 316 VVKLISHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVS 375
QY 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
DB 376 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

RESULT 8

US-08-153-799-18
Sequence 18, Application US/08153799
Patent No. 5766883
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
CORRESPONDENCE ADDRESSES: 23
ADDRESS: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991
ATTORNEY/AGENT INFORMATION:

```

; FILING DATE: 30-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42444
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: protein
; MOLECULE TYPE: protein
US-08-967-024C-25

Query Match 100.0%; Score 1508; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.3e-148;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPPELKFQCCQKTLRPFKIIIGGFTTIENQPFALYYRHRGGSVTVVCGGSLIS 60
DB 91 KPSSPPPELKFQCCQKTLRPFKIIIGGFTTIENQPFALYYRHRGGSVTVVCGGSLIS 150

QY 61 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENILHKOYSADTLAHND 120
DB 151 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENILHKOYSADTLAHND 210

QY 121 IALLKIRSEKRCQAPSRITQIICLPMSYNDPQGTSCETIGFGKENSTDYLYPEQLKWT 180
DB 211 IALLKIRSEKRCQAPSRITQIICLPMSYNDPQGTSCETIGFGKENSTDYLYPEQLKWT 270

QY 181 VVKLISHRECQPHYGVSEVTTKMLCAADPWKTDSCQSGSGPLVCSLQGRMTLTGIVS 240
DB 271 VVKLISHRECQPHYGVSEVTTKMLCAADPWKTDSCQSGSGPLVCSLQGRMTLTGIVS 330

QY 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
DB 331 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 366

RESULT 6
US-08-087-163-1
; Sequence 1, Application US/08087163
; Patent No. 5472692
; GENERAL INFORMATION:
; APPLICANT: Liu, Jian-Ning
; APPLICANT: Gurewicz, Victor
; TITLE OF INVENTION: PRO-UKINASE MUTANTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,163
; FILING DATE: 07/02/93
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983

; FILING DATE: 30-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42444
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
US-08-087-163-1

Query Match 100.0%; Score 1508; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 3.6e-148;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPSSPPPELKFQCCQKTLRPFKIIIGGFTTIENQPFALYYRHRGGSVTVVCGGSLIS 60
DB 136 KPSSPPPELKFQCCQKTLRPFKIIIGGFTTIENQPFALYYRHRGGSVTVVCGGSLIS 195

QY 61 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENILHKOYSADTLAHND 120
DB 196 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENILHKOYSADTLAHND 255

QY 121 IALLKIRSEKRCQAPSRITQIICLPMSYNDPQGTSCETIGFGKENSTDYLYPEQLKWT 180
DB 256 IALLKIRSEKRCQAPSRITQIICLPMSYNDPQGTSCETIGFGKENSTDYLYPEQLKWT 315

QY 181 VVKLISHRECQPHYGVSEVTTKMLCAADPWKTDSCQSGSGPLVCSLQGRMTLTGIVS 240
DB 316 VVKLISHRECQPHYGVSEVTTKMLCAADPWKTDSCQSGSGPLVCSLQGRMTLTGIVS 375

QY 241 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 276
DB 376 WGRGALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

RESULT 7
US-08-286-748B-18
; Sequence 18, Application US/08286748B
; Patent No. 5759542
; GENERAL INFORMATION:
; APPLICANT: Victor Gurewicz
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
; TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,748B
; FILING DATE: August 5, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J. Peter Fasse
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04547/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
```

SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-098A-44

Query Match 100.0%; Score 1508; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.3e-148;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSPPEELKFCQCKTLRPRFKIIGGEFTTIENQWFAAIYRHRGGSVTVYCGSLIS 60
DB 91 KPSPPEELKFCQCKTLRPRFKIIGGEFTTIENQWFAAIYRHRGGSVTVYCGSLIS 150
QY 61 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
DB 151 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 210
QY 121 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGKENSTDYLYPEQLKMT 180
DB 211 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGKENSTDYLYPEQLKMT 270
QY 181 VVKLISHRECOOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGLVCSLQGRMTLTGIVS 240
DB 271 VVKLISHRECOOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGLVCSLQGRMTLTGIVS 330
QY 241 WGRGCAKDKPGVYTRVSHFLPWIRSHTKENGIAL 276
DB 331 WGRGCAKDKPGVYTRVSHFLPWIRSHTKENGIAL 366

RESULT 4
US-08-967-024C-24
Sequence 24, Application US/08967024C
Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: WNEEDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOSCH, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967.024C
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-024C-24
Query Match 100.0%; Score 1508; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 3.3e-148;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPSPPEELKFCQCKTLRPRFKIIGGEFTTIENQWFAAIYRHRGGSVTVYCGSLIS 60
DB 91 KPSPPEELKFCQCKTLRPRFKIIGGEFTTIENQWFAAIYRHRGGSVTVYCGSLIS 150
QY 61 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 120
DB 151 PCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHND 210
QY 121 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGKENSTDYLYPEQLKMT 180
DB 211 IALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGKENSTDYLYPEQLKMT 270
QY 181 VVKLISHRECOOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGLVCSLQGRMTLTGIVS 240
DB 271 VVKLISHRECOOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGLVCSLQGRMTLTGIVS 330
QY 241 WGRGCAKDKPGVYTRVSHFLPWIRSHTKENGIAL 276
DB 331 WGRGCAKDKPGVYTRVSHFLPWIRSHTKENGIAL 366

RESULT 5
US-08-967-024C-25
Sequence 25, Application US/08967024C
Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: WNEEDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOSCH, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967.024C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8

	PROPEP	22	33	BY SIMILARITY.
F	CHAIN	34	566	TISSUE-TYPE PLASMINOGEN ACTIVATOR. A
F	CHAIN	34	314	TISSUE-TYPE PLASMINOGEN ACTIVATOR B
F	CHAIN	315	566	CHAIN
F	CHAIN	315	566	CHAIN
F	DOMAIN	40	82	PIRONECTIN TYPE-I.
F	DOMAIN	83	121	EGF-LIKE.
F	DOMAIN	128	209	KRINGLE 1.
F	DOMAIN	219	300	KRINGLE 2.
F	DOMAIN	315	566	SERINE PROTEASE.
F	ACT SITE	361	361	CHARGE RELAY SYSTEM.
F	ACT SITE	410	410	CHARGE RELAY SYSTEM.
F	ACT SITE	517	517	CHARGE RELAY SYSTEM.
F	DISULFID	42	72	BY SIMILARITY.
F	DISULFID	70	79	BY SIMILARITY.
F	DISULFID	87	98	BY SIMILARITY.
F	DISULFID	92	109	BY SIMILARITY.
F	DISULFID	111	120	BY SIMILARITY.
F	DISULFID	128	209	BY SIMILARITY.
F	DISULFID	149	191	BY SIMILARITY.
F	DISULFID	180	204	BY SIMILARITY.
F	DISULFID	219	300	BY SIMILARITY.
F	DISULFID	240	282	BY SIMILARITY.
F	DISULFID	271	295	BY SIMILARITY.
F	DISULFID	303	434	INTERCHAIN (BY SIMILARITY).
F	DISULFID	346	362	BY SIMILARITY.
F	DISULFID	354	423	BY SIMILARITY.
F	DISULFID	448	523	BY SIMILARITY.
F	DISULFID	480	496	BY SIMILARITY.
F	DISULFID	513	541	BY SIMILARITY.
F	CARBOHYD	153	153	N-LINKED (GLCNAC. .) (POTENTIAL).
F	CARBOHYD	487	487	N-LINKED (GLCNAC. .) (POTENTIAL).
F	SEQUENCE	566 AA;	63701 MW;	2EB56BE4E32276C3 CRC64;
uery Match		36.1%;	Score 814;	DB 1; Length 566;
eat Local Similarity		35.8%;	Pred. No. 4.7e-58;	
atches 176;	Conservative	60;	Mismatches 155;	Indels 100; Gaps 9;
C	3	ELH0VP-SNCD---	CLNGSGTCVSNKYFSLNHWCNPKFGGQHCIDKSKTCYEGNGHFY	58
I	78	QCHSVPRSRSEPCWFCFNGGTCRQALYSSDF-VQCPGEGMGLCEIDATATCYKDOGVAY	136	
C	59	RGKASTDTMGRPCLPWNSTATVLOQTYHAHRSDALQGLGKHNYCNPNRRRPPCYVQVG	118	
D	137	RGTWSTAESGAECANWNSGLAMKPYSGRRPNAIRLGLGNHNYCNPNDDQSKPCYVFEKA	196	
C	119	LKPLVQBCMHDCR-----	132	
D	197	GKYISEFCSTPACAKVAEEDGDCYTNGNLAYRGTSHTKSGASCLPWNVSFLTSKIITAW	256	
C	133	-----DGKLRQ-----	CG-QKTLRPRKII 152	
I	257	KSNAPALGLGKHCHRNPDGDAQPWCWVKRQLTWECYCDVPCQVTCGLROYKEPQFRIK	316	
C	153	GGEFTTENQWPAAY-RRHRGGSVTVCGGSLISPCWVTSATHCFIDYPKKEDIYVYL	211	
D	317	GGLPADITSHPWQAAIFVQVRRSPGRFLCGGILISSCWVLSSAAHCFQERYPPHHLKVFL	376	
C	212	GRSLRNSNTQGMKFEVENILHKDYSADTLAHNDIALLKIRSEKGRCAOPSRITOTIC	271	
I	377	GRVTLVPGEEQTFVEVKIHKFFDDT--YNDIALHLKSDLSLTCASESASVRTIC	434	
C	272	LPSMYNDPQFQTSCEITFGKENSTDYLPQKMTVVKLI SHRECOQPHYGVSEVTTKM	331	
D	435	LPDASLQPDWTECELSYKGKHSPPFFSERLKEARVELYPSRCSCTSHLFNRTVTNNM	494	
C	332	LCAADPQW-----KTDSQCGDSGGLVCSLQGRWMTLTGIVSWGRCALKKQKPGVYTVFS	385	
I	495	LCAGDTRGGGHTNLHACQDSGGLVCMKONHMTLVGLISWGJCGGRKQVPGVYTKVT	554	
C	386	HFLPWIRSHTX 396		

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DB          555 NYLDWIRNTR 565

RESULT 15
URTG_DESRO STANDARD; PRT; 394 AA.
URTG_ID      URTG_DESRO
AC          P49150;
DT          01-FEB-1996 (Rel. 33, Created)
DT          01-FEB-1996 (Rel. 33, Last sequence update)
DT          28-FEB-2003 (Rel. 41, Last annotation update)
DE          Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
DE          gamma).
OS          Desmodus rotundus (Vampire bat).
OC          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC          Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
OC          Desmodontinae; Desmodus.
OC          NCBI_TaxID=9430;
OX          [1]
RN          SEQUENCE FROM N.A.
RP          TISSUE=Salivary gland;
RX          MEDLINE=92039036; PubMed=1937019;
RA          Kraetzschmar J., Haendler B., Langer G., Beidol W., Bringmann P.,
RT          Alagon A., Donner P., Schleuning W.D.;
RT          "The plasminogen activator family from the salivary gland of the
RT          vampire bat Desmodus rotundus: cloning and expression.";
RL          Gene 105:229-237(1991).
RN          [2]
RP          CHARACTERIZATION.
RX          MEDLINE=93393059; PubMed=1309059;
RA          Schleuning W.-D., Alagon A., Beidol W., Bringmann P., Petri T.,
RA          Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
RA          Donner P.;
RT          "Plasminogen activators from the saliva of Desmodus rotundus (common
RT          vampire bat): unique fibrin specificity.";
RL          Ann. N.Y. Acad. Sci. 667:395-403(1992).
CC          -!- FUNCTION: Probably essential to support the feeding habits of this
CC          exclusively haematophagous animal. Probable potent thrombolytic
CC          agent.
CC          -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC          plasminogen to form plasmin.
CC          -!- SUBUNIT: Monomer.
CC          -!- SIMILARITY: Belongs to peptidase family S1.
CC          -!- SIMILARITY: Contains 1 kringle domain.
CC          -----
CC          This SWISS-PROT entry is copyright. It is produced through a collaboration
CC          between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC          the European Bioinformatics Institute. There are no restrictions on its
CC          use by non-profit institutions as long as its content is in no way
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CC          entities requires a license agreement (See http://www.isb-sib.ch/
CC          or send an email to license@sib.ch).

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CC -----
DR EMBL; MG3990; AAA31595.1; -.
DR PIR; J50600; J50600.
DR HSP; P98119; IAS1.
DR MEROPS; S01.239; -.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase Sl.
DR InterPro; IPR013114; Peptidase_SlA.
DR Pfam; PF00031; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PLASMOGEN; PLASMOGEN activation; Hydrolase; Ser
KW

```

"Molecular cloning and sequence analysis of the cDNA for a human serine protease responsible for activation of hepatocyte growth factor. Structural similarity of the protease precursor to blood coagulation factor XII." J. Biol. Chem. 268:10024-10028(1993).

[2]

SEQUENCE OF 40-655 FROM N.A.

Zhao S., Odeh C., Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Activates hepatocyte growth factor (HGF) by converting it from a single chain to a heterodimeric form.

-1- SUBUNIT: Dimer of a short chain and a long chain linked by a disulfide bond.

-1- SUBCELLULAR LOCATION: Secreted as an inactive single-chain precursor and is then activated to a heterodimeric form.

-1- TISSUE SPECIFICITY: Liver.

-1- SIMILARITY: Belongs to peptidase family S1.

-1- SIMILARITY: Contains 2 EGF-like domains.

-1- SIMILARITY: Contains 1 fibronectin type I domain.

-1- SIMILARITY: Contains 1 fibronectin type II domain.

-1- SIMILARITY: Contains 1 kringle domain.

-1- CAUTION: it is uncertain whether Met-1 is the initiator.

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EMBL: D14012; BAA03113.1; -
ENBL; Z69923; -; NOT_ANNOTATED_CDS.
PIR: A46688; A46688.
HSP: P00763; LDPO.
MEROPS: S01.228; -;
Genew; HGNC:4894; HGFA.
MTM; 604552; -
GO: GO:0005576; C:extracellular; TAS.
GO: GO:0004252; F:serine-type endopeptidase activity; TAS.
GO: GO:0006508; P:proteolysis and peptidolysis; TAS.
InterPro: IPR009003; Cys Ser trypsin.
InterPro: IPR000742; EGF_2.
InterPro: IPR006209; EGF-like.
InterPro: IPR000083; FibrinctnI.
InterPro: IPR000562; FN_Type_II.
InterPro: IPR006210; IEGF.
InterPro: IPR000001; Kringle.
InterPro: IPR001254; Peptidase_S1.
InterPro: IPR001314; Peptidase_S1A.
Pfam: PF00008; EGF; 2.
Pfam: PF00039; fn1; 1.
Pfam: PF00040; fn2; 1.
Pfam: PF00051; kringle; 1.
Pfam: PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
PRINTS: PR00013; ENTPEPIL.
PRINTS: PR00018; KRINGLE.
ProDom: PD000995; FN_Type_II; 1.
ProDom: PD000395; Kringle; 1.
SMART: SM00181; EGF; 2.
SMART: SM00058; FN1; 1.
SMART: SM00059; FN2; 1.
SMART: SM00330; KR; 1.
SMART: SM00020; Tryp_Spc; 1.
PROSITE: PS00022; EGF_1; 2.
PROSITE: PS01186; EGF_2; 1.
PROSITE: PS50036; EGF_3; 2.
PROSITE: PS01253; FIBRONECTIN_1; 1.
PROSITE: PS00023; FIBRONECTIN_2; 1.
PROSITE: PS00021; KRINGLE_1; 1.
PROSITE: PS50070; KRINGLE_2; 1.
PROSITE: PS50240; TRYPSIN_DOM; 1.

RF	SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605.	RP	VARIANT TENRI CYS-53.
RJ	Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,	RA	MEDLINE=99290785; PubMed=10361128;
RK	Rajkumar N., Toth E.J., Yi O., Nickerson D.A.;	RB	Kondo S., Tokunaga F., Kawano S., Oono Y., Kumagai S., Koide T.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	RC	"Factor XII Tenri, a novel cross-reacting material negative factor XII
RM	[3]	RD	deficiency, occurs through a proteasome-mediated degradation.";
RN	SEQUENCE OF 4-615 FROM N.A.	RE	Blood 93:4300-4308(1999).
RO	MEDLINE=86176794; PubMed=3754331;	RF	-!- FUNCTION: Factor XII is a serum glycoprotein that participates in
RP	Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,	RG	the initiation of blood coagulation, fibrinolysis, and the
RQ	Cortese R.;	RH	generation of bradykinin and angiotensin.
RR	"cDNA sequence coding for human coagulation factor XII (Hageman).";	RI	-!- CATALYTIC ACTIVITY: Cleaves selectively Arg- -Ile bonds in factor
RS	Nucleic Acids. Res. 14:3146-3146(1986).	RJ	VII to form factor VIIa and factor XI to form factor XIa.
RT	[4]	RK	-!- PTM: O- AND N-GLYCOSYLATED.
RU	SEQUENCE OF 14-615 FROM N.A.	RL	-!- DISEASE: Defects in F12 do not cause any clinical symptoms. The
RV	MEDLINE=86033830; PubMed=3877053;	RM	sole effect is that whole-blood clotting time is prolonged. There
RW	Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.,	RN	-!- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a
RX	McGillivray R.T.A.;	RO	complex bound to an anionic surface. Prekallikrein is cleaved by
RY	"Characterization of human blood coagulation factor XII cDNA.	RP	factor XII to form kallikrein, which then cleaves factor XII first
RZ	"Characterization of the primary structure of factor XII and the tertiary	RQ	to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor
RA	structure of beta-factor XIIa.";	RR	XIIa activates factor XI to factor XIa.
RB	J. Biol. Chem. 260:13666-13676(1985).	RS	-!- SIMILARITY: Belongs to peptidase family S1.
RC	[5]	RT	-!- SIMILARITY: Contains 2 EGF-like domains.
RD	SEQUENCE OF 146-615 FROM N.A.	RU	-!- SIMILARITY: Contains 1 fibronectin type I domain.
RE	MEDLINE=86216049; PubMed=3011063;	RV	-!- SIMILARITY: Contains 1 fibronectin type II domain.
RF	Que B.G., Davie E.W.;	RW	-!- SIMILARITY: Contains 1 kringle domain.
RG	"Characterization of a cDNA coding for human factor XII (Hageman	RX	factor).";
RH	Biochemistry 25:1525-1528(1986).	RY	[6]
RI	[6]	RZ	SEQUENCE OF 20-379.
RJ	MEDLINE=85182674; PubMed=3886554;	RA	McMullen B.A., Fujikawa K.;
RK	"Amino acid sequence of the heavy chain of human alpha-factor XIIa	RB	(activated Hageman factor).";
RL	J. Biol. Chem. 260:5328-5341(1985).	RC	[7]
RM	SEQUENCE OF 561-615 FROM N.A.	RD	TISSUE=Blood;
RN	MEDLINE=96133302; PubMed=8528215;	RE	SEQUENCE OF 354-362 AND 373-615.
RO	Schloesser M., Hoferbert S., Bartz U., Lutze G., Lammle B., Engel W.;	RF	MEDLINE=83291041; PubMed=6604055;
RP	"The novel acceptor splice site mutation 11396(G->A) in the factor	RG	Fujikawa K., McMullen B.A.;
RQ	XII gene causes a truncated transcript in cross-reacting material	RH	"Amino acid sequence of human beta-factor XIIa.";
RR	negative patients.";	RI	J. Biol. Chem. 258:10924-10933(1983).
RS	Hum. Mol. Genet. 4:1235-1237(1995).	RJ	[8]
RT	[9]	RK	SEQUENCE OF 561-615 FROM N.A.
RU	CARBOHYDRATE-LINKAGE SITE THR-109.	RL	TISSUE=Blood;
RV	MEDLINE=92184750; PubMed=1544894;	RM	MEDLINE=96133302; PubMed=8528215;
RW	Harris R.J., Ling V.T., Spellman M.W.;	RO	"O-linked fucose is present in the first epidermal growth factor
RX	domain of factor XII but not protein C.";	RP	J. Biol. Chem. 267:5102-5107(1992).
RY	[10]	RQ	VARIANT WASHINGTON D.C. SER-590.
RZ	MEDLINE=90046788; PubMed=2510163;	RA	Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
RB	Saito H.;	RB	"Coagulation factor XII (Hageman factor) Washington D.C.: inactive
RC	factor XIIa results from Cys-571->Ser substitution.";	RC	Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
RD	[11]	RD	VARIANT LOCARNO PRO-372.
RE	MEDLINE=94325559; PubMed=8049433;	RE	Hovanga J.K., Schaller J., Stricker H., Wullemmin W.A., Furian M.,
RF	Laemmle B.;	RF	"Coagulation factor XII Locarno: the functional defect is caused by
RG	the amino acid substitution Arg-353->Pro leading to loss of a	RG	kallikrein cleavage site.";
RH	Blood 84:1173-1181(1994).	RH	

```
SMART: SM00020; Trp_SPC; 1.
I PROSITE; PS00022; EGF_1; 2.
I PROSITE; PS01186; EGF_2; 1.
I PROSITE; PS00026; EGF_3; 2.
I PROSITE; PS01253; FIBRONECTIN_1; 1.
I PROSITE; PS00023; FIBRONECTIN_2; 1.
I PROSITE; PS00021; KRINGLE_1; 1.
I PROSITE; PS00070; KRINGLE_2; 1.
I PROSITE; PS02040; TRYPSIN_DOM; 1.
I PROSITE; PS00134; TRYPSIN_HIS; 1.
I PROSITE; PS00135; TRYPSIN_SER; 1.
I Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
I Hydrolase; Fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen;
I Polymorphism; Disease mutation.
F SIGNAL 1 19
F CHAIN 20 372 ALPHA-FACTOR XIIA HEAVY CHAIN.
F CHAIN 373 615 ALPHA-FACTOR XIIA LIGHT CHAIN.
F CHAIN 354 362 BETA-FACTOR XIIA PART 1.
F CHAIN 373 615 BETA-FACTOR XIIA PART 2.
F DOMAIN 47 88 FIBRONECTIN TYPE-II.
F DOMAIN 94 131 EGF-LIKE 1.
F DOMAIN 133 173 FIBRONECTIN TYPE-I.
F DOMAIN 174 210 EGF-LIKE 2.
F DOMAIN 217 295 KRINGLE.
F DOMAIN 296 349 PRO-RICH.
F DOMAIN 373 615 SERINE PROTEASE.
F CARBOHYD 109 109 O-LINKED (FUC).
F CARBOHYD 249 249 N-LINKED (GLCNAC. . .).
F CARBOHYD 299 299 O-LINKED (POTENTIAL).
F CARBOHYD 305 305 O-LINKED (POTENTIAL).
F CARBOHYD 308 308 O-LINKED (POTENTIAL).
F CARBOHYD 328 328 O-LINKED (POTENTIAL).
F CARBOHYD 329 329 O-LINKED (POTENTIAL).
I very Match 30.2%; Score 681; DB 1; Length 615;
I est Local Similarity 34.1%; Pred. No. 2.6e-47;
I atches 152; Conservative 58; Mismatches 158; Indels 78; Gaps 10;
I 13 CLINGTCVSNKYSNIHNCNPKKFGQHCIDKSKTCYEGNGHFYRGKASTDTMGRCL 72
I 183 CLHGRCLE---VEGHRCHCPGVYTGPFCDVTKASCVDGRGLSYRGARTLTSGAPCQ 239
I 73 PMSATVLOQTY-HAHRSDALQGLGKHNYCRNPNRRPWCYVQVGLPLVQECMVHDC 131
I 240 PMAS-----EATYENVTAQARNWGLGHGAFCRPNNDIRPWCPLVNRDRLSWEYCDLAQC 295
I 132 -----ADGKL----- 136
I 296 QTETQAPPTVPSRLVPLMPAQAPPKPQPTTRTPPOSQTFGALPAKREQPPSLTRNG 355
I 137 KFOGQ---XTLRPRFKIIGFTTIENQWFAIYRRHRGSGSVTVVCGSLISPCWITS 193
I 356 PLSCGQLRSLSSMTFVVGVLRCAGHYIALTWGHS-----FCAGSLIAPCWILT 409
I 194 ATHCFIDYPKEDYIVYLGSRSLNSNTQGMKEFEVENLILHKDYSADTLAHHNDIALKI 253
I 410 AAHCLQDRPAPEDLTVVLGQERRNHSCEPQTLAVRSYRLHEAFS--PVSQCHDLALLRL 467
I 254 R-SKEGRCAPSRITQICLPSMYNDPQFGTSCETIGFGKENSTDYLYPEQLKMTVVKLI 312
I 468 QEDADGSCALLSPVQVCLPSPGAARESETTLQVAGNGHQFGAEYASFLEGAQVPEL 527
I 313 SHRECOQPHYVGSVTTKMLCAADPQWKTDSCQGDGGPLVCSLQG---RMTLTGVSWG 369
I 528 SLERCSAPDVHSGSILPEMLCAGFLGGTDACQGDGSGPLVCSVCDQAERRLTLQGIISWG 587
I 370 RGCALKDKPGVYTVSHFLPIRSHT 395
I 588 SGQGDNRNKPQVYTDVAYLAWIREHT 613
I ULT 20
I 2_BOVIN
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ID FA12_BOVIN STANDARD; PRT; 593 AA.
AC P98140;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
DE (HAF) (Fragment).
GN F12.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94242782; PubMed=8186251;
RA Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;
RT "Primary structure of bovine Hageman factor (blood coagulation factor
RT XII): comparison with human and guinea pig molecules.";
RL Biochim. Biophys. Acta 1206:63-70(1994).
RN [2]
RP SEQUENCE OF 10-21; 350-364 AND 525-550.
RX MEDLINE=77182112; PubMed=861210;
RA Fujikawa K., Walsh A.K., Davie W.E.;
RT "Isolation and characterization of bovine factor XII (Hageman
RT factor).";
RL Biochemistry 16:2270-2278(1977).
CC -!- FUNCTION: Factor XII is a serum glycoprotein that participates in
CC the initiation of blood coagulation, fibrinolysis, and the
CC generation of bradykinin and angiotensin.
CC -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
CC VII to form factor VIIa and factor XI to form factor XIa.
CC -!- PTM: O- AND N-GLYCOSYLATED (BY SIMILARITY).
CC -!- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor
CC XIIa activates factor XI to factor XIa. Bovine factor XII is
CC cleaved only to alpha-factor XIIa as it lacks the trypsin/
CC kallikrein cleavage site.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; S70164; AAB30804.2; -
CC PIR; S45281; S45281.
CC HSP; P00763; 1DPO.
CC -----
CC MEROPS; S01.211; -.
CC InterPro; IPR009003; Cys_ser_trypsin.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR00083; Fibrnctnl.
CC InterPro; IPR00562; FN_Type_II.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00008; EGF_2.
CC Pfam; PF00039; fn1; 1.
CC Pfam; PF00040; fn2; 1.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
```


-1- PTM: N-LINKED GLYCAN CONTAINS N-ACETYLACTOSAMINE, SIALIC ACID AND IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).

-1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

-1- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily. PIR: S03733; PLPG.

HSP: P00747; SHPG.

MEROPS: S01.233.

GlycosultedB: P06867; Cys_ser trypsin.

InterPro: IPR009003; Cys_ser trypsin.

InterPro: IPR000001; Kringle.

InterPro: IPR003014; PAN.

InterPro: IPR003609; Pan app.

InterPro: IPR001254; Peptidase_S1.

InterPro: IPR001314; Peptidase_S1A.

InterPro: IPR003966; Peptidase_S1A_pr.

Pfam: PF000051; Kringle; 5.

Pfam: PF000024; PAN; 1.

Pfam: PF00089; trypsin; 1.

PRINTS: PR00722; CHYMOTRYPSIN.

PRINTS: PR001018; KRINGLE.

PRINTS: PR01505; PROTHROMBIN.

ProDom: PD000395; Kringle; 5.

SMART: SM00130; KR; 5.

SMART: SM00473; PAN AP; 1.

SMART: SM00020; Tryp_Spc; 1.

PROSITE: PS00021; KRINGLE 1; 5.

PROSITE: PS00070; KRINGLE 2; 5.

PROSITE: PS00240; TRYPSIN_DOM; 1.

PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.

PROSITE: PS00135; TRYPSIN_SER; 1.

Hydrolase: Serine protease; Plasma; Glycoprotein; Fibrinolysis; Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.

CHAIN 1 560 PLASMIN HEAVY CHAIN A.

CHAIN 1 561 790 SERINE PROTEASE.

DOMAIN 1 84 162 KRINGLE 1.

DOMAIN 1 166 243 KRINGLE 2.

DOMAIN 1 256 333 KRINGLE 3.

DOMAIN 1 358 435 KRINGLE 4.

DOMAIN 1 461 540 KRINGLE 5.

ACT_SITE 602 602 CHARGE RELAY SYSTEM.

ACT_SITE 645 645 CHARGE RELAY SYSTEM.

ACT_SITE 740 740 CHARGE RELAY SYSTEM.

CARBOHYD 289 289 N-LINKED (GLCNAC...).

CARBOHYD 340 340 O-LINKED (GALNAc...).

SEQUENCE 730 AA; 88592 MW; F04EA06E74BCD58E CRC64;

Query Match 22.5%; Score 508.5; DB 1; Length 790;

est Local Similarity 36.2%; Pred. No. 2.6e-33;

atches 130; Conservative 45; Mismatches 141; Indels 43; Gaps 14;

45 DKSKTCYEGNGHFYRGKASTDTMRPCLPWNASATVLOQTVAHNR---SDALQLGLGKH 100

456 DLSEDCMGNGKRYRGKREATTAGVPCQEWAA---QEPHRHSIFPTETNPRAGLEK-N 509

101 YCRNPD-NRRPWCYVQVLKPLVQECMWHDCAGKLFQCGQKTLRPR---FKLIGCF 156

510 YCRNPDGDDNGPWCYT-TNPQKLFYCDVPCQVTS--SFDGCKPKVFKKCPARWGGCV 566

157 TTENQPFPAAYRRHRGGSVTVYCGSLISPCWVISATHCFIDYPKKEDYVVLGRSRL 216

567 SIPHSWFWQISLRVYRG---HFCGGTLLSPFWLTKHCLKESSPSSVKVLGAHEE 622

217 NSNTOGEMKFEVENIILHKVSDATLHNDIALLKTRSGRCAQPSRTQTTCLPSMY 276

623 YHLGSGVQEIDVSKLF--KEPS-----EADIALKLSSP-----AVITDKVIPACLET-- 668

277 NDPOF---GTSCEITGFGKENSTDYLYPEQLKMTVVVKL-SHRECOQPHYGVSEVTTKML 332

669 --PNVWVADRTPACVITGWTGKT--YGAGLLKEARLPVIEKVCNEYVLGGKVSFNL 724

333 CAADPQWKTDSCQDGGPLVCSLQGRMTLTGVISWGGCALDKPKGVTYTVSHFLPKWI 391

725 CAGHLAGGIDSCQDGGPLVCFKFDKYLIOGVTSWGLGALPNKPGVYVVSFVWI 783

RESULT 22

PLMN MOUSE

ID PLMN MOUSE STANDARD; PRT; 812 AA.

AC P20918; Q8CIS2; Q91WU5;

DT 01-FEB-1991 (Rel. 17, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].

GN PLG.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

ON NCBI_TaxID=10090;

RX SEQUENCE FROM N.A.

RX MEDLINE=91184812; PubMed=2081600;

RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;

RT "Characterization of the cDNA coding for mouse plasminogen and localization of the gene to mouse chromosome 17.";

RL Genomics 8:49-61(1990).

RN [2]

RC STRAIN=129/SV;

RA Brathwaite M., Waeltz P., Qian Y., Dudekula D., Schlessinger D., Nagaraja R.;

RT "Genomic sequence analysis in the mouse t-complex region.";

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RP TISSUE=Liver;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Soares M.B., Bonaldo M.F., Caban R.C., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guraratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [4]

RP SEQUENCE OF 1-16 FROM N.A.

RC STRAIN=129/SVJ; TISSUE=Liver;

RX PubMed=12149246;

RA Bannach F.G., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L., Farmer R.J., Miles L.A.;

RT "Localization of regulatory elements mediating constitutive and cytokine-stimulated plasminogen gene expression.";

RL J. Biol. Chem. 277:38579-38588(2002).

RN [5]

CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.

RP MEDLINE=95042728; PubMed=7525077;

RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,

Moses M., Lané W.S., Cao Y., Sage E.H., Folkman J.;
"Angiostatin: a novel angiogenesis inhibitor that mediates the
suppression of metastases by a Lewis lung carcinoma."; *Cell*
Cell 79:315-328(1994).
-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including
embryonic development, tissue remodeling, tumor invasion, and
inflammation; in ovulation it weakens the walls of the Graafian
follicle. It activates the urokinase-type plasminogen activator,
collagenases and several complement zymogens, such as C1 and C5.
It cleaves fibrin, fibronectin, thrombospondin, laminin and von
Willebrand factor.
-!- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks
neovascularization and growth of experimental primary and
metastatic tumors in vivo.
-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
products.
-!- ENZYME REGULATION: Converted into plasmin by plasminogen
activators, both plasminogen and its activator being bound to
fibrin. Cannot be activated with streptokinase.
-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
immediately after dissociation from the clot.
-!- MISCELLANEOUS: In the presence of the inhibitor, the activation
involves only cleavage after Arg-581, resulting in 2 chains held
together by 2 disulfide bonds. Without the inhibitor, the
activation involves also removal of the activation peptide.
-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Contains 5 kringle domains.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; J04766; AAA50168.1; --
EMBL; AF481053; AAM22156.1; --
EMBL; BC014773; AAH14773.1; --
EMBL; BC057186; AAH57186.1; --
EMBL; AY134430; AAN15805.1; --
PIR; A38514; PLMS.
HSP; P00747; IPMK.
MEROPS; S01.233; --
MGD; MGI:97620; Pfg.
GO; GO:0016506; F:apoptosis activator activity; IDA.
GO; GO:0006915; P:apoptosis; IDA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR003966; Peptidase_S1A_pr.
Pfam; PF00051; kringle; 5.
Pfam; PF00024; PAN; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
PRINTS; PR01505; PROTHROMBIN.
ProDom; PD000395; Kringle; 4.
SMART; SM00130; KR; 5.
SMART; SM00473; PAN AP; 1.
SMART; SM00020; TRY SPc; 1.
PROSITE; PS00021; KRINGLE_1; 5.
PROSITE; PS50070; KRINGLE-2; 5.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; plasma; Glycoprotein; Fibrinolysis;
Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;

[illegible]

345 QDSGGPLVCSLQRMWLTGIVSGRCALKDKRGVYTVSHPLPHI 391
 759 QDSGGPLVCFKDXKYLQVLTGIVSGRCALKDKRGVYTVSHPLPHI 805
 ULT 23
 N MACMU STANDARD; PRT; 810 AA.
 P12545;
 01-OCT-1989 (Rel. 12, Created)
 01-OCT-1989 (Rel. 12, Last sequence update)
 28-FEB-2003 (Rel. 41, Last annotation update)
 Plasminogen precursor (EC 3.4.21.7).
 PLG.
 Macaca mulatta (Rhesus macaque).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 NCBI_TaxID=9544;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=89174660; PubMed=2925643;
 Tomlinson J.E., McLean J.W., Lawn R.M.;
 "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
 synthesis.";
 J. Biol. Chem. 264:5957-5965(1989).
 -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 a proteolytic factor in a variety of other processes including
 embryonic development, tissue remodeling, tumor invasion, and
 inflammation; in ovulation it weakens the walls of the Graafian
 follicle. It activates the urokinase-type plasminogen activator,
 collagenases and several complement zymogens, such as C1 and C5.
 It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 Willebrand factor.
 -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa]-Arg-[Xaa];
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 activators, both plasminogen and its activator being bound to
 fibrin. Activated with catalytic amounts of streptokinase.
 -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 immediately after dissociation from the clot.
 -!- MISCELLANEOUS: In the presence of the inhibitor, the activation
 involves only cleavage after Arg-580, resulting in 2 chains held
 together by 2 disulfide bonds. Without the inhibitor, the
 activation involves also removal of the activation peptide.
 -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 -!- SIMILARITY: Contains 5 kringle domains.

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 or send an email to license@sib-sib.ch).

 EMBL; J04697; AAA36901.1; -;
 PIR; B32869; B30848.
 HSSP; P00747; 1PMK.
 I MEROPS; S01.233; -;
 InterPro; IPR009003; Cys Ser trypsin.
 InterPro; IPR000001; Kringle.
 InterPro; IPR003014; PAN.
 InterPro; IPR003609; Pan_app.
 InterPro; IPR001254; Peptidase S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR003966; Peptidase_S1A_pr.
 Pfam; PF00051; kringle; 5.
 Pfam; PF00024; PAN; 1.
 Pfam; PF00089; trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR001018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR PRODOM; PD000399; Kringle; 5.
 DR SMART; SMO0130; KR; 4.
 DR SMART; SMO0473; PAN_AP; 1.
 DR SMART; SMO0020; TRYD_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
 FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 581 810 SERINE PROTEASE.
 FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
 FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 134 134 FIBRIN.
 FT BINDING 136 136 FIBRIN.
 FT BINDING 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 185 262 BY SIMILARITY.
 FT DISULFID 188 316 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 567 685 BY SIMILARITY.
 FT DISULFID 577 585 BY SIMILARITY.
 FT DISULFID 607 623 BY SIMILARITY.
 FT DISULFID 659 766 BY SIMILARITY.
 FT DISULFID 728 745 BY SIMILARITY.
 FT DISULFID 756 784 BY SIMILARITY.
 FT CARBOHYD 365 365 O-LINKED (GALNAc...) (BY SIMILARITY).
 SQ SEQUENCE 810 AA; 90255 MW; A75E1C51A1A0F24A CRC64;

Query Match 22.2%; Score 501; DB 1; Length 810;
 Best Local Similarity 34.4%; Pred No. 1,le-32;
 Matches 140; Conservative 46; Mismatches 165; Indels 56; Gaps 16;
 QY 10 NCDCUNGTCVSNKYFSNIHWCNCPKFGGQ-----HCEIDKSKTCYEGNGH 56
 Db 428 NPDAKGPWCFTTDPDSVRWEYCNLKKCSGTSGSVAAPPVLAQLPDAETPSBEDCMFGNGK 487
 QY 57 FYRGKASTDTMGRCLPWSNATVLOQTVHAHR-----SDALQGLGKHVNCNPD-NRRRP 111
 PRINTS; PR00722; CHYMOTRYPSIN.

488 GYRKGKATVTGTPTCEWAA-----QEPHSHRIFTPTNPRAGLEK-NYCRNPDGVGGP 541

112 WCYVQVGLKPLVQSCVHDCADGKLFQCGQKTLRPR---FKIIGGEFTTIENQWFAAI 168

542 WCYT-TNPKLFDYCDVPOCAAS--SFDCKPQVEPKCGRVVGCVAPHSWPW--QI 596

169 YRRHGGSTVYVCGSIIISPCWISATHCTIDVPKEDYIVYIGRGRNLNTGEMKFEV 228

597 SLRTRLG--NHFCGGTILSPWVLTAAHCKSKSRPSFYKVLGAHR-----EVHLEPHV 649

229 ENLILHKDYSADTLAHHNDTALKIRSKGRCQPSRTIOTICLPSMYNDPQS---GTS 284

650 QEIVSRQWSEPARA---DIALKLSPP-----AIITKVIAPCLPS-----PNVIVADRT 698

285 CEITFGKGNSTLYPEQLKMTVVKLISHRECOQPHYGYSEVTTKMLCAADPQWKDSC 344

699 CFITGWGETQGT--YGAGLLKEARLPVIENKVCNRYEFLNGTVKTKTELCAHLAGGTDSC 756

345 QDSGGPLVCLSGRMVLTIGVSGRCALKDKRGVTVRVSHLPWI 391

757 QDSGGPLVCEPKDKYILQGVTSWGLGCAHPKRGVTVRVSRFTWTI 803

LT 24

HUMAN

PLAN HUMAN STANDARD; PRT; 810 AA.

P00747;

21-JUL-1986 (Rel. 01, Created)

01-MAR-1989 (Rel. 10, Last sequence update)

15-MAR-2004 (Rel. 43, Last annotation update)

Plasminogen precursor (EC 3.4.21.7) (Contains: Angiostatin).

PLG.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A., AND VARIANT ASN-472.

MEDLINE=90202879; PubMed=2318848;

Petersen T.E., Marten M.R., Ichinose A., Davis E.W.;

"Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system.";

J. Biol. Chem. 265:6104-6111(1990).

[2]

SEQUENCE FROM N.A.

MEDLINE=87162490; PubMed=3030813;

Forsgren M., Raden B., Israelsson M., Larsson K., Heden L.-O.;

"Molecular cloning and characterization of a full-length cDNA clone for human plasminogen.";

FEBS Lett. 213:254-260(1987).

[3]

SEQUENCE FROM N.A., AND VARIANTS LYS-57; GLN-133; HIS-261; TRP-408;

ASN-472; VAL-494 AND TRP-523.

Rieder M.J., Arnel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;

Submitted (DEC-2002) to the ENBL/GenBank/DBJ databases.

[4]

SEQUENCE OF 20-810, AND VARIANT ASN-472.

Sottrup-Jensen L., Petersen T.E., Magnusson S.;

Submitted (JUL-1977) to the PIR data bank.

[5]

SEQUENCE OF 292-810 FROM N.A.

MEDLINE=85023311; PubMed=6148961;

Malinowski D.P., Sadler J.E., Davis E.W.;

"Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.";

Biochemistry 23:4243-4250(1984).

[6]

SEQUENCE OF 20-100.

MEDLINE=75093329; PubMed=122932;

Wiman B., Wallen P.;

"Structural relationship between 'glutamic acid' and 'lysine' forms of human plasminogen and their interaction with the NH2-terminal

activation peptide as studied by affinity chromatography.";

Eur. J. Biochem. 50:489-494(1975).

[7]

SEQUENCE OF 95-580; 581-626; 657-700 AND 732-810, AND VARIANT ASN-472.

Sottrup-Jensen L., Claess H., Zajdel M., Petersen T.E., Magnusson S.;

(in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);

Progress in chemical fibrinolysis and thrombolysis, pp.3:191-205,

Raven Press, New York (1978).

[8]

SEQUENCE OF 483-604.

MEDLINE=76043692; PubMed=126863;

Wiman B., Wallen P.;

"Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that forms the linkage between the plasmin chains.";

Eur. J. Biochem. 58:539-547(1975).

[9]

SEQUENCE OF 581-810.

MEDLINE=77225245; PubMed=142009;

Wiman B.;

"Primary structure of the B-chain of human plasmin.";

Eur. J. Biochem. 76:129-137(1977).

[10]

ACTIVE SITE.

MEDLINE=73149248; PubMed=4694729;

Robbins K.C., Bernabe P., Arzadon L., Summaria L.;

"The primary structure of human plasminogen. II. The histidine loop of human plasmin: light (B) chain active center histidine sequence.";

J. Biol. Chem. 248:1631-1633(1973).

[11]

ACTIVE SITE.

MEDLINE=69234739; PubMed=4240117;

Groeskopf W.R., Summaria L., Robbins K.C.;

"Studies on the active center of human plasmin. Partial amino acid sequence of a peptide containing the active center serine residue.";

J. Biol. Chem. 244:3590-3597(1969).

[12]

OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.

MEDLINE=82213905; PubMed=6919539;

Trexler M., Vali Z., Pathy L.;

"Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen. Arginine 70 and aspartic acid 56 are essential for binding of ligand by kringle 4.";

J. Biol. Chem. 257:7401-7406(1982).

[13]

FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.

MEDLINE=85054794; PubMed=6094526;

Vali Z., Pathy L.;

"The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin affinity of the kringle 1 domain.";

J. Biol. Chem. 259:13690-13694(1984).

[14]

PHOSPHORYLATION SITE SER-597.

MEDLINE=97345939; PubMed=9201958;

Wang H., Prorok M., Bretthauer R.K., Castellino F.J.;

"Serine-578 is a major phosphorylation locus in human plasma plasminogen.";

Biochemistry 36:8100-8106(1997).

[15]

CARBOHYDRATE-LINKAGE SITES.

MEDLINE=88185329; PubMed=3356193;

Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P., Gerwig G.J., van Halbeek H., Vliegenthart J.F.;

"The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Spectes specificity in relation to sialylation and fucosylation patterns.";

Eur. J. Biochem. 173:57-63(1988).

[16]

CARBOHYDRATE-LINKAGE SITE SER-268.

MEDLINE=97207306; PubMed=9054441;

Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J., Pizzo S.V.;

"Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of human plasminogen 2.";

J. Biol. Chem. 272:7408-7411(1997).
[17]
CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
MEDLINE=95042728; PubMed=7525077;
O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.,
"Angiostatin: a novel angiogenesis inhibitor that mediates the
suppression of metastases by a Lewis lung carcinoma.",
Cell 79:315-328(1994).
[18]
CHARACTERIZATION OF ANGIOSTATIN.
MEDLINE=97238710; PubMed=9102221;
Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
Lapcevich R., Nacy C.A.,
"A recombinant human angiotatin protein inhibits experimental primary
and metastatic cancer.",
Cancer Res. 57:1329-1334(1997).
[19]
X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
MEDLINE=92031503; PubMed=1657149;
Mulichak A.M., Tulinsky A., Ravichandran K.G.,
"Crystal and molecular structure of human plasminogen kringle 4
refined at 1.9-A resolution.",
Biochemistry 30:10576-10588(1991).
[20]
X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
MEDLINE=92031503; PubMed=1657149;
Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.,
"The refined structure of the epsilon-aminocaproic acid complex of
human plasminogen kringle 4.",
Biochemistry 30:10589-10594(1991).
[21]
X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
Stec B., Yamano A., Whitlow M., Teeter M.M.,
"Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
A possible structural role of disordered residues.",
Acta Crystallogr. D 53:169-178(1997).
[22]
X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
MEDLINE=96180681; PubMed=8611560;
Mathews I.I., Vandernhoff-Hanover P., Castellino F.J., Tulinsky A.,
"Crystal structures of the recombinant kringle 1 domain of human
plasminogen in complexes with the ligands epsilon-aminocaproic acid
and trans-4-(aminomethyl)cyclohexane-1-carboxylic Acid.",
Biochemistry 35:2567-2576(1996).
[23]
X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
MEDLINE=96198034; PubMed=8521645;
Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
Castellino F.J.,
"Structure and ligand binding determinants of the recombinant kringle
5 domain of human plasminogen.",
Biochemistry 37:3258-3271(1998).
[24]
STRUCTURE BY NMR OF 96-184.
MEDLINE=94237157; PubMed=8181475;
Rejante M.R., Llinas M.,
"1H-NMR assignments and secondary structure of human plasminogen
kringle 1.",
Eur. J. Biochem. 221:927-937(1994).
[25]
STRUCTURE BY NMR OF 96-184.
MEDLINE=94237158; PubMed=8181476;
Rejante M.R., Llinas M.,
"Solution structure of the epsilon-aminohexanoic acid complex of
human plasminogen kringle 1.",
Eur. J. Biochem. 221:939-949(1994).
[26]
STRUCTURE BY NMR OF 183-354.
MEDLINE=96194156; PubMed=8652577;
Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
Rickli E.E.,
"Recombinant gene expression and 1H NMR characteristics of the

RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains.",
RL Biochemistry 35:2357-2364(1996).
RN [27]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE=90219023; PubMed=2157850;
Query Match 22.1%; Score 499; DB 1; Length 810;
Best Local Similarity 33.7%; Pred. No. 1.6e-32;
Matches 137; Conservative 44; Mismatches 170; Indels 56; Gaps 15;
QY 10 NCDCLNGTGVSNKYFSNIHWCNCPKFGGO-----HCEIDKSKTCYEGNGH 56
Db 428 NPDADKGMCTTDPFSEWEYCNLKCSGTSEASVAPPVLLPDVETPSEDCWFGNGK 487
QY 57 FYRGKASDTMGRPCLPWNSATVLQOTYHAHR----SDALQLGLGKNYCNPD-NRRRP 111
Db 488 GYRGKATVTGTGTCQDWA-----QEPHRSITPTETNPRAGLEK-NYCRNPQDVGCP 541
QY 112 WCYVQVGLKPLVQECMVHDCADGKLKFCQGKTLRPR---FKIIGBFTTIENQFWFAA 168
Db 542 WCYT-TNPKLYDYCDVPCQA--APSFDCGKQVEPKPCGRVVGCGVAHPSWQVSL 598
QY 169 YRHGGSVTVYCGSLSPCWVISATHCFIDYPKEDYIVYLGSRSLNNTQGMKEEV 228
Db 599 --RTRFG--MHFCGTLISPEWVITAHCLKSPSPSYKVILGAHQEVNLEPHVQETEV 654
QY 229 ENLIHKDYSADTLAHNDIALKIRSKGRCAPSRITQITICLPSMTNDPQF----GTS 284
Db 655 SELFLEPT-----RKDIALKLSSP---AVITDKVIPACLPS----PNVVADRTE 698
QY 285 CEITGFGKENSTDYLYPEQLKTVYKLIHSHRECOQPHYGVSEVITOMLCAADPOWKDSC 344
Db 699 CFITGWGTQGT--FGAGLLKEAQLPVIEKNRYEFLNGRVQSTELCAGHLAGGTDSC 756
QY 345 QQDSGGPLVCSLQGRMTLTGTVSGRGCAKDKPGVTVRSHFLPWI 391
Db 757 QQDSGGPLVCFEKOKYILQGVTSWGLGCAKPNKGVYVVRSEFVTWI 803
RESULT 25
PLMN CANFA
ID PLMN CANFA STANDARD; PRT; 333 AA.
AC P80009;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=90175323; PubMed=2626424;
RA Schaller J., Straub C., Kaempfer U., Rickli E.E.,
"Complete amino acid sequence of canine miniplasminogen.",
Protein Seq. Data Anal. 2:445-450(1989).
RL -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including
embryonic development, tissue remodeling, tumor invasion, and
inflammation; in ovulation it weakens the walls of the Graafian
follicle. It activates the urokinase-type plasminogen activator,
collagenases and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
CC Willembrand factor.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to

fibrin. Activated with urokinase and high concentrations of streptokinase.

-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.

-!- SIMILARITY: Contains at least 1 kringle domain.

HSP; P00747; SHPG.

MEROFS; S01.233; Cys_Ser_trypsin.

InterPro; IPR009003; Cys_Ser_trypsin.

InterPro; IPR000001; Kringle.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR003966; Peptidase_S1A_pr.

Pfam; PF00051; kringle; 1.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00018; KRINGLE.

PRINTS; PR01505; PROTHROMBIN.

ProDom; PD000395; Kringle; 1.

SMART; SMO0130; KR; 1.

SMART; SMO0020; tryp_Spc; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS00070; KRINGLE_2; 1.

PROSITE; PS00240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; Tissue remodeling; Blood coagulation; Kringle; Zymogen.

NON_TER 1

CHAIN 1

CHAIN 103

CHAIN 333

DOMAIN 4

DOMAIN 104

DOMAIN 333

DISULFID 4

DISULFID 25

DISULFID 66

DISULFID 54

DISULFID 78

DISULFID 90

DISULFID 208

DISULFID 100

DISULFID 108

DISULFID 130

DISULFID 146

DISULFID 222

DISULFID 289

DISULFID 252

DISULFID 268

DISULFID 279

ACT_SITE 145

ACT_SITE 145

ACT_SITE 145

ACT_SITE 188

ACT_SITE 188

ACT_SITE 283

ACT_SITE 283

SITE 152

SITE 152

SITE 186

SITE 186

SITE 264

SITE 264

SITE 277

SITE 277

SEQUENCE 333 AA; 36678 MW; C8C0271B6C6AC8D4 CRC64;

ry Match 22.1%; Score 498.5; DB 1; Length 333;

st Local Similarity 35.6%; Pred. No. 6.2e-33;

ches 126; Conservative 49; Mismatches 136; Indels 43; Gaps 14;

50 CYEGNGHYRGKASTDTMGRCPLWNSATVLIQYTHAHR----SDALQLGLGHNYCRNP 105

4 CMFGNGKYRKXKATWTNGICQEWAA-----QEPHRSIFPTPTNQAGLEK-NYCRNP 57

106 D-NRRRPMCTVQVGLKPLVQSCMVHDCADGKLTQCGQKTLRPR---FKIIGBEFTIEN 161

58 DGDVNGPWCYT-MNQRKLFDCYDPQCV--STSPDCGKQVPEPKCFGRVVGCVANPHS 114

162 QPWFAAIYRRHGGSVTVVCGSLSPSCWVTSATHCFDYPKEDYIVYLGSRSLNNTQ 221

115 WFWQISLSTRVG----KHFQGGTILSPENWVTAHCLRSRSPASYKVLG-----AHKE 165

222 GEMKFEVENLHKDYSADTIAHNDIALKIRKEGSCAPSTIQTICLPSMYNDPQF 281

166 VNLESDVQIEVYKLFLEFTRA---DIALKLSSP----AVITSKVIPACLP-----PENY 214

282 ----GTSCEITGFGKENSTDIYLPQLKWTVVKLISHRECOQPHYGVSEVTTKMLCAADP 337

215 VVADRTLCYITGWGTQGT--YCGALLKEAQLFVIEKNCNRYEYLNKGRVKSCTELCAGNL 272

338 QWKTDSCQSGSGPLVCSLQGRMTLGTIVSWGCGCALKDKPGVYTVVSHPLPW 391

273 AGGTDSCQSGSGPLVCFEYDKYILOGVTISWGLGTCARPNKPGVYVRSRFTWTI 326

RESULT 26

PLMN_SHEEP

ID PLMN_SHEEP STANDARD; PRT; 343 AA.

AC P81286;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Plasminogen (EC 3.4.21.7) (Fragment).

GN PLG.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE.

RX MEDLINE=93149995; PubMed=1492092;

RA Schaller J., Straub C., Kamper J., Rickli E.B.;

RT "Complete amino acid sequence of ovine miniplasminogen."

RL Protein Seq. Data Anal. 5:21-25(1992).

CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. CANNOT be activated with streptokinase.

CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.

CC -!- SIMILARITY: Contains at least 2 kringle domains.

DR PIR; B61545; B61545.

DR HSP; P00747; SHPG.

DR MEROFS; S01.233; -.

DR InterPro; IPR009003; Cys_Ser_trypsin.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR001254; Peptidase S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR InterPro; IPR003966; Peptidase_S1A_pr.

Pfam; PF00051; kringle; 1.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

PRINTS; PR00018; KRINGLE.

PRINTS; PR01505; PROTHROMBIN.

ProDom; PD000395; Kringle; 1.

SMART; SMO0130; KR; 1.

SMART; SMO0020; tryp_Spc; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS00021; KRINGLE_1; 1.

PROSITE; PS00070; KRINGLE_2; 1.

PROSITE; PS00240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.

NON_TER 1

CHAIN 1

CHAIN 140

DOMAIN <1 140

DOMAIN 141 >343

DOMAIN <1 17

DOMAIN <1 17

F DOMAIN 41 120 KRINGLE 5.
F DOMAIN 114 341 SERINE PROTEASE.
F ACT_SITE 181 181 CHARGE RELAY SYSTEM.
F ACT_SITE 224 224 CHARGE RELAY SYSTEM.
F ACT_SITE 319 319 CHARGE RELAY SYSTEM.
F NON_TER 343 343
F SEQUENCE 343 AA; 37662 MW; 8DF6EBA92D596EE0 CRC64;
very March 21.8%; Score 493; DB 1; Length 343;
est Local Similarity 35.6%; Pred. No. 1.8e-32;
atches 126; Conservative 42; Mismatches 142; Indels 44; Gaps 13;
C 50 CYENGHFVYRGKASTMTGRPCLPWNSATVLOQTYAH----RSDALQIGLGHNYCRNP 105
I 15 CMLGIGKGVYRGKATTVAGVPCQWAA-----QEPHRRHGIFPTNPFRAGLEK-NYCRNP 68
C 106 D-NRRPWCVVQGLKPLVQCMVHCADKLKFCQGXLTLPK---FKIIGCEFTTN 161
L 69 DGDVNGFWCT-TNPKLFYCDIPQC---ESSFDCGKPKVFKPCPARVVGCVATPHS 124
C 162 QPWFAAIYRRHGGSVTYVCGSLISPCWVISATHCFIDYPKKEDYVYVGRSLNSNTQ 221
I 125 WPMQVSLRRSR-----EHFCGGTLISPEWLTAAHCLDSILGPSFYTIVLGAHYEMARE 180
C 222 GEMKFEVNLILHKDYSDTLAHNDIALKIKSKGRCQAQPSRTIQTICLPSWYNDPOF 281
D 181 SVGEIPVSRFLPEPSRA-----DIALKISPP-----AVTDEVIPACLES----FNY 224
C 282 ----GTSCEITGFKXENSTDYLPKQMTVVKLISHRECOQPHYGSVTTNMLCAADP 337
D 225 VVADKTVYITNGETQGT--FGVGRLEKARLPVIEKNVCNRYEYLVGRVKSTELCAGDL 282
C 338 QWITDSQGSGLFVCLSGRMTLGVISWGGCCALKQKPGYTVAVSHFLPW 391
I 283 AGGTSQGSGLFVCLSGRMTLGVISWGGCCALKQKPGYTVAVSHFLPW 336
F ULT 27
F N_BOVIN STANDARD; PRG; 812 AA.
F PLMN_BOVIN
F P06868; Q28462;
D 01-JAN-1988 (Rel. 06, Created)
D 01-NOV-1997 (Rel. 35, Last sequence update)
D 15-MAR-2004 (Rel. 43, Last annotation update)
F Plasminogen precursor (EC 3.4.21.7).
F PLG.
C Bos taurus (Bovine).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
C Bovidae; Bovinae; Bos.
C NCBI_TaxID=9913;
F [1]
F SEQUENCE FROM N.A.
F Tissue=Liver;
F Berglund L., Andersen M.D., Petersen T.E.;
F "Cloning and characterization of the bovine plasminogen cDNA."
F Int. Dairy J. 5:593-603(1995).
F [2]
F SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
F MEDLINE=85203906; PubMed=3846532;
F Schaller J., Moser P.W., Danneberg-Muller G.A.K., Rosselet S.J.,
F Kampfer U., Rickli E.S.;
F "Complete amino acid sequence of bovine plasminogen. Comparison with
F human plasminogen."
F Eur. J. Biochem. 149:267-278(1985).
F [3]
F SEQUENCE OF 706-812 FROM N.A.
F MEDLINE=85023311; PubMed=6148961;
F Malinowski D.P., Sadler J.E., Davie E.W.;
F "Characterization of a complementary deoxyribonucleic acid coding for
F human and bovine plasminogen."
F Biochemistry 23:4243-4250(1984).
F [4]

RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegenthart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns."
RL Eur. J. Biochem. 173:57-63(1988).
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion,
CC and inflammation; in ovulation it weakens the walls of the
CC Graafian follicle. It activates the urokinase-type plasminogen
CC activator, collagenases and several complement zymogens, such
CC as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin,
CC laminin and von Willebrand factor.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[]-Xaa > Arg-[]-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products
CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Cannot be activated with streptokinase.
CC -!- PTM: N-LINKED GLYCANS CONTAIN N-ACETYLGLUCOSAMINE AND SIALIC ACID.
CC O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS
CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clot
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 5 kringle domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X79402; CAA55939.1; -;
DR EMBL; K02935; AAA30714.1; -;
DR PIR; S45046; PLEO.
DR HSP; P00747; 2PK4.
DR MEROPS; S01.233; -;
DR GlycoSuiteDB; P06868; -;
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL. 1 26
FT CHAIN 27 812 PLASMINOGEN.
FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.

FT DOMAIN 110 188 KRINGLE 1.
 FT DOMAIN 192 269 KRINGLE 2.
 FT DOMAIN 282 359 KRINGLE 3.
 FT DOMAIN 384 461 KRINGLE 4.
 FT DOMAIN 485 564 KRINGLE 5.
 FT DOMAIN 584 812 SERINE PROTEASE.
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 365 365 /FTID=CAR 000014.
 FT CARBOHYD 624 624 O-LINKED (GALNAC. . .).
 FT ACT_SITE 667 762 CHARGE RELAY SYSTEM.
 FT ACT_SITE 762 762 CHARGE RELAY SYSTEM.
 FT CONFLICT 335 335 N -> D (IN REF. 2).
 FT CONFLICT 516 516 Q -> H (IN REF. 2).
 FT CONFLICT 555 555 P -> L (IN REF. 2).
 FT CONFLICT 744 744 T -> R (IN REF. 3).
 SC SEQUENCE 812 AA, 51216 MW, 386A6A91E220946 CRC64;
 ary Match 21.5%; Score 484.5; DB 1; Length 812;
 at Local Similarity 35.4%; Pred. No. 2.3e-31;
 ches 123; Conservative 42; Mismatches 151; Indels 31; Gaps 11;
 QY 50 CYEGNGHYRGKASDTWGRCLPNSATVLQOTVHAHRSDALQGLGKHYCRNPD-NR 108
 DL 485 CMIGTKSYRGKATTVAGVPCQEWAAQEPHQHSIFTPETNP-OSGL-ERNYCRNPDGV 542
 QY 109 RRPWCYVQGLKPLVQECWHDGADGKLFQCGQKTLRPR---PKIIGGEFTTIENQPF 165
 DL 543 NGPWCTYTNPKPF-DYCDVQPC---ESSFQCGPKVPEKCKSGRIYGGCVKSPHSPWQ 598
 QY 166 AAIYRHRGGVYVCGSLSPCWVISATHCDFIDYFKEDYIVYLGSRILNSVTOGEMK 225
 DL 599 VSLRHSR-----HFCGGLTSPKWLTAACHLNLALSFKYVILGAHNEKREQVQE 653
 QY 226 FEVENLILHKQYSADTLAHHNDIALIKRSKEGRCAQPSRTIQTICLPSMYNDPQFQTS 285
 DL 654 IPVSLFREPQSA-----DIALKL-----SRPAITKEVIPACLPNPNVVAARTEC 701
 QY 286 EITGFKENSTNYLPE-OLKMTVVKLISHRECQOPHYGVSEVTKMLCAADPQWKTDC 344
 DL 702 YITGNETQGT---FGEGLLKEAHLPIENKVCNREYLDGRVKPTELCAHGLGGTDC 758
 QY 345 QDSGGPLVCSLQGRMTLTGIVSWRGCAKDKPGVYTRVSHFLPWI 391
 DL 759 QDSGGPLVCEKDKVILQGVTSWGLGCAKPNKGVYRVSPYVPI 805
 RE LT 28
 AI HUMAN
 IL APOA HUMAN STANDARD; PRT; 4548 AA.
 AC P08519;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
 GN LPA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OY NCBI_TaxID=9606;
 RA [1]
 RF SEQUENCE FROM N.A.
 RX MEDLINE=88039109; PubMed=3670400;
 RA McLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
 RA Fless G.M., Scanu A.M., Lawn R.M.;
 RA "cDNA sequence of human apolipoprotein(a) is homologous to
 RV plasminogen.";
 RI Nature 330:132-137 (1987).
 RN [2]
 RE SERINE PROTEASE ACTIVITY.
 RI MEDLINE=90076123; PubMed=2531657;
 RJ Salonen E.-M., Jaubert M., Zardi L., Vaheri A., Ehrnholm C.;

"Lipoprotein(a) binds to fibronectin and has serine proteinase activity capable of cleaving it.";
 EMBO J. 8:4035-4040 (1989).
 [3]
 RP MEDLINE=90049223; PubMed=2530631;
 RX Utermann G.;
 RA "The mysteries of lipoprotein(a).";
 RL Science 246:904-910 (1989).
 RN [4]
 RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
 RX MEDLINE=21303595; PubMed=11294842;
 RA Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
 RT "Structural elucidation of the N- and O-glycans of human apolipoprotein(a): role of o-glycans in conferring protease resistance.";
 RL J. Biol. Chem. 276:22200-22208 (2001).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
 RX MEDLINE=96217891; PubMed=8642595;
 RA Mikol V., Lograsso P.V., Boettcher B.R.;
 RT "Crystal structures of apolipoprotein(a) kringle IV37 free and complexed with 6-aminocaproic acid and with p-aminomethylbenzoic acid: existence of novel and expected binding modes.";
 RL J. Mol. Biol. 256:751-761 (1996).
 RN [6]
 RP VARIANT ARG-4193.
 RX MEDLINE=95002201; PubMed=7918682;
 RA Scanu A.M., Pfaffinger D., Lee J.C., Hinman J.;
 RT "A single point mutation (Trp72-->Arg) in human apo(a) kringle 4-37 associated with a lysine binding defect in Lp(a).";
 RL Biochim. Biophys. Acta 1227:41-45 (1994).
 CC -!- FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinase activity and is able of autolysis. Inhibits tissue-type plasminogen activator 1.
 CC Lp(a) may be a ligand for megalin/Gp 330.
 CC -!- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and decorin.
 CC -!- PTM: N- and O-glycosylated. The N-glycans are complex biantennary structures present in either a mono- or disialylated state. The O-glycans are mostly (80%) represented by the monosialylated core type 1 structure, NeuNacalpha2-3galbeta1-3galNAc, with smaller amounts of disialylated and non-sialylated O-glycans also detected.
 CC -!- DISEASE: Elevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with atherosclerosis. Homology with plasminogen kringle IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrin(ogen) binding.
 CC -!- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-Lp(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of proteolytic fragmentation.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 CC -!- SIMILARITY: Contains 38 kringle domains.
 CC -----
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 CC -----
 CC EMBL; X06290; CAA29618.1; -.
 DR PIR; S00657; S00657.
 DR PDB; 1I71; 13-JUN-01.
 DR PDB; 1JFN; 28-JUN-02.
 DR PDB; 1KIV; 18-MAY-99.
 DR PDB; 3KIV; 18-MAY-99.
 DR PDB; 4KIV; 18-MAY-99.
 DR MEROPS; S01.226; -.

Genew; HGNC:6667; LPA.
MIM; 152200; ..
GO; GO:0004866; F:endopeptidase inhibitor activity; TAS.
GO; GO:0008015; P:circulation; TAS.
GO; GO:0009405; P:patogenesis; TAS.
InterPro; IPR009003; Cys_Ser_cryptin.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00051; kringle; 38.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 38.
SMART; SM00130; KR; 38.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE 1; 38.
PROSITE; PS00070; KRINGLE 2; 38.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
HydroLase; Serine protease; Lipid transport; Plasma; Glycoprotein; Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
SIGNAL 1 19
F CHAIN 20 4548 APOLIPOPROTEIN(A).
F DOMAIN 20 130 KRINGLE TYPE IV, 1.
F DOMAIN 131 244 KRINGLE TYPE IV, 2.
F DOMAIN 245 358 KRINGLE TYPE IV, 3.
F DOMAIN 359 472 KRINGLE TYPE IV, 4.
F DOMAIN 473 586 KRINGLE TYPE IV, 5.
F DOMAIN 587 700 KRINGLE TYPE IV, 6.
F DOMAIN 701 814 KRINGLE TYPE IV, 7.
F DOMAIN 815 928 KRINGLE TYPE IV, 8.
F DOMAIN 929 1042 KRINGLE TYPE IV, 9.
F DOMAIN 1043 1156 KRINGLE TYPE IV, 10.
F DOMAIN 1157 1270 KRINGLE TYPE IV, 11.
F DOMAIN 1271 1384 KRINGLE TYPE IV, 12.
F DOMAIN 1385 1498 KRINGLE TYPE IV, 13.
F DOMAIN 1499 1612 KRINGLE TYPE IV, 14.
F DOMAIN 1613 1726 KRINGLE TYPE IV, 15.
F DOMAIN 1727 1840 KRINGLE TYPE IV, 16.
F DOMAIN 1841 1954 KRINGLE TYPE IV, 17.
F DOMAIN 1955 2068 KRINGLE TYPE IV, 18.
F DOMAIN 2069 2182 KRINGLE TYPE IV, 19.
F DOMAIN 2183 2296 KRINGLE TYPE IV, 20.
F DOMAIN 2297 2410 KRINGLE TYPE IV, 21.
F DOMAIN 2411 2524 KRINGLE TYPE IV, 22.
F DOMAIN 2525 2638 KRINGLE TYPE IV, 23.
F DOMAIN 2639 2752 KRINGLE TYPE IV, 24.
F DOMAIN 2753 2866 KRINGLE TYPE IV, 25.
F DOMAIN 2867 2980 KRINGLE TYPE IV, 26.
F DOMAIN 2981 3094 KRINGLE TYPE IV, 27.
F DOMAIN 3095 3208 KRINGLE TYPE IV, 28.
F DOMAIN 3209 3322 KRINGLE TYPE IV, 29.
F DOMAIN 3323 3436 KRINGLE TYPE IV, 30.
F DOMAIN 3437 3550 KRINGLE TYPE IV, 31.
F DOMAIN 3551 3664 KRINGLE TYPE IV, 32.
F DOMAIN 3665 3778 KRINGLE TYPE IV, 33.
F DOMAIN 3779 3892 KRINGLE TYPE IV, 34.
F DOMAIN 3893 3998 KRINGLE TYPE IV, 35.
F DOMAIN 3999 4112 KRINGLE TYPE IV, 36.
F DOMAIN 4113 4226 KRINGLE TYPE IV, 37.
F DOMAIN 4227 4340 KRINGLE TYPE V.
F DOMAIN 4341 4454 SERINE PROTEASE.
F DOMAIN 4455 4568 CHARGE RELAY SYSTEM.
F ACT SITE 4369 CHARGE RELAY SYSTEM.
F ACT SITE 4412 CHARGE RELAY SYSTEM.
F ACT SITE 4498 CHARGE RELAY SYSTEM.
F VARIANT 4193 W -> R (LOSS OF LYSINE-SEPHAROSE BINDING)
F SEQUENCE 4548 AA; 501313 MW; 96921BE96A465C5F CRC64;
F 21.2%; Score 478; DB 1; Length 4548;
F very Match

Best Local Similarity 36.0%; Pred. No. 5.5e-30;
Matches 129; Conservative 36; Mismatches 133; Indels 60; Gaps 17;
QY 50 CYEGNGHYRGKASTDTMGSPCLPWNATVLTQTYHAHRSDALQLGLGK-----HNYCRN 104
DB 4228 CMFGNGKGYRGKATVTGTPCQEW-----AAQEPHRSHTFIPGNKAGLEKKNYCRN 4280
QY 105 PD-NRRRPWCYVQGLKPLVQECNVHDCADGKLKFCQGKTLRPR---FKIIGSEFTTIE 160
DB 4281 PDGDIINGPWCYT-MNPRKLFYCDIPLCASS--SFDGCKPQVEPKPCPGSIGVGCVAHPH 4337
QY 161 NOPWFAALYRRHGGSVTYVCGGSLSPCWVTSATHCFIDYPKKEDYVVLGRSR---LN 217
DB 4338 SWPQVSL--RTRFGK--HFCGGTLSPWVLTAAHCKKSSRPSSFKVILGAHOEVNLE 4393
QY 218 SNTQENKFEVENLILHKDYSADTLAHHNDIALIKIRSKGRCQAQPSRTIQTICLPSPMYN 277
DB 4394 SHVQ---EIEVSRLEFLEPTQA-----DIALKL---SRPAVITDKVMPACLPS--- 4435
QY 278 DPQF----GTSCETGFGKENSVDLYPEOLKMTVVKLVSHRECCQPHYGVSEVTTQMLC 333
DB 4436 -PDMVTARTCEYITGWEVQGT--FGTGLKGAQLLVIEVCN--HY-----KYIC 4483
QY 334 AADPQWKTDCQSGDGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTVRVSHPFPMI 391
DB 4484 AEHLARGTDCQSGDGGPLVCFEKKDYLOGVTSWGLGCARPKNKPGYVARVSRFVTWI 4541

RESULT 29
ID APOA MACMU STANDARD; PRT; 1420 AA.
AC P14417;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment).
GN LPA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RX MEDLINE=89174660; PubMed=29256543;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.";
RL J. Biol. Chem. 264:5957-5965(1989).
CC -!- FUNCTION: Apo(a) is the main constituent of lipoprotein(a) (Lp(a)). It has serine proteinase activity and is able of autolysis. Inhibits tissue-type plasminogen activator 1.
CC Lp(a) may be a ligand for megalin/Gp 330.
CC -!- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and decorin (By similarity).
CC -!- PTM: N- and O-glycosylated (By similarity).
CC -!- DISEASE: Elevated plasma concentrations of apo(a) and its naturally occurring proteolytic fragments are correlated with atherosclerosis. Homology with plasminogen kringle IV and V is thought to underlie the atherogenicity of the protein, because the fragments are competing with plasminogen for fibrinogen binding.
CC -!- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved, leading to the formation of the so called mini-Lp(a). Apo(a) fragments accumulate in atherosclerotic lesions, where they may promote thrombogenesis. O-glycosylation may limit the extent of proteolytic fragmentation (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily. Contains at least 10 kringle domains.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announcement/> or send an email to license@isb-sib.ch).

EMBL: J04635; AAA36833.1; -
PIR: A32869; A32869.
HASP: P00747; 2PK4.
MEROPS: S01.226; -
InterPro: IPR009003; Cys_Ser_trypsin.
InterPro: IPR000001; Kringle.
InterPro: IPR001254; Peptidase_S1.
InterPro: IPR001314; Peptidase_S1A.
Pfam: PF00051; kringle; 1.
Pfam: PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
PRINTS: PR00018; KRINGLE.
ProDom: PD000395; Kringle; 10.
SMART: SM00130; KR; 10.
SMART: SM00020; Tryp_SPC; 1.
PROSITE: PS00021; KRINGLE 1; 10.
PROSITE: PS00070; KRINGLE 2; 10.
PROSITE: PS00240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; FALSE NEG.
PROSITE: PS00135; TRYPSIN_SER; FALSE NEG.
Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein;
Kringle; Repeat; Atherosclerosis.
NON_TER 1
DOMAIN 1 49 127 KRINGLE 1.
DOMAIN 2 163 241 KRINGLE 2.
DOMAIN 3 277 355 KRINGLE 3.
DOMAIN 4 391 469 KRINGLE 4.
DOMAIN 5 505 583 KRINGLE 5.
DOMAIN 6 619 697 KRINGLE 6.
DOMAIN 7 725 803 KRINGLE 7.
DOMAIN 8 839 917 KRINGLE 8.
DOMAIN 9 953 1031 KRINGLE 9.
DOMAIN 10 1067 1145 KRINGLE 10.
DOMAIN 1191 1420 SERINE PROTEASE.
SEQUENCE 1420 AA; 158367 MW; BE102949E03C5B0E CRC64;

ery Match 21.1%; Score 477; DB 1; Length 1420;
st Local Similarity 34.0%; Pred. No. 1.7e-30;
ches 129; Conservative 43; Mismatches 137; Indels 70; Gaps 15;

50 CYENGHYRKAATDTRGCLPWSATVLQ--QTHAHSRALQLGLKHYCRNPDN 107
1068 CYHNGQSYRGTFSTVTGRTCSQSSMTPHQKRTPEHFNDDLTN-----NYCRNPD 1122
108 RRRPWCYVQVGLKLVOS--QWVHDCAD-----GKLKFCQGO 142
1123 DTGWCFT---MDSVREYCNLRCSDTGTEVTPTVTPVPSLEAPSQASSPDCGK 1179
143 KTLRPR---FKIIGGEFTTIENQPFMAIYRRHGGSVTVYCGSLISPCWVISATHCFI 199
1180 PQVEPKKCFGSIYGCVAHPHSWPQVSL--RTRFGK--HPCGGTLISPEWVLTAAACLE 1235
200 DYPKKEDIVYVLRGR---LNSNTQGMKPEVENLILHKDYSADTLAHHNDIALLKIRSK 256
1236 TFSRFSFKVILGAHQVNLSEHVQ---EIEVSRLEFLEPGA-----DIALLKL--- 1281
257 EGRCAQPERT:QTICLPMSYNDPQF---GTSCEITGFGKENSTDIYLPQLKMTVVKLI 312
1282 -SRPAITDKVIPACLPs---PNVITAMTECVITGWEQTQT--FGAGLLKEAQLHVI 1334
313 SHRECCQPHYGVSEVTTKMLCAAPQWKTDSCQDSGGLYCSLQGRMTLTGIVSGRGC 372
1335 ENTVCNHFELNGRVYKSTELCAGHLAGGTDRCCQDNGGPPVCFDKYILRGITSWGPGC 1394
373 ALKDRPGYVTRVSHPLPI 391
1395 ACPNKEGVYVRSFVTWI 1413

RESULT 30
PLMN HORSE
ID PLMN HORSE STANDARD; PRT; 338 AA.
AC P80010;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=92052077; PubMed=1946332;
RA Schaller J., Straub C., Kaempfer U., Rickli E.E.;
RT "Complete amino acid sequence of equine miniplasminogen.";
RL Protein Seq. Data Anal. 4:69-74(1991).
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion, and
CC inflammation; in ovulation it weakens the walls of the Graafian
CC follicle. It activates the urokinase-type plasminogen activator,
CC collagenases and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
CC Willebrand factor.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Activated with catalytic amounts of streptokinase.
CC -!- MISCELLANEOUS: plasmin is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clot.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains at least 1 kringle domain.
DR PIR; A61545; A61545.
DR HSSP; P00747; SHEP.
DR MEROPS; S01.233; -
DR InterPro: IPR009003; Cys_Ser_trypsin.
DR InterPro: IPR000001; Kringle_
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR InterPro: IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
FT NON_TER 1
FT CHAIN <1 108 PLASMIN HEAVY CHAIN A.
FT CHAIN 109 338 PLASMIN LIGHT CHAIN B.
FT DOMAIN 9 88 KRINGLE 5.
FT DOMAIN 109 338 SERINE PROTEASE.
FT DISULFID 9 88 BY SIMILARITY.
FT DISULFID 30 71 BY SIMILARITY.
FT DISULFID 59 83 BY SIMILARITY.
FT DISULFID 95 213 INTERCHAIN (BY SIMILARITY).
FT DISULFID 105 113 INTERCHAIN (BY SIMILARITY).
FT DISULFID 135 151 BY SIMILARITY.
FT DISULFID 227 294 BY SIMILARITY.

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-!- TISSUE SPECIFICITY: Brian and Leydig cells of the testis.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 Kringle domain.
-!- SIMILARITY: Contains 4 SRCR domains.
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EMBL; AJ001531; CRA04816.1; -
EMBL; AF077298; AAD25919.1; -
HSSP; P00763; IDPO.
GeneW; HGNC:9477; PRSS12.
MIM; 606709; -
MEROPS; S01.237; -
GO; GO:0008236; F:serine-type peptidase activity; TAS.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00051; kringle; 1.
Pfam; PF00530; SRCR; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00258; SPERACTRCPTR.
ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
SMART; SM00202; SR; 4.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS00420; SRCR_1; 3.
PROSITE; PS00287; SRCR_2; 4.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; serine protease; Glycoprotein; Kringle; Repeat; Signal.
SIGNAL 1
CHAIN 1 875
FT CHAIN 21 875 NEUTROTRYPSIN.
FT DOMAIN 23 92 PRO-RICH.
FT DOMAIN 93 165 KRINGLE.
FT DOMAIN 170 271 SRCR 1.
FT DOMAIN 280 381 SRCR 2.
FT DOMAIN 387 487 SRCR 3.
FT DOMAIN 500 601 SRCR 4.
FT DOMAIN 619 875 SERINE PROTEASE.
FT DOMAIN 619 630 ZYMOGEN ACTIVATION REGION.
FT ACT_SITE 630 631 REACTIVE BOND (POTENTIAL).
FT ACT_SITE 676 676 CHARGE RELAY SYSTEM.
FT ACT_SITE 726 726 CHARGE RELAY SYSTEM.
FT ACT_SITE 825 825 CHARGE RELAY SYSTEM.
FT DISULFID 619 750 POTENTIAL.
FT CARBOHYD 26 26 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 683 683 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 663 663 A -> V (IN REF. 2).
FT CONFLICT 701 701 E -> V (IN REF. 2).
FT CONFLICT 839 841 WVY -> AAL (IN REF. 2).
FT CONFLICT 875 AA; 97011 MW; B66EC946DC208DC8 CRC64;
SEQUENCE 875 AA; 97011 MW; B66EC946DC208DC8 CRC64;
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Query Match 19.8%; Score 447; DB 1; Length 875;
Best Local Similarity 29.7%; Pred.No. 2.6e-28;
Matches 128; Conservative 60; Mismatches 155; Indels 88; Gaps 17;
-----
33 CPKFKGGQH-C-EIDKSKTCYEG-----NGHF--- 57
465 CSRQQRGHDCSHREDVSIACYPGGHGRLSLGFPVRLMDGNKKKGKRVVEIFNGQGTI 524
58 -----YRGKASTDTM---GRPCLPWNSATVLOQTVAHRSDSLALQGL 96

```

525 CDGWTDKDAVICRQLGYKPARARTMAVFGSGKPIHVDNVKCTGNSLADCIKQDI 584
 97 GKNNYCRNPDRRPPWYGVGLKPLVQECVNDHCDAG-----KLKPCQCGQKTLRPFK- 150
 585 GRN-CHSEADAGVICY--FGKK-----ASGNSNKESLSVCGRLUHRQRK 630
 151 IIGSEFTIENQPFIAIYRRHRGGSVYVCGSLISPCWVIGATCFIDYPRK-EDYIV 209
 631 IIGKNSLRGGWPQVSLRLKSSHGDRLLCGATLLSSCVLTAACHCFKYGNSRYSYAV 690
 210 YLGRSLRNSNTQGMKEVENLILHKDYSADTLAHNDIALIKRSKEGCAQPSITQI 269
 691 RVGDYHTLVPEEFEEIGVQIVIHREYRDRSDY--DIALVLQPEECARFSSHVL 748
 270 ICLFSMYNDPO-FGTSCEITGFGKENSTDYLYPEQLQNTVVKLISHRECCQPHYGVSEVT 328
 749 ACLPWRERPKTASNYITGNG---DTGRAYSETLQQAALPLPKFCEE--RYKGRFT 803
 329 TKMLCAAD--PQWNTDSCQDSGSGPLVCSLQGR-MTLGTIVSGRGCAKDKGVTRVS 395
 804 GRMLCAGNLHKEKVDSCQDSGSGPLCERPGESVWVYGVTSWGYGCVKXSPGVTRVS 863
 386 HFLPWIRSHTK 396
 864 AFVFWIKSVTK 874

IT 32
 MOUSE
 NEUTR MOUSE STANDARD; PRT; 761 AA.
 O0872;
 30-MAY-2000 (Rel. 39, Created)
 30-MAY-2000 (Rel. 39, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Neurotrypsin precursor (EC 3.4.21.-) (Motopsin) (Brain-specific serine
 protease 3) (BSSP-3).
 PRS12 OR BSGP3.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Brain;
 MEDLINE=97401523; PubMed=9245503;
 Geschwend T.P., Krueger S.R., Kozlov S.V., Wolter D.P., Sonderegger P.,
 "Neurotrypsin, a novel multidomain serine protease expressed in the
 nervous system.",
 Mol. Cell. Neurosci. 9:207-219(1997).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=98008948; PubMed=9344839;
 Yamamura Y., Yamashiro K., Teurukua N., Nakazato H., Tsujimura A.,
 Yamaguchi N.,
 "Molecular cloning of a novel brain-specific serine protease with a
 kringle-like structure and three scavenger receptor cysteine-rich
 motifs.",
 Biochem. Biophys. Res. Commun. 239:386-392(1997).
 [3]
 SEQUENCE FROM N.A.
 STRAIN=C57BL/6J; TISSUE=Mammary gland;
 MEDLINE=22388257; PubMed=12477932;
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Udell T.B., Roehlyuk S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihay S.J.,
 Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Pahey J., Helton E., Kettman M., Madao A., Rodrigues S., Sanchez A.,
 Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences",
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC - FUNCTION: Plays a role in neuronal plasticity and the proteolytic
 action may subserve structural reorganizations associated with
 learning and memory operations.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - TISSUE SPECIFICITY: Most abundant in cerebral cortex, hippocampus
 and amygdala.
 CC - SIMILARITY: Belongs to peptidase family S1.
 CC - SIMILARITY: Contains 1 kringle domain.
 CC - SIMILARITY: Contains 3 SRCR domains.
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 entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
 or send an email to license@isb-sib.ch).
 EMBL; Y13192; CAA73646.1; -
 EMBL; D89871; BAA23966.1; -
 EMBL; BC031429; AAH31429.1; -
 HSSP; P00763; 1DPO.
 MEROPS; S01.237; -
 MGD; MGI:1100881; Ptas12.
 InterPro; IPR009003; Cys_Ser_trypsin.
 InterPro; IPR000001; Kringle.
 InterPro; IPR001254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR001190; Srcr_receptor.
 Pfam; PF00051; Kringle; 1.
 Pfam; PF00530; SRCR; 3.
 Pfam; PF00089; trypsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 PRINTS; PR00256; SPERACTRCPTR.
 ProDom; PD000395; Kringle; 1.
 SMART; SM00130; KS; 1.
 SMART; SM00020; Tryp_Spc; 1.
 PROSITE; PS00021; KRINGLE_1; 1.
 PROSITE; PS00070; KRINGLE_2; 1.
 PROSITE; PS00420; SRCR_1; 3.
 PROSITE; PS00287; SRCR_2; 3.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.
 SIGNAL 1 21
 POTENTIAL
 CHAIN 22 761
 NEUTROTRYPsin.
 DOMAIN 85 157
 KRINGLE.
 FT DOMAIN 166 267
 SRCR 1.
 FT DOMAIN 273 373
 SRCR 2.
 FT DOMAIN 386 487
 SRCR 3.
 FT DOMAIN 505 761
 SERINE PROTEASE.
 FT DOMAIN 505 516
 ZINCEN ACTIVATION REGION.
 FT ACT_SITE 516 517
 REACTIVE BOND (POTENTIAL).
 FT ACT_SITE 562 562
 CHARGE RELAY SYSTEM.
 FT ACT_SITE 612 612
 CHARGE RELAY SYSTEM.
 FT ACT_SITE 711 711
 CHARGE RELAY SYSTEM.
 FT DISULFID 505 636
 POTENTIAL.
 FT CARBOHYD 93 93
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 521 521
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 569 569
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 761 AA; 84118 MW; DF507B03712164E6 CRC64;

Query Match 19.2%; Score 434; DB 1; Length 761;
est Local Similarity 29.0%; Pred. No. 2.5e-27;
atches 126; Conservative 62; Mismatches 159; Indels 88; Gaps 16;
C 28 IHCNCPKPGGQH-C--EIDKSKTCY-EGNGH-----56
I 346 VSPQSRQRQWGRHDSHREDVGLTCYPSDGHRLSPGPIRLVDGENKKEGRVEVFNAG 405
C 57 -----FYRKASDTTW---GRPCLPWN SATVLQQTTHAHRSDA 91
I 406 QWGTICDDGWTDXAAVIGCQLGYKGPARTWAFEGEGKGPIMHNDVXCTGNEKALADC 465
C 92 LQGLGHKNYCRPNDRRRPCVQ-----VGLKPLVQSCVHDCADGKLCQCGKTLR 146
I 466 VKQDIGHN-CRSEDAGVTCYLEKASSGNKEM-----LSSGCGRLRLH 511
C 147 PRFK-IIGGEFTIENQWPAALVYRHRGGSVTVCGSLIPSCWVISATHCFIDY-PRK 204
I 512 RQKRIIGNNLSRGAWPQASLRSAHGDGRLGATLSSCWLTAAHCFKRYGNN 571
C 205 EDIVYIGRLNSNTGEMKFEVENILHKYSADTLAHNDIALKTRSEKRCQAQPS 264
I 572 RSYAVRVDGYHTLVPEFEQEIYVQOVIHNRYPDRSDY--DIALVRLQGPGEQCARLS 629
C 265 RTIQTICLPSMYNDPO-FGTSCEITGFGKENSIDYLPKMTVVKLISHRECCQPHY 323
I 630 THVLPACLPWRREPQKTASCHITGW---DTGRAYSRTLQAAVPLPKFKCKE--RY 684
C 324 GSEVTRMLCAADPQW-KTDSQCGSGGGLVCLQGR-MTLGIVSWRGKALKDKPGV 380
I 685 KGLFTGRMLCAGNLQEDNRVDSQCGSGGLMCKEKPDESVMVYGVTSWGYCGVXKDPGV 744
C 381 YTRVSHPLPWIRSH 395
I 745 YTRVPAFPWIKSVT 759
ULT 33
F N ERIEU STANDARD; PRT; 810 AA.
Q29485;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, last sequence update)
28-FEB-2003 (Rel. 41, last annotation update)
Plasminogen precursor (EC 3.4.21.7).
PLG.
Erinaceus europaeus (Western European hedgehog).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
C NCBI_TaxID=9365;
F [1] -
F TISSUE=Liver;
F MEDLINE=96025778; PubMed=7592597;
F Lawn R.M., Boommark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
F Byrne C.D., Fong K.J., Meer K., Patchy L.,
F "The recurring evolution of lipoprotein(a). Insights from cloning of
F hedgehog apolipoprotein(a).";
F J. Biol. Chem. 270:24004-24009 (1995).
F [2]
F REVISIONS.
F Lawn R.M.;
F Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
F -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
F a proteolytic factor in a variety of other processes including
F embryonic development, tissue remodeling, tumor invasion, and
F inflammation; in ovulation it weakens the walls of the Graafian
F follicle. It activates the urokinase-type plasminogen activator,
F collagenases and several complement zymogens, such as C1 and C5.
F It cleaves fibrin, fibronectin, thrombospondin, laminin and von
F Willebrand factor.
F -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;

higher selectivity than trypsin. Converts fibrin into soluble
products.
-!- ENZYME REGULATION: Converted into plasmin by plasminogen
activators, both plasminogen and its activator being bound to
fibrin. Cannot be activated with streptokinase.
-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
immediately after dissociation from the clot.
-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Contains 5 kringle domains.
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EMBL; U33171; AAC48717.1; -
PIR; I46260; I46260.
HSP; P00747; 1PMK.
MEROPS; S01.233; -
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan app.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE 1; 5.
DR PROSITE; PS00070; KRINGLE 2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
FT DOMAIN 583 810 SERINE PROTEASE.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 185 262 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 379 456 KRINGLE 4.
FT DOMAIN 482 561 KRINGLE 5.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT CARBOHYD 339 339 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 810 AA; 90902 MW; 8E75780946017A16 CRC64;
Query Match 19.1%; Score 431; DB 1; Length 810;
Best Local Similarity 30.7%; Pred. No. 4.6e-27;
Matches 122; Conservative 49; Mismatches 157; Indels 70; Gaps 16;
QY 27 NIHW--CNCPKKFGQGHCEIDKS-----KTCVEGNHGFYRGKASTDTMGRPCL 72
DB 445 SVRWFECNLKCKSGTGMTSATNSSPVQVSSASESSQDCIIDNGKYGRTKATGTAGTPCQ 504
QY 73 PWN SATVLQQTTHA-----RSDALQLGLGHKNYCRPNDR--NRRPWCVTQVGLKPL 122

DF	PROSITE; PS01209; LDLRA_1; 1.	AC	O35453; Q9CWN7;
DF	PROSITE; PS0068; LDLRA_2; 3.	DT	15-JUL-1998 (Rel. 36, Created)
DF	PROSITE; PS0240; TRYPsin_DOM; 1.	DT	10-OCT-2003 (Rel. 42, Last sequence update)
DF	PROSITE; PS00134; TRYPsin_HIS; 1.	DT	10-OCT-2003 (Rel. 42, Last annotation update)
DF	PROSITE; PS00135; TRYPsin_SER; 1.	DE	Serine protease hepsin (EC 3.4.21.-).
KX	Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane;	GN	HPN
KX	Glycoprotein; Alternative splicing;	OS	Mus musculus (Mouse).
FT	DOMAIN 1 55	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
FT	TRANSMEM 56 76	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
FT		OX	NCBI_TaxID=10090;
FT		RN	[1] SEQUENCE FROM N.A. (ISOFORM 2).
FT		RP	SEQUENCE FROM N.A. (ISOFORM 2).
FT		RC	TISSUE=Liver;
FT		RX	MEDLINE=98058912; PubMed=9395459;
FT		RA	Vu T.-K.H., Liu R.W., Haakema C., Tonasek J.J., Howard E.W.;
FT		RA	"Identification and cloning of the membrane-associated serine
FT		RT	protease, hepsin, from mouse preimplantation embryos.";
FT		RL	Eur. J. Biol. Chem. 272:31315-31320(1997).
FT		RN	[2]
FT		RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
FT		RX	MEDLINE=99339944; PubMed=10411637;
FT		RA	Kawamura S., Kurachi S., Dayashiki Y., Kurachi K.;
FT		RT	"Complete nucleotide sequence, origin of isoform and functional
FT		RT	characterization of the mouse hepsin gene.";
FT		RL	Eur. J. Biochem. 262:755-764(1999).
FT		RN	[3]
FT		RP	SEQUENCE FROM N.A. (ISOFORM 1).
FT		RC	STRAIN=C57BL/6J; TISSUE=Kidney;
FT		RX	MEDLINE=21086560; PubMed=11217851;
FT		RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
FT		RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
FT		RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
FT		RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
FT		RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
FT		RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
FT		RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
FT		RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
FT		RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
FT		RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
FT		RA	Brownstein M.J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
FT		RA	Gustingich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
FT		RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
FT		RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
FT		RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
FT		RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
FT		RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
FT		RA	Hayashizaki Y.;
FT		RL	"Functional annotation of a full-length mouse cDNA collection.";
FT		RL	Nature 409:685-690(2001).
CC	-!- FUNCTION: Plays an essential role in cell growth and maintenance	CC	-!- of cell morphology.
CC	-!- SUBCELLULAR LOCATION: Type II membrane protein.	CC	-!- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;	CC	Name=1; Synonyms=1a;
CC	Isoid=Q35453-1; Sequence=Displayed;	CC	Note=Minor isoform;
CC	Name=2; Synonyms=2a;	CC	Isoid=Q35453-2; Sequence=VSP_007232;
CC	Note=Major isoform;	CC	-!- SIMILARITY: Belongs to peptidase family S1.
CC	-!- CAUTION: Ref.3 sequence differs from that shown due to	CC	frameshifts in positions 155, 191 and 233.
CC	-----	CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC	modified and this statement is not removed. Usage by and for commercial	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).	CC	-----
CC	-----	CC	-----
CC	EMBL; AF030065; AAB84221.1; --	CC	-----

QY	2	NELHQPNSDCLNGGTCVSNKYFSNIHWC-----NCPKFGGHCEDKSKTCVGGNGHF	57
DL	453	NQSDPCGCEFLCSVNGLCVPA-----CDGVKDCNGLDRCNCVCRATFQCKEDSTCI	504
QY	58	YRGKASTDTMGRP-CLPWSNATVLIQQ-----TYHAHRSDALQLGLGKKNYCRNPDRR	109
DL	505	SLPKVCD---QOPDCLNGSDEQCQGVPCGTFTFQCEDRSCKVK-----PNPQCDG	553
QY	110	RPWCVOVGLKPLVQECWHDCKLFCQKQNTLRPFKTIIGGFTTIENOPWFAAY	169
DL	554	RP-----DCRGSDEHCDGLOGPSSRIVGGAVSSGEPWQASLQ	595
QY	170	RRHGGSVTVYVCGSLISPCWVISATHCFIDYPKKED-----YIVYLGSRSLNSNTQG	222
DL	596	VRGR-----HICGALLIADRWITAAHCF-----QEDSMASITVLWTFLGKWNQSRWPG	645
QY	223	EMKPEVENLIHKDYSADTLAHNDIALKIRSEKGCAPQPSRTIOTICLPMSYNDPQFG	282
DL	646	EVSPKVELLHPHFEED---SHDYDVALLQLDHPVR-----SAARVPCVLPASHFEFG	699
QY	283	TSCEITGFG---KENSTDYLYPEQLKMTVKLISHRECCQPHYTGSEVITTMCAADPQWK	340
DL	700	LHCWITGVALREGGP---ISNALQKVDQLIPQDLCSEVRY---QVTPMLCAGYRKKG	754
QY	341	TDSCGGSGGLVLC-SLOGRMTLGIYSGWGCALKDKPGYITVSHFLPWIR	392
DL	755	KDACQGSGLPLVCKAUSGRWFLAGLSWGLGCGRPNYFGVYTRITGVISMIQ	807
RI	LT 36		
HF	HEPS_MOUSE		
II	STANDARD; PRT; 436 AA.		

EMBL; AK002694; BAB22289.2; ALT_FRAME.

HSP; P00763; IDPO.

MEROFS; S01.224; -.

MGI; 1196620; Hpn.

InterPro; IPR009003; Cys Ser trypsin.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1A.

InterPro; IPR001190; Src_rceptor.

Pfam; PF00089; trypsin; 1.

PRINTS; P00722; CHYMOTRYPSIN.

SMART; SM00202; SR; 1.

SMART; SM00202; TRYP_SPC; 1.

PROSITE; PS00240; TRYPsin DOM; 1.

PROSITE; PS00134; TRYPsin HIS; 1.

PROSITE; PS00135; TRYPsin SER; 1.

Hydrolase; Serine protease; Transmembrane; Signal-anchor;

Alternative splicing.

CHAIN 1 181

CHAIN 182 436

DOMAIN 21 36

TRANSMEM 37 63

EXTRACELLULAR (POTENTIAL).

SERINE PROTEASE, NON-CATALYTIC

CHAIN (POTENTIAL).

SERINE PROTEASE, CATALYTIC CHAIN

(POTENTIAL).

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).

EXTRACELLULAR (POTENTIAL).

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

Missing (in isoform 2).

FTid=VSP_007232.

L -> F (IN REF. 2 AND 3).

T -> Y (IN REF. 3).

G -> R (IN REF. 3).

NR -> ET (IN REF. 3).

P -> L (IN REF. 3).

H -> N (IN REF. 3).

SEQUENCE 436 AA; 46787 MW; 4A0993148C620BD0 CRC64;

very Match 18.5%; Score 417; DB 1; Length 436;

est Local Similarity 34.8%; Pred. No. 3e-26;

atches 111; Conservative 59; Mismatches 98; Indels 52; Gaps 18;

112 WCYVQVGLKPLVQECM----VHDCADGKLF---CQGGKTLRPRFKIIGGEFTTIENQP 163

137 FCVDEGL-FLAQLLDVISCDCPGEFLATQDCGRKL-FVDRIVGQDSGLGRWP 194

164 WFAALYRHRGSGVTYVCGSLISPCWVISATHCFIDYPKEDYI-----VVLGRSLNSN 219

195 WQVSL--RYDG---THLCGSLSGDWLTAHCF---PERNVLNRWRFVAG--AVART 244

220 TQGENKPEVNLILH-----KDYSDTLAHNDIALIKIRSEKGRCAQSPRTTQICLP 273

245 SPHAVQLGVAVIYHGGVLPDPFDID--ENSNDIALVHLS--LPLTEYIQVCLP 298

274 SMYNDPQGTGCEITFGKENSVDLYPEQ---LMTVVKLISHRECOQPHYGSEVTK 330

299 AAGQALVDGKVTWGTGNTQ----FYGQAVLQEARVPIISNEVCNSPDPFGNQIKPK 354

331 MLCRADPQWKTDSCGDSGGLVC--SLQG--RWLTGIVSGRCALKDKPGVTVRVSH 386

355 MFCAGYPEGIDACGDSGPGPVCBDSISGTSRWLGLGVWGTCCALARPGVTVTKTD 414

387 FLPW----IRSHKTEENGL 401

415 PREWIFKAIKTHS--EASGM 432

RESULT 37

TMS6 MOUSE

ID TMS6 MOUSE

AC Q9DBI0;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Transmembrane protease, serine 6 (EC 3.4.21.-) (Matrptase-2).

GN TMS6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.

RC STRAIN=C57BL/6J;

EX MEDLINE=22755759; PubMed=12744720;

RA Hooper J.D.; Campagnolo L.; Goodarzi G.; Truong T.N.; Stuhlmann H.;

RA Quigley J.P.;

RT "Mouse matritase-2: identification, characterization and comparative

RT mRNA expression analysis with mouse hepsin in adult and embryonic

RT tissues.";

RL Biochem. J. 373:689-702(2003).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Liver;

RX MEDLINE=22354683; PubMed=12468651;

RA Okazaki Y.; Furuno M.; Kasukawa T.; Adachi J.; Bono H.; Kondo S.;

RA Nakai I.; Osato N.; Saito R.; Suzuki H.; Yamanaka I.; Kiyosawa H.;

RA Yagi K.; Tomaru Y.; Hasegawa Y.; Nogami A.; Schonbach C.; Gojohori T.;

RA Baldarelli R.; Hill D.P.; Bult C.; Hume D.A.; Quackenbush J.;

RA Schriml L.M.; Kanapin A.; Matsuda H.; Batalov S.; Beisel K.W.;

RA Blake J.A.; Bradt D.; Brusic V.; Chothia C.; Corbani L.E.; Cousins S.;

RA Dalla E.; Dragani T.A.; Fletcher C.F.; Forrest A.; Frazer K.S.;

RA Gaasterland T.; Gariboldi M.; Gissi C.; Godzik A.; Gough J.;

RA Grimmond S.; Gustinchich S.; Hirokawa N.; Jackson I.J.; Jarvis E.D.;

RA Kanai A.; Kawai H.; Kawasaki Y.; Kedzierski R.M.; King B.L.;

RA Konagaya A.; Kurochkin I.V.; Lee Y.; Lenhard B.; Lyons P.A.;

RA Maglott D.R.; Maltais L.; Marchionni L.; McKenzie L.; Miki H.;

RA Nagashima T.; Numata K.; Okido T.; Pavan W.J.; Pertea G.; Pesole G.;

RA Petrovsky N.; Pillai R.; Pontius J.U.; Qi D.; Ramachandran S.;

RA Ravasi T.; Reed J.C.; Reed D.J.; Reid J.; Ring B.Z.; Ringwald M.;

RA Sandelin A.; Schneider C.; Semple C.A.; Setou M.; Shinada K.;

RA Sultana R.; Takenaka Y.; Taylor M.S.; Teasdale R.D.; Tomita M.;

RA Verardo R.; Wagner L.; Wahlestedt C.; Wang Y.; Watanabe Y.; Wells C.;

RA Wilming L.G.; Wyszewski-Boris A.; Yanagisawa M.; Yang I.; Yang L.;

RA Hirozane-Kishikawa T.; Konno H.; Nakamura M.; Sakazume N.; Sato K.;

RA Shiraki T.; Waki K.; Kawai J.; Aizawa K.; Arakawa T.; Fukuda S.;

RA Hara A.; Hashizume W.; Imotani K.; Iehli Y.; Itoh M.; Kagawa I.;

RA Miyazaki A.; Sakai K.; Sasaki D.; Shibata K.; Shinagawa A.;

RA Yasunishi A.; Yoshino M.; Waterston R.; Lander E.S.; Rogers J.;

RA Birney E.; Hayashizaki Y.;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;

RA Klausner R.D.; Collins F.S.; Wagner L.; Shellen C.M.; Schuler G.D.;

RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;

RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;

RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;

RA Brownstein M.J.; Udén T.B.; Toshiyuki S.; Carninci P.; Prange C.;

RA Raha S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullany S.J.;

RA Boeak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.D.; Hulyk S.W.;

RA Vallalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

RA Fahey J.; Helton E.; Kettman M.; Madan A.; Rodrigues S.; Sanchez A.;

RA Whitting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield I.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 R7 "Generation and initial analysis of more than 15,000 full-length human
 R1 and mouse cDNA sequences.";
 R1 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 R1 [4]
 RE REVIEW
 RX MEDLINE=2268120; PubMed=12784999;
 RA Netzel-Arnett S., Hooper J.D., Szabo R., Madison E.L., Quigley J.P.,
 RA Bugge T.H., Antalis T.M.;
 R1 "Membrane anchored serine proteases: a rapidly expanding group of cell
 R1 surface proteolytic enzymes with potential roles in cancer.";
 R1 Cancer Metastasis Rev. 22:237-258(2003).
 CC -!- FUNCTION: May play a specialized role in matrix remodeling
 CC processes in liver (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed at highest levels in liver, kidney
 CC and uterus.
 CC -!- DEVELOPMENTAL STAGE: Expressed at higher levels from 12.5 dpc to
 CC 15.5 dpc with a peak at 13.5 dpc. Expression in the developing
 CC liver as well as a restricted set of embryonic epithelial cells of
 CC the nasal cavity and pharyngo-tympanic tubes.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 2 CUB domains.
 CC -!- SIMILARITY: Contains 3 LDL-receptor class A domains.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 CC EMBL; AY240929; AAP69827.1; -;
 CC EMBL; AK004939; BAB23684.2; -;
 CC EMBL; BC029645; BAH29645.2; -;
 CC HSRF; P00763; IDPO.
 CC MEROPS; S01.308; -;
 CC MGD; MGI:1919003; TMPRSS6.
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR009003; Cys Ser trypsin.
 CC InterPro; IPR002172; LDL_receptor_A.
 CC InterPro; IPR001254; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1a.
 CC Pfam; PF00057; ldl_recept_a; 2.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00261; LDLRECEPTOR.
 CC PROSITE; PS01180; CUB; 1.
 CC PROSITE; PS01209; LDLRA_1; 1.
 CC PROSITE; PS00068; LDLRA_2; 3.
 CC PROSITE; PS00240; TRYPsin_DOM; 1.
 CC PROSITE; PS00134; TRYPsin_HIS; 1.
 CC PROSITE; PS00135; TRYPsin_SER; 1.
 CC Hydrolase; Serine protease; Repeat; Signal-anchor; Transmembrane;
 CC Glycoprotein.
 CC DOMAIN 1 59 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 60 80 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 CC (POTENTIAL).
 CC DOMAIN 81 811 EXTRACELLULAR (POTENTIAL).
 CC DOMAIN 213 336 CUB 1.
 CC DOMAIN 323 440 CUB 2.
 CC DOMAIN 445 477 LDL-RECEPTOR CLASS A 1.
 CC DOMAIN 478 514 LDL-RECEPTOR CLASS A 2.
 CC DOMAIN 518 555 LDL-RECEPTOR CLASS A 3.
 CC DOMAIN 565 799 SERINE PROTEASE.
 CC ACT SITE 617 617 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT SITE 668 668 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC ACT SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC CARBOHYD 138 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 216 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 433 433 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 518 518 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 690 P -> PP (IN REF. 2).
 SQ SEQUENCE 811 AA; 90978 MW; 32EB3E7C3127801B CRC64;
 Query Match 18.4%; Score 415.5; DB 1; Length 811;
 Best Local Similarity 37.0%; Pred. No. 8.2e-26;
 Matches 102; Conservative 47; Mismatches 90; Indels 37; Gaps 11;
 QY 130 DCADG--KLKPCQCGKTLRPRFKIIGFETIENQPFWFAIYRHRHGGSVTVYCGGLSIS 187
 Db DCRDGSDECHDCGLQLSSR--IVGGTVSEGEWPMQASLQIRGR-----HICGGALIA 608
 QY 198 PCWISATHCIDYPKED-----YIVYLGRSLNSNTGEMKKEVENLIHKDYSD 240
 Db DRWVITAAHCF-----QEDSWASPKLMTVFLGKQRQSRWPGEVSVKVSRLFLHPYHEED 663
 QY 241 TLAHNDIALLKIRSKGRCQAQP---SRTIQTICLPMSYNDPQFGTSCETITFGKENSST 297
 Db --SHDYDVALQL-----DHPVVYSATVRPCLPARSHFFEPQCHCWITGWAQREGG 714
 QY 298 VLYPEQLKMTVVKLISHRECOQPHYGVSEVTTMLCAADPQWKTDSCGDSGGILVC-SL 356
 Db PV-SNTLOKVDVQLVPDLCSEAYRY--QVSPRLCAGYRKGDACQDGGSGPLVCREP 771
 QY 357 QGRMTLTGIVSWGRGCAKDKPGVYTVRSHPLPWIR 392
 Db SCRWFAGLVNGLGCGRPNFFGVYTVTRVINMIQ 807
 RESULT 38
 PSS8 HUMAN STANDARD; PRT; 343 AA.
 AC Q16651; Q9UCA3;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Proctasin precursor (EC 3.4.21.-).
 GN PRS88.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Prostate;
 RX MEDLINE=95286644; PubMed=7768952;
 RA Yu J.X., Chao L., Chao J.;
 RT "Molecular cloning, tissue-specific expression, and cellular
 RL localization of human proctasin mRNA.";
 RN J. Biol. Chem. 270:13483-13489(1995).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton J., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3].

SEQUENCE OF 45-64.

TISSUE=semen;

MEDLINE=94308140; PubMed=8034538;

Yu J.X., Chao L.J.; "Proctasin is a novel human serine proteinase from seminal fluid. Purification, tissue distribution, and localization in prostate gland"; Chem. 269:18843-18848(1994).

J. Biol.

-!- FUNCTION: Possesses a trypsin-like cleavage specificity.

-!- SUBUNIT: Heterodimer of two chains, light and heavy, held by a disulfide bond.

-!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. SECRETED AFTER CLEAVAGE OF ITS C-TERMINUS.

-!- TISSUE SPECIFICITY: Found in prostate, liver, salivary gland, kidney, lung, pancreas, colon, bronchus and renal proximal tubular cells. In the prostate gland it may be synthesized in epithelial cells, secreted into the ducts, and excreted into the seminal fluid.

-!- SIMILARITY: Belongs to peptidase family S1.

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EMBL; L41351; AAC41759.1; --
EMBL; U33446; AAB19071.1; --
EMBL; BC001462; AAB01462.1; --
PIR; A57014; A57014.
HSP; P00763; LDPO.
MEROPS; S01.159; --
Gene; HGNC:9491; PRSS8.
MIM; 600823; --
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Zymogen; Signal; Glycoprotein; Transmembrane.

SIGNAL	1	29
PROPEP	30	32
CHAIN	33	44
CHAIN	45	322
PROPEP	323	343
TRANSMEM	320	340
DOMAIN	45	286
DISULFID	37	154
DISULFID	70	86
DISULFID	168	244
DISULFID	201	223
DISULFID	234	262
ACT_SITE	85	85
ACT_SITE	134	134
ACT_SITE	238	238
CARBOHYD	159	159

POTENTIAL.
ACTIVATION PEPTIDE.
PROSTATIN LIGHT CHAIN.
PROSTATIN HEAVY CHAIN.
POTENTIAL.
SERINE PROTEASE.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.
N-LINKED (GLCNAC. . .) (POTENTIAL).

```

SQ SEQUENCE 343 AA; 36431 MW; 98DD6447F5A8C1E2 CRC64;
Query Match 18.1%; Score 408.5; DB 1; Length 343;
Best Local Similarity 36.6%; Pred. No. 1.1e-25;
Matches 100; Conservative 36; Mismatches 100; Indels 37; Gaps 8;

QY 140 CQKTLRPFKIIGGEFTTINQWFAAIYRRHGGSVTY-----VCGGSLISPCWVTSAT 195
DQ 37 CG---VAPQARITGSSAVAGQWPQV-----SITVEGVHVCGGSLVSEQWLSAA 84
QY 196 HCFIDVPKEDYIVYLGSRSLNSNTQGBMKPEVENLILHKDYSADTLAHENDALLKIRS 255
DQ 85 HCFPSEHHKEAVEVKGHAHQDLSVEDAKVSTLKDIIHPHSYLQE--GSGQDIALLOL-- 140
QY 256 KEGRCQAQPSRTIQTICLSMYNDPQFGTSCBITGFGK-ENSTDYLYPEQLKMTVVKLISH 314
DQ 141 --SRPITTSRYIRPICLPAANASFPNGHLHCTVTGTGHWAPSVSLITPKPLQQLQEVPLIS 198
QY 315 REC-----QOPHYVGSSEVTKMLCAADPOKWTSCQGGSGGGLVCSLQGRMTLTG 364
DQ 199 EFCNGLYNIDAKPEBPHF----VQEDMVACGVGGKDKACQGGSGGLPCFVPELWYLTG 254
QY 365 IVSWRGCGALKDPGVYTRVSHFLFWIRSHTKPE 397
DQ 255 IVSWGDACARRPGVYTLASSVASWISQSKVTE 287

RESULT 39
KAL_MOUSE
ID KAL_MOUSE STANDARD; PRT; 638 AA.
AC F26262;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasma kallikrein precursor (EC 3.4.21.34) (Plasma prekallikrein)
DE (Kininogenin) (Fletcher factor).
DE KUKBI OR KUK3 OR PK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=91090844; PubMed=2264928;
RA Seidah N.G., Sawyer N., Hamelin J., Mion P., Beaubien G.,
RA Brachepa L., Rochemont J., Mbikay M., Chretien M.;
RT "Mouse plasma kallikrein: cDNA structure, enzyme characterization,
RT and comparison of protein and mRNA levels among species.";
RL DNA Cell Biol. 9:737-748(1990).
CC -!- FUNCTION: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It
CC activates, in a reciprocal reaction, factor XII after its binding
CC to a negatively charged surface. It also releases bradykinin from
CC HMW kininogen and may also play a role in the renin-angiotensin
CC system by converting prorenin into renin.
CC -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Xaa and Lys-|-Xaa
CC bonds, including Lys-|-Arg and Arg-|-Ser bonds in (human)
CC kininogen to release bradykinin.
CC -!- SUBUNIT: The zymogen is activated by factor XIIa, which cleaves
CC the molecule into a light chain, which contains the active site,
CC and a heavy chain, which associates with HMW kininogen. These
CC chains are linked by one or more disulfide bonds.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasma kallikrein
CC subfamily.
CC -!- SIMILARITY: Contains 4 apple domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).

```

CC EMBL; M59588; AAA63393.1; --
DR PIR; A36557; KONSPL.
DR HGSP; P00750; IATF.
DR MEROPS; S01.212; Kikbl.
DR MGD; MGI:102849; Kikbl.
DR InterPro; IPR00177; Apple.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00024; PAN; 4.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00005; APPLIEDOMAIN.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00223; APPLE; 4.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00495; APPLE; 4.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Plasma; Zymogen; Signal;
KW Fibrinolytic; Blood coagulation; Inflammatory response; Liver;
KW Repeat.
FT SIGNAL 1 19
FT CHAIN 20 390 PLASMA KALLIKREIN HEAVY CHAIN.
FT CHAIN 391 638 PLASMA KALLIKREIN LIGHT CHAIN.
FT DOMAIN 120 105 APPLE 1.
FT DOMAIN 110 195 APPLE 2.
FT DOMAIN 200 285 APPLE 3.
FT DOMAIN 291 376 APPLE 4.
FT DOMAIN 389 621 SERINE PROTEASE.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 453 453 O-LINKED (PROBABLE).
FT CARBOHYD 434 434 N-LINKED (GLCNAC. . .) (PROBABLE).
FT ACT_SITE 434 434 CHARGE RELAY SYSTEM.
FT ACT_SITE 483 483 CHARGE RELAY SYSTEM.
FT ACT_SITE 578 578 CHARGE RELAY SYSTEM.
FT DISULFID 21 104 BY SIMILARITY.
FT DISULFID 47 77 BY SIMILARITY.
FT DISULFID 51 57 BY SIMILARITY.
FT DISULFID 111 194 BY SIMILARITY.
FT DISULFID 137 166 BY SIMILARITY.
FT DISULFID 141 147 BY SIMILARITY.
FT DISULFID 201 284 BY SIMILARITY.
FT DISULFID 227 256 BY SIMILARITY.
FT DISULFID 231 237 BY SIMILARITY.
FT DISULFID 292 375 BY SIMILARITY.
FT DISULFID 318 347 BY SIMILARITY.
FT DISULFID 322 328 BY SIMILARITY.
FT DISULFID 340 345 BY SIMILARITY.
FT DISULFID 383 503 BY SIMILARITY.
FT DISULFID 419 435 BY SIMILARITY.
FT DISULFID 517 584 BY SIMILARITY.
FT DISULFID 548 563 BY SIMILARITY.
FT DISULFID 574 602 BY SIMILARITY.
SQ SEQUENCE 638 AA; 71368 MW; CC27C93AB1086599 CRC64;

ery Match 18.1%; Score 407.5; DB 1; Length 638;
st Local Similarity 33.1%; Pred No. 2.7e-25;
tches 93; Conservative 56; Mismatches 107; Indels 25; Gaps 8;

QY 126 CAVHDCAGKLFQCGQKTLPRKFIIGETTTIENOPWFAIYRHRGGSVTVCGSL 185
Df 375 CKLVDSPD-----C---TTKINARIVGTTNAGLGPWQVSL--QVKLVSTQLCGGSI 423
QY 186 ISPCWVIGATHCFIDYRKEDYIVYLGSRSLNSQTGEMKFEVENLILHKDYSDATLAHH 245
Df 424 IGRQWLPAACFGDIPDPVWRVYGGILSSEITKETPSSRIKELIHQEKYS--EGN 481
QY 246 NDIALKIRSEGRCAQPSRTIQTICLPSMYNDPFGTSCBITGFG---KENSTDYLYPE 302

Db 482 YDIALIKLQTP-----LNYTEFQKICLPSKADTNTIYTNWVTGWGTYKEQGETQNI--- 534
QY 303 QKMTVVKLISHRECCQPHYVGSVTTKMLCAADPQWKTDSCQDSDGGLVCSLQGRWTL 362
Db 535 -LQKATPLVNEECQK-KYRDYVINKQMICAGYKEGTDACKDSDGGLVCKHSGRWL 592
QY 363 TGVSWGRGCALKDKPGVYTRVSHFLPWIRSHYKKEENGLAL 403
Db 593 VGIISWGECCGRKDPQGVYTKVSEYMDWILEKTSQSDVRAL 633
RESULT 40
TMSS_MOUSE
ID TMSS_MOUSE STANDARD; PRT; 455 AA.
AC Q9ER04; Q9ER02; Q9ER03;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
GN TMPS5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "cDNA cloning of mouse spinesin."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 4).
RC TISSUE=Brain;
RA Mitsui S., Yamaguchi N.;
RT "Molecular cloning of mouse type 4 spinesin."
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -! SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -! ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=4;
CC Name=4;
CC IsoId=Q9ER04-1; Sequence=Displayed;
CC Name=1;
CC IsoId=Q9ER04-2; Sequence=VSP_005397, VSP_005398;
CC Name=2;
CC IsoId=Q9ER04-3; Sequence=VSP_005395;
CC Name=3;
CC IsoId=Q9ER04-4; Sequence=VSP_005396;
CC -! SIMILARITY: Belongs to peptidase family S1.
CC -! SIMILARITY: Contains 1 SRCR domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB016229; BAB20276.1; --
DR EMBL; AB016230; BAB20277.1; --
DR EMBL; AB016423; BAB20278.1; --
DR EMBL; AB041037; BAB40328.1; --
DR HSSP; P00763; 1DPO.
DR MEROPS; S01.313; --
DR MGD; MGI:1933407; Tmpres5.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_Spc; 1.

D PROSITE; PS00240; TRYPSIN DOM; 1.
E PROSITE; PS00134; TRYPSIN HIS; 1.
F PROSITE; PS00135; TRYPSIN SER; 1.
D PROSITE; PS00420; SRCR_1; FALSE_NEG.
F PROSITE; PS00287; SRCR_2; 1.
F Hydroxylase; Serine protease; Transmembrane; Signal-anchor;
F Glycoprotein; Alternative splicing.
F DOMAIN 1 49 CYTOPLASMIC (POTENTIAL).
F TRANSMEM 50 70 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
F DOMAIN 71 455 EXTRACELLULAR (POTENTIAL).
F DOMAIN 112 207 SRCR.
F DOMAIN 218 455 SERINE PROTEASE.
F ACT_SITE 258 308 CHARGE RELAY SYSTEM (BY SIMILARITY).
F ACT_SITE 308 308 CHARGE RELAY SYSTEM (BY SIMILARITY).
F ACT_SITE 405 405 CHARGE RELAY SYSTEM (BY SIMILARITY).
F SITE 217 218 CLEAVAGE (POTENTIAL).
F DISULFID 135 195 BY SIMILARITY.
F DISULFID 148 206 BY SIMILARITY.
F DISULFID 209 328 BY SIMILARITY.
F DISULFID 243 259 BY SIMILARITY.
F DISULFID 374 390 BY SIMILARITY.
F DISULFID 401 429 BY SIMILARITY.
F CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 319 319 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 375 375 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 375 375 Missing (in isoform 2).
F VARSPLIC 1 144 /Ftid=VSP_005395.
F VARSPLIC 1 10 Missing (in isoform 3).
F VARSPLIC 1 182 /Ftid=VSP_005396.
F VARSPLIC 1 182 /Ftid=VSP_005397.
F VARSPLIC 183 192 /Ftid=VSP_005398.
F VARSPLIC 325 325 D -> G (IN REF. 1; BAB20277).
F CONFLICT 325 325
F SEQUENCE 455 AA; 49632 MW; 50FC31789C6899AA CRC64;
18.08; Score 406.5; DB 1; Length 455;
1st Local Similarity 29.38; Pred. No. 2.2e-25;
atches 120; Conservative 55; Mismatches 132; Indels 103; Gaps 16;
32 NCPKFGQGHCEIDKSKTCYEGNGHYRKGASTDTMGRPLCP-----WNSATVLOQTVH 85
92 NCP-----GVSCBEL-----LPSLPKTVSPRINGEDLLQLQVQV 125
86 AHRSDALQL-----GLGKHYCNPNDR-----RPMCYVGVGLKP-- 121
126 RARPDWLLVCHEGWSPALGMH-ICKSLGHLRLQTHKAVNLSDIKLNRQFAQLSARPGG 184
122 LVQECM--VHDCADGKLK----FQCGQKTLRPFKTIIGGEFTTIENQPWFAATYRRHGG 175
185 LVEAWKPSANCPSPGRIVSLKSCGCGARPLASR--IVGQAVASGRWFWQASVNLGSR-- 240
176 SVTVCGSLSPCWVTSATHCPIDYPKEDYIVLGRSLNS-----NTQ 221
241 ---HTCGASVLAPHVWVTAACHMYSF-----RLSLSSWRVHAGLVSHGAVRQHQ 287
222 GEMKPEVENLILHKDYADTLAHENDIALKIRSKRCACQPSRTIOTICLPSPWINDPQF 281
288 GTM---VEKIIPHLYSAQN--HDYDVALLQLRTP----INFSTVDVAVCLPAKEQYFPW 338
282 GTSCEITGFKENSTDYLYPQLKMTVVVKLISHRECQOPHYGEVTTKMLCAADPOKWT 341
339 GSQCWVSGWGTDPDPSHTSSDTLQDTWVPLLSLTHLNCSSCMYSGALLTHRLMCLCAGYLDGRA 398
342 DSCQDSGGPVLCSLQGRMTLTGVSWGRGALKDKPGVYTRVSHFLPWI 391
399 DACQDSGGPLVCFPSGDTWHLVGVVSWGRGCAENRFGVAKVAEFLDWI 448
very Match
1st Local Similarity 29.38; Pred. No. 2.2e-25;
atches 120; Conservative 55; Mismatches 132; Indels 103; Gaps 16;
32 NCPKFGQGHCEIDKSKTCYEGNGHYRKGASTDTMGRPLCP-----WNSATVLOQTVH 85
92 NCP-----GVSCBEL-----LPSLPKTVSPRINGEDLLQLQVQV 125
86 AHRSDALQL-----GLGKHYCNPNDR-----RPMCYVGVGLKP-- 121
126 RARPDWLLVCHEGWSPALGMH-ICKSLGHLRLQTHKAVNLSDIKLNRQFAQLSARPGG 184
122 LVQECM--VHDCADGKLK----FQCGQKTLRPFKTIIGGEFTTIENQPWFAATYRRHGG 175
185 LVEAWKPSANCPSPGRIVSLKSCGCGARPLASR--IVGQAVASGRWFWQASVNLGSR-- 240
176 SVTVCGSLSPCWVTSATHCPIDYPKEDYIVLGRSLNS-----NTQ 221
241 ---HTCGASVLAPHVWVTAACHMYSF-----RLSLSSWRVHAGLVSHGAVRQHQ 287
222 GEMKPEVENLILHKDYADTLAHENDIALKIRSKRCACQPSRTIOTICLPSPWINDPQF 281
288 GTM---VEKIIPHLYSAQN--HDYDVALLQLRTP----INFSTVDVAVCLPAKEQYFPW 338
282 GTSCEITGFKENSTDYLYPQLKMTVVVKLISHRECQOPHYGEVTTKMLCAADPOKWT 341
339 GSQCWVSGWGTDPDPSHTSSDTLQDTWVPLLSLTHLNCSSCMYSGALLTHRLMCLCAGYLDGRA 398
342 DSCQDSGGPVLCSLQGRMTLTGVSWGRGALKDKPGVYTRVSHFLPWI 391
399 DACQDSGGPLVCFPSGDTWHLVGVVSWGRGCAENRFGVAKVAEFLDWI 448
ID KLKD_HUMAN STANDARD; PRT; 277 AA.
AC Q9UKR3; Q9Y433;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Kallikrein 13 precursor (EC 3.4.21.-) (Kallikrein-like protein 4)
(KUK-L4).
GN KUK13 OR KUKL4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20229789; PubMed=10766816;
RA Yousef G.M., Chang A., Diamandis E.P.;
RT "Identification and characterization of KUK-L4, a new kallikrein-like
gene that appears to be down-regulated in breast cancer tissues";
J. Biol. Chem. 275:11891-11898(2000).
RL [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
RA Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Ganes J.,
RA Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu S.,
RA Andreise T., Frankheim M., Attix C., Amico-Keller G., Coefield J.,
RA Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
RA Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,
RA Olsen A.S., Carrano A.V.;
RT "Sequence analysis of chromosome 19q13.4";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-180 FROM N.A.
RC TISSUE=Uterus;
RA Anserge W., Wirkner U., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Expressed in prostate, breast, testis and
salivary gland.
CC -!- SIMILARITY: Belongs to peptidase family S1. Kallikrein subfamily.
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or send an email to license@isb-sib.ch).
CC EMBL; AF135024; AAD26425.2; -;
DR EMBL; AC011473; AAG33259.1; -;
DR EMBL; AL050220; CAB43320.1; ALT_INIT.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.306; -;
DR Genew; HGNC:6361; KUK13.
DR MIM; 605505; -;
DR GO; GO:0005576; Cxetracellular; NAS.
DR GO; GO:0004252; F-serine-type endopeptidase activity; NAS.
DR GO; GO:0006508; P-proteolysis and peptidolysis; NAS.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00689; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydroxylase; Serine protease; Glycoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 277 KALLIKREIN 13.
FT ACT_SITE 76 76 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 124 124 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT

FT ACT_SITE 218 218 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 42 178 BY SIMILARITY.
 FT DISULFID 61 177 BY SIMILARITY.
 FT DISULFID 157 224 BY SIMILARITY.
 FT DISULFID 189 203 BY SIMILARITY.
 FT DISULFID 214 239 BY SIMILARITY.
 FT CARBOHYD 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 170 180 VNYPKTLQCAN -> GHHPHRWPEAP (IN REF. 3).
 SQ SEQUENCE 277 AA; 30570 MW; BAB9B8DFB5D542 CRC64;
 seq Match 17.9%; Score 405; DB 1; Length 277;
 st Local Similarity 41.1%; Pred. No. 1.7e-25;
 ches 101; Conservative 34; Mismatches 81; Indels 30; Gaps 10;
 Qy 153 GGEFTTTEPFAAIYRRHGGSVTVCGGSLISPCWVISAICHIDIPKEDYIVYLG 212
 Db 38 GGYTCFPHSQPWAALVQGR-----LLCGVLVHPKWLTAACHL-----REGKLVYLG 87
 Qy 213 RSLRNSNTQCEMKFEVENLILKDY--SADTLAHHNDIALKRSKEGRCQAQPSRIQTI 270
 Db 88 KHALGRVEAGEQVREVHSHIPHEYSRSPHLNHDHIMLELQSP-----VQLTGYIQI- 142
 Qy 271 CLPSMYND---PQGTSCBITGFKENSTYLYPEQLAMTVVKLISHRECCQPHYGVSEV 327
 Dt 143 -LPLSHNNRLTP--GTTCTRVSGWGTTSPOVNPYKTLQCANIQLSDECRQ--VYPGKI 197
 Qy 328 TTKMLCAADPOWTKDSQGGSGGLVCSLQGRMTLGTIVSGWR-GCALKDXPGVYTRVSH 386
 Db 198 TDNMLCAGTRGGKSGGGLVCSN-----RTLYGIVSGWDFPGQDPGPGVYTRVSR 253
 Qy 387 FLPMIR 392
 Dt 254 YVLWIR 259
 RE JT 42
 HE HUMAN
 ID HEPES HUMAN STANDARD; PRT; 417 AA.
 AC P05981,
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Serine protease hepsin (EC 3.4.21.-) (Transmembrane protease, serine
 1).
 GN HPN OR TMPSR51.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RI SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=88209431; PubMed=2835076;
 RT Leytus S.P., Loeb K.R., Hagen F.S., Kurachi K., Davie E.W.;
 R1 "A novel trypsin-like serine protease (hepsin) with a putative
 transmembrane domain expressed by human liver and hepatoma cells.";
 RL Biochemistry 27:1067-1074 (1988).
 RN [2]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Pancreas, and Spleen;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marushina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.D.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skaleks U., Smallus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.;
 "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=91358502; PubMed=1885621;
 RA Tsui A., Torres-Rosado A., Arai T., le Beau M.M., Lemons R.S.,
 Chou S.H., Kurachi K.;
 RT "Hepsin, a cell membrane-associated protease. Characterization,
 tissue distribution, and gene localization.";
 J. Biol. Chem. 266:16948-16953 (1991).
 RL [4]
 RP CHARACTERIZATION.
 RX MEDLINE=93348237; PubMed=8346233;
 RA Torres-Rosado A., O'Shea K.S., Tsui A., Chou S.H., Kurachi K.;
 RT "Hepsin, a putative cell-surface serine protease, is required for
 mammalian cell growth.";
 Proc. Natl. Acad. Sci. U.S.A. 90:7181-7187 (1993).
 RL -!- FUNCTION: Plays an essential role in cell growth and maintenance
 of cell morphology.
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -!- TISSUE SPECIFICITY: Present in most tissues, with the highest
 level in liver.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC
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 CC
 CC EMBL; M18930; AAA36013.1; .
 DR EMBL; X07732; CAA30558.1; .
 DR EMBL; X07002; CAA30058.1; .
 DR EMBL; BC025716; AAH25716.1; .
 DR F01; S00845; S00845.
 DR HSP; P00763; IDPO.
 DR MEROPS; S01.224; .
 DR Genew; HGNC:5155; HPN.
 DR MIM; 142440; .
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0008236; F:serine-type peptidase activity; TAS.
 DR GO; GO:0008151; P:cell growth and/or maintenance; TAS.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolyase; Serine protease; Transmembrane; Signal-anchor.
 FT CHAIN 1 162
 FT SERINE PROTEASE HEPSPIN, NON-CATALYTIC
 FT CHAIN (POTENTIAL).
 FT SERINE PROTEASE HEPSPIN, CATALYTIC CHAIN
 FT (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT SERINE PROTEASE.
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 203 203
 FT ACT_SITE 257 257
 FT ACT_SITE 353 353

KW Fibrinolysis; Blood coagulation; Inflammatory response; Liver;
Repeat; Polymorphism.

FT SIGNAL 1 19

FT CHAIN 20 390 PLASMA KALLIKREIN HEAVY CHAIN.

FT CHAIN 391 638 PLASMA KALLIKREIN LIGHT CHAIN.

FT DOMAIN 20 105 APPLE 1.

FT DOMAIN 110 195 APPLE 2.

FT DOMAIN 200 285 APPLE 3.

FT DOMAIN 291 376 APPLE 4.

FT DOMAIN 389 621 SERINE PROTEASE.

FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .)

FT CARBOHYD 308 308 N-LINKED (GLCNAC. . .)

FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .)

FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .)

FT CARBOHYD 494 494 N-LINKED (GLCNAC. . .)

FT ACT SITE 434 434 CHARGE RELAY SYSTEM.

FT ACT SITE 483 483 CHARGE RELAY SYSTEM.

FT ACT SITE 578 578 CHARGE RELAY SYSTEM.

FT DISULFID 21 104

FT DISULFID 47 77

FT DISULFID 51 57

FT DISULFID 111 194

FT DISULFID 137 166

FT DISULFID 141 147

FT DISULFID 201 284

FT DISULFID 227 256

FT DISULFID 231 237

FT DISULFID 292 375

FT DISULFID 318 347

FT DISULFID 322 328

FT DISULFID 340 345

FT DISULFID 383 503

FT DISULFID 419 435

FT DISULFID 517 584

FT DISULFID 548 563

FT DISULFID 574 602

FT VARIANT 143 143

FT VARIANT 178 178

FT VARIANT 202 202

FT VARIANT 208 208

FT VARIANT 269 269

FT VARIANT 311 311

FT VARIANT 358 358

FT VARIANT 381 381

FT VARIANT 442 442

FT VARIANT 560 560

FT SEQUENCE 638 AA; 71369 MW; 862F9C1053838F84 CRC64;

try Match 17.8%; Score 402; DB 1; Length 638;

at Local Similarity 33.1%; Pred. No. 7.6e-25;

ches 88; Conservative 56; Mismatches 98; Indels 24; Gaps 7;

144 TLPRFKLIGETIENQPPFAIY-----RRHGGSVTVCGGSLISPCWISATHCF 198

384 TTKTSTRVGGTNSWGWPMQVSLKVLTAQRH-----LGGSLIGHQWLVTAHCF 436

199 IDPKKEDYIYGLGRSLNSNTQEMFVENLILHKDYSADTLAHNDIALKIRSKG 258

437 DGLPLQDVWRIYSGILNSLDTKTPPSQIKELIHHQNYKVSQGNH--DIALIKLQAP-- 492

259 RQAQPSRTIQICLPSMYNDPQTSCEITGFG--KENSSTDYLPQGLKMTVVKLSHRE 316

493 --LNYTFEQKICLPSKSGDSTIYTNCTWGTWGFSEKGE---IQNLQKVNPLVTNEE 547

1000

QY 317 CQPHYGVSEVTTKMLCAADPQWKTDSCQDPSGGLVCSLQGRMTLTGIVSWGRGCALKD 376

DB 548 CQK-RYQDYKITQRMVCAVKEGKGKDGKSGGLVCKNGWRLVIGITSWEGGCARRE 606

QY 377 KPGYTVRSHLPWIRSHTRKEENGLA 402

DB 607 QPGYTKVAYEYMDWILEKTSOSDGA 632

RESULT 44

ST14 HUMAN

ID ST14 HUMAN STANDARD; PRT: 855 AA.

AC Q915F6; Q9BS01; Q9H3S0; Q9HB36; Q9HCA3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 10-OCT-2003 (Rel. 42, Last annotation update)

DE Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Membrane-

DE type serine protease 1) (MT-SP1) (Prostamin) (Serine protease TADG-15)

DE (Tumor associated differentially-expressed gene-15 protein).

GN ST14 OR PRSS14 OR SNC19 OR TADG15.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. PubMed=10373424;

RX MEDLINE=99303581; PubMed=10500122;

RA Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;

RT "Molecular cloning of cDNA for matriptase, a matrix-degrading serine

RT protease with trypsin-like activity.;"

RL J. Biol. Chem. 274:18231-18236(1999).

RN [2]

RP SEQUENCE FROM N.A. PubMed=10500122;

RX MEDLINE=99432178; PubMed=10500122;

RA Takeuchi T., Shuman M.A., Craik C.S.;

RT "Reverse biochemistry: Use of macromolecular protease inhibitors to

RT dissect complex biological processes and identify a membrane-type

RT serine protease in epithelial cancer and normal tissue.;"

RL Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).

RN [3]

RP SEQUENCE FROM N.A.

RX TissueProstate;

RA Yamaguchi N., Mitsui S.;

RT "Molecular cloning of a novel transmembrane serine protease expressed

RT in human prostate.;"

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Tanimoto H., Underwood L.J., Wang Y., Shigemasa K., Parmley T.H.,

RA O'Brien T.J.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood, and Muscle;

RX MEDLINE=22388257; PubMed=12477932;

RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kesteman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).

[6] SEQUENCE OF 340-664 FROM N.A.
Cao J., Fan W., Zheng S.;
"Genomic analysis of a novel human serine protease SNCI19.";
Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

[7] CHARACTERIZATION.
TISSUE=Milk.

MEDLINE=99303582; PubMed=10373425;
Lin C.Y., Anders J., Johnson M., Dickson R.B.;
"Purification and characterization of a complex containing matrixinase and a Kunitz-type serine protease inhibitor from human milk.";
J. Biol. Chem. 274:18237-18242(1999).

-|- FUNCTION: Degrades extracellular matrix. Proposed to play a role in breast cancer invasion and metastasis. Exhibits trypsin-like activity as defined by cleavage of synthetic substrates with Arg or Lys as the P1 site.

-|- SUBCELLULAR LOCATION: Type II membrane protein (Probable).

-|- SIMILARITY: Belongs to peptidase family S1.

-|- SIMILARITY: Contains 2 CUB domains.

-|- SIMILARITY: Contains 4 LDL-receptor class A domains.

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EMBL; AF118224; AD42765.2; -
EMBL; AF133086; AAF00109.1; -
EMBL; AB030036; BAB20376.1; -
EMBL; AF057145; AAG15395.1; -
EMBL; BC005826; AAH05826.1; -
EMBL; BC030532; AAH30532.1; -
EMBL; AF283256; AAG13949.1; -
HSP; P00763; IDPO.
Genew; HGNC:11344; ST14.
MIM; 606797; -
MEROPS; S01.302; -
GO; GO:0005887; C:Integral to plasma membrane; TAS.
GO; GO:0008236; F:serine-type peptidase activity; TAS.
GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
InterPro; IPR000859; CUB.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR02172; LDL_receptor_A.
InterPro; IPR01254; Peptidase_S1.
InterPro; IPR01314; Peptidase_S1A.
Pfam; PF00431; CUB_2
Pfam; PF00057; ldl_recept_a; 4.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00261; LDLRECEPTOR.
SMART; SM00042; CUB; 2.
SMART; SM00192; LDLA; 3.
SMART; SM00020; TRYD_SPC; 1.
PROSITE; PS01180; CUB_2.
PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS00068; LDLRA_2; 4.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
Transmembrane; Repeat.
DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
DOMAIN 2 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
TRANSNEM 56 (POTENTIAL).
DOMAIN 77 855 EXTRACELLULAR (POTENTIAL).
DOMAIN 214 334 CUB 1.

FT	DOMAIN	340	447	CUB 2.
FT	DOMAIN	452	487	LDL-RECEPTOR CLASS A 1.
FT	DOMAIN	487	524	LDL-RECEPTOR CLASS A 2.
FT	DOMAIN	524	560	LDL-RECEPTOR CLASS A 3.
FT	DOMAIN	566	603	LDL-RECEPTOR CLASS A 4.
FT	DOMAIN	615	854	SERINE PROTEASE.
FT	ACT SITE	656	656	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT SITE	711	711	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT SITE	805	805	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CARBOHYD	109	109	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	302	302	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	485	485	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	772	772	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	327	329	FEA -> GTR (IN REF. 5; AAH05826).
FT	CONFLICT	381	381	R -> S (IN REF. 4).
FT	CONFLICT	674	674	A -> V (IN REF. 3).
SQ	SEQUENCE	855 AA;	94769 MW;	26143132C01F99C9 CRC64;

Query Match 17.8%; Score 401.5; DB 1; Length 855;
Best Local Similarity 28.1%; Pred. No. 1.2e-24;
Matches 119; Conservative 65; Mismatches 157; Indels 83; Gaps 20;

QY	5	HOVPSNCDCLNGG--TCVSNKYPSNIHW-----CNCPK---KFGQHCE	43
Db	480	HSDELNSCDAGHQFTC-KKKCKPLFWVCDSDVNDGDSDEQCSCPAQTRCSNGKC-	537
QY	44	IDKSKTCYEGNGHFYRGKASTDTMGRCPLPNSATVLQOTYHAHRSALQLGLGKHYCR	103
Db	538	LSKSQCC---NGKDDCGDSDEA---SCPKNVVTCTKHTVYCLNGLCLSGK-----	583
QY	104	NPDRNRPCWYVGLKPLVQEC--WVHDCAG--KLKFCQCGQKTLRPRFKLIGGEFTTIE	160
Db	594	NP-----ECGKEDSCDSGDEKDCDCLRSFTQARVVGTDADG	624
QY	161	NQWFAAIYRHRGSGVTVCGGSLISPCWVISATHCFID-----YPKKEDIYVLG-RS	214
Db	625	EWPMQVSLHALQGQ---HICGASLISPNMLVSAHCYIDDRGRFYSDDPTQWTAFLGHD	680
QY	215	RLNSNTQGMKFEVENILHKDYSADTLAHNDTALLKIRSKRGRCQAQPSFTICLPS	274
Db	681	QSRSAPGVQERRLKRITISHPFNDFTFDY--DIALLELE---KPAEYSMWVRPICLPD	734
QY	275	MYNDPQFGTSCIEITGFG--KENSTDYLYPEQLKVTYVVKLISHRECQCPHYVGSVTKML	332
Db	735	ASHVFPAGKAIWTVGWGHTVQGTGALI---LQKGEIRVINQTTCE--NULLPQGITPRM	789
QY	333	CAADPQWKTDSCQDSDGGPL-VCSLQGRMLTGVSWGRGALKDKPGVYTRVSHFLPWI	391
Db	790	CVGFLSGGVSDSCQDSDGGPLSSVEADGRIFQAGVYVSWGDCGAQRNKPGVYTRLPFLFRDWI	849
QY	392	RSHT 395	
Db	850	KENT 853	

RESULT 45
ST14 MOUSE
ID ST14 MOUSE STANDARD; PRN; 855 AA.
AC P56677;
DT 15-JUL-1999 (Rel. 38, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Epithin).
GN ST14 OR PRSS14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.B.17SCID; TISSUE=Thymus;
RX MEDLINE=99216440; PubMed=10199918;
RA Kim M.G., Chen C., Lyu M.S., Cho E.G., Park D., Kozak C.,

Schwartz R.H.,
"Cloning and Chromosomal mapping of a gene isolated from thymic
stromal cells encoding a new mouse type II membrane serine protease,
epithin, containing four LDL receptor modules and two CUB domains.",
Immunogenetics 49:420-428(1999).
[2]
REVISTONS: TO 23; 321; 325; 343; 409-410 AND C-TERMINUS.
RP STRAIN=C.B.17SCID; TISSUE=Thymus;
RC STRAIN=G. Chen C. Cho E.G. Park D., Schwartz R.H.;
R2 Kim M.G.;
R1 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RN TISSUE=Breast; tumor;
RF MEDLINE=22398257; PubMed=12477932;
R3 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
R2 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
R1 Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
R4 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
R3 Diachenko L., Marsden K., Farmer A.A., Rubin G.M., Hong L.,
R2 Stapleton M., Soares M.B., Bonaldo M.F., Casavani T.L., Scheetz T.E.,
R4 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
R1 Roha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
R3 Beak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
R2 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R4 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R3 Phehy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
R2 Whiting J., Touchman J.W., Green E.D., Dickson M.C.,
R4 Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
R3 Rodriguez A.C., Krzywinski M.I., Skalek U., Smalls D.E.,
R1 Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalls D.E.,
R4 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
R3 "Generation and initial analysis of more than 15,000 full-length
R2 human and mouse cDNA sequences";
R1 Proc. Natl. Acad. Sci. U.S.A. 99:15899-15903(2002).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: Highly expressed in intestine, kidney, lung,
CC and thymus. Not expressed in skeletal muscle, liver, heart,
CC testis and brain.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 CUB domains.
CC -1- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC
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CC or send an email to license@isb-sib.ch.
CC
CC EMBL; AF042822; AA02230.3; -
CC EMBL; BC005456; AA05496.1; -
CC HSRP; F20231; IAAO.
CC MEROPS; S01.302; -
CC MGD; MGI:133881; St14.
CC GO; GO:0005576; C:extracellular; IDA.
CC GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
CC GO; GO:0008236; F:serine-type peptidase activity; IDA.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR002172; LDL_receptor_A.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00431; CUB; 2.
CC Pfam; PF00057; ldl_recept_a; 4.
CC Pfam; PF00089; trypsin_1;
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00261; LDLRECEPTOR.
CC SMART; SM00042; CUB; 2.
CC SMART; SM00132; LDLa; 4.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS01180; CUB; 2.
CC PROSITE; PS01209; LDLRA 1; 2.

DR	PROSITE; PS50068; LDLRA 2; 4.
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.
KW	Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
FT	Transmembrane; Repeat.
FW	CYTOPLASMIC (POTENTIAL).
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
DOMAIN	(POTENTIAL).
TRANSMEM	56 76
FT	DOMAIN 77 855
FT	EXTRACELLULAR (POTENTIAL).
FT	CUB 1.
FT	CUB 2.
FT	LDL-RECEPTOR CLASS A 1.
FT	LDL-RECEPTOR CLASS A 2.
FT	LDL-RECEPTOR CLASS A 3.
FT	LDL-RECEPTOR CLASS A 4.
FT	SERINE PROTEASE.
FT	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE	855 AA; 94654 MW; 4F10B84DA2146DD5 CRC64;
Query Match	17.8%; Score 401.5; DB 1; Length 855;
Best Local Similarity	27.9%; Pred. No. 1.2e-24;
Matches 117; Conservative 68; Mismatches 147; Indels 87; Gaps 20	
QY	11 CDCLNGGTCVSNKYFNSIHW-----CNCPKKFGGHCB-----IDKSKTC 50
DB	488 CNATHQFTC-KNQCFKPFLFWCDSDVDGDSDEGCSCPA--GSFKCSNGKCLPQSQC 544
QY	51 YEGNCHFRYGKASDTMGRCPLPNWSATVLQQTYHAHRSDALQLGLCKNYCNPDNR 110
DB	545 ---NGKDNGDGSDEA---SCDSVVNVVCTKYTRYCONGLCLKSG-----NP----- 585
QY	111 PWCYVQVGLKPLVEEC-MVHDCADG--KLKFCQGOKTLPRFKIIIGBEFTTIENOF 167
DB	586 -----ECDGKTDCSDGSEKNKDCGLRSFTKQARVVGTTNADEGEWPQVS 631
QY	168 IYRRHGGSVTYCGGSLISPCWVISATHCFIDYP--KKEDIIVY-----LGSRSLASN 219
DB	632 LHALGG---HLGCASLISPDWLVAHAFQDDKNFKYSDYTNMTWTFATFLGLDQSKRSAS 687
QY	220 TGCEMKFEVENLIHKDYSADTLLAHNDIALLKIRSEGRCAQPSRTIOTICLPMSYNDP 279
DB	688 --GVQELKLRITTHSPENDTPDY--DIALLELE---KSVEYSTVRVPICLPDATHVF 739
QY	280 QGTSCETGG--KENSTDLYPEQLKMVTWKLSHRCQOPHYGYGSEVTKMLCAADP 337
DB	740 PAKGAIWWTGMGHTKEGGTGALI---LOKEIRVINOTTCED--LMPQGITPRMCMCVGEL 794
QY	338 QWKTDSCGDSDGGLP-VCSLQGRMTLTGIYSWGRCALKDKPGVYTVRSHFLPWIRSHT 395
DB	795 SGGVDSQCGSDGGLSSAEKDGMRFAQGVWSWEGCAQRNKPGVYTRLPFWRDWIKEHT 853
RESULT 46	
ID	HEPS RAT STANDARD; PRG; 416 AA.
AC	Q0551;
DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Serine protease hepsin (EC 3.4.21.-).
GN	HFN.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
 [1]
 SEQUENCE FROM N.A.
 TISSUE=Liver;
 MEDLINE=93305733; PubMed=8318546;
 Parley D., Reymond P., Nick H.;
 "Cloning and sequence analysis of rat hepsin, a cell surface serine
 proteinase";
 Biochim. Biophys. Acta 1173:350-352(1993).
 -!- FUNCTION: Plays an essential role in cell growth and maintenance
 of cell morphology.
 -!- SUBCELLULAR LOCATION: Type II membrane protein.
 -!- SIMILARITY: Belongs to peptidase family S1.

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 or send an email to license@isb-sib.ch).

 EMBL; X70900; CAA50256.1; -.
 PIR; S33777; S33777.
 HSSP; P00763; IDPO.
 MEROPS; S01.224; -.
 InterPro; IPR009003; Cys Ser trypsin.
 InterPro; IPR01254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 InterPro; IPR001190; Srcr_receptor.
 Pfam; PF00089; tryptsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 SMART; SM00202; SR; 1.
 SMART; SM00202; Tryp_Spc; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Hydrolase; Serine protease; Signal-anchor.
 CHAIN 1 161
 CHAIN (POTENTIAL).
 SERINE PROTEASE HEPsin, NON-CATALYTIC
 CHAIN (POTENTIAL).
 CHAIN 162 416
 CHAIN (POTENTIAL).
 CYTOPLASMIC (POTENTIAL).
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 SERINE PROTEASE.
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 INTERCHAIN (BY SIMILARITY).
 BY SIMILARITY.
 BY SIMILARITY.
 N-LINKED (GLCNAC... (POTENTIAL).
 SEQUENCE 416 AA; 44926 MW; 85A9F8FA9550E180 CRC64;
 17.8%; Score 401; DB 1; Length 416;
 est Local Similarity 34.2%; Pred. No. 5.6e-25;
 atches 109; Conservative 55; Mismatches 103; Indels 52; Gaps 17;

 112 WCYVQGLKPLVQECM-----VHDCADGKLF-----CQSQKTLPRFKIIGGEFTTENOP 163
 117 FVDEGGL-PLAQLLDVISVCDPCRFILATQCDCGRKL-FVDRIVGQSLSLRWP 174
 164 WFAAYRRHRGGSYYVCGSLSPWCWISATHCFIDYPKKEYI-----VYLGRSLNSN 219
 175 WQVSL--RYDG---THLCGSLSGDWLTAACHF---PERNVLRSRWFAG--AVAT 224
 220 TQGEKKEVENLILH-----KQYSADTLAHNDIALKIRSEGRCAQSRRTOTICLP 273
 225 SPHAVQLGVQAVIYHGGVLPFRDPTD--ENSDIALVHLSSS-----LPLTEVIQVCLP 278

Qy 274 SMYNDPQFGTSCITGKGENSTDYLPQO---LKMVTVKLISHRECCQOPHYVYGVSEVTK 330
 Db 279 AAGQALVDGKVCITVGNQ-----FYQQAUVLQEARVPIISNEVCNSDFYGNQIKPK 334
 Qy 331 MLCAADPQWKTDCQDSDGGPLVC---SLQGRMTLTGVSWGRGCAKDKKPGVYTRVSH 386
 Db 335 MFCAGYEGGIDACQDSDGGHFCVCEDRISGTSRWRLCGIVSWGTGCAKARKPGVYTKVID 394
 Qy 387 FLPW-----IRSHYKEENGL 401
 Db 395 FREFIFOAKTHS-EATGM 412

 RESULT 47
 TRY3_CHICK
 ID TRY3_CHICK STANDARD; PRT; 248 AA.
 AC Q90629;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Trypsin II-P29 precursor (EC 3.4.21.4).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RX MEDLINE=95251611; PubMed=7733885;
 RT Wang K., Gan L., Lee I., Hood L.B.;
 RA "Isolation and characterization of the chicken trypsinogen gene
 family.";
 RL Biochem. J. 307:471-479(1995).
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: High levels are seen in the pancreas while
 lower levels are found in the liver, spleen and thymus.
 CC -!- SIMILARITY: Belongs to peptidase family S1.

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 or send an email to license@isb-sib.ch).

 EMBL; U15157; AAA79914.1; -.
 PIR; S55066; S55066.
 HSSP; P00763; IDPO.
 MEROPS; S01.151; -.
 InterPro; IPR009003; Cys Ser trypsin.
 InterPro; IPR01254; Peptidase_S1.
 InterPro; IPR001314; Peptidase_S1A.
 Pfam; PF00089; tryptsin; 1.
 PRINTS; PR00722; CHYMOTRYPSIN.
 SMART; SM00202; Tryp_Spc; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 PROSITE; PS00135; TRYPSIN_SER; 1.
 Hydrolase; Serine protease; Digestion; Pancreas; Zymogen;
 Calcium-binding; Signal; Multigene family.
 SIGNAL 1 16
 BY SIMILARITY.
 FT PROPEP 17 25
 ACTIVATION PEPTIDE (BY SIMILARITY).
 FT CHAIN 26 248
 TRYPSIN II-P29.
 FT ACT_SITE 65 65
 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT METAL 77 77
 CALCIUM (BY SIMILARITY).
 FT METAL 79 79
 CALCIUM (VIA CARBONYL OXYGEN)
 (BY SIMILARITY).
 FT METAL 82 82
 CALCIUM (VIA CARBONYL OXYGEN)
 (BY SIMILARITY).

FT METAL 87 87 CALCIUM (BY SIMILARITY).
FT ACT_SITE 109 109 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 202 202 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 32 162 BY SIMILARITY.
FT DISULFID 50 66 BY SIMILARITY.
FT DISULFID 134 235 BY SIMILARITY.
FT DISULFID 141 208 BY SIMILARITY.
FT DISULFID 173 187 BY SIMILARITY.
FT DISULFID 198 222 BY SIMILARITY.
FT SITE 196 196 REQUIRED FOR SPECIFICITY (BY SIMILARITY).
SC SEQUENCE 248 AA; 26622 MW; 55E16B07622B588E CRC64;

ry Match 17.5%; Score 395.5; DB 1; Length 248;
at Local Similarity 38.7%; Pred. No. 8.5e-25;
ches 94; Conservative 40; Mismatches 84; Indels 25; Gaps 7;

Qy 150 KIIGSGTTIENQWFAAIYRRHGGSVTVVCGSLISPCWISATHCFIDYPKEDYIV 209
De 25 KIVGVCYCPHSVPYQVSL-----NSGYHFCGSLNSQWLSAACY-----KSRIOV 73

Qy 210 YLGRSLNSNTQGMKEFEVENLILKDYSDTIAHNDIALIKRSGRCAQSPSTIQ 269
De 74 RLGSYNDIVQEDSEVRSSSVIIRHPKYSSITL--NNDIMLIKLAS-----AVEYSADIQ 127

Qy 270 ICLPSMNDPOFGNSCITGFGKENSVDLYPEQLKMTVVKLISHRECQOPHYVGSVTT 329
De 128 IALPS--SCAAGTECLISGNTLSNGVYPELLQCLNAPILSDQCEA--YPGDITS 183

Qy 330 KMLCAADPQWKTDCQGDGSGPLVCSLQGRMTLTGIVSWGRGKALDKPKGVYTRVSHFLP 389
De 184 NMICVGFLEGGKDCQGDGSGFVNCGE---LQGVSWIGCALGKPGVYTKVNCVND 239

Qy 390 WIR 392
De 240 WIQ 242

LT 48
TR BOVIN
IF TRY1 BOVIN STANDARD; PRT; 243 RA.
AC P00760;
DT 21-JUL-1986 (Rel. 01, Created)
D1 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trypsinogen, cationic precursor (EC 3.4.21.4) (Beta-trypsin)
DE (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RA [1]
RE SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Okajima T., Maniwa M., Nagao S., Fujikawa H., Goto S.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RE SEQUENCE OF 15-243, AND DISULFIDE BONDS.
RX MEDLINE=67168848; PubMed=5967094;
RA Mikes O., Holeysovsky V., Tomasek V., Sorm F.;
RT "Covalent structure of bovine trypsinogen. The position of the
remaining amides".
RL Biochem. Biophys. Res. Commun. 24:346-352(1966).
RN [3]
RE REVISIONS.
RX MEDLINE=72035053; PubMed=4399051;
RA Hartley B.S.;
RT "Homologies in serine proteinases".
RL Philos. Trans. R. Soc. Lond., B, Biol. Sci. 257:77-87(1970).
RN [4]
RE REVISIONS.
RX MEDLINE=75146445; PubMed=1092332;
RA Titani K., Ericsson L.H., Neurath H., Walsh K.A.;

"Amino acid sequence of dogfish trypsin.";
Biochemistry 14:1358-1366(1975).
[5]
RX X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF CALCIUM-BINDING SITE.
RX MEDLINE=78072097; PubMed=512;
RA Bode W., Schwager P.;
RT "The refined crystal structure of bovine beta-trypsin at 1.8-A
resolution. II. Crystallographic refinement, calcium binding site,
benzamide binding site and active site at pH 7.0.";
J. Mol. Biol. 98:693-717(1975).
[6]
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=71112431; PubMed=556951;
RA Kosiakoff A.A., Chambers J.L., Kay L.M., Stroud R.M.;
RT "Structure of bovine trypsinogen at 1.9-A resolution.";
Biochemistry 16:654-664(1977).
[7]
RX DISULFIDE BONDS.
RX MEDLINE=66079271; PubMed=5892911;
RA Kauffman D.L.;
RT "The disulfide bridges of trypsin.";
J. Mol. Biol. 12:929-932(1965).
CC -- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Xaa, Lys-|-Xaa.
CC -- COFACTOR: Binds 1 calcium ion per subunit.
CC -- SUBCELLULAR LOCATION: Extracellular.
CC -- TISSUE SPECIFICITY: Synthesized in the acinar cells of the
pancreas
CC -- PTM: AUTOCATALYTIC CLEAVAGE AFTER LYS-20 LEADS TO BETA-TRYPSIN BY
RELEASING A TERMINAL HEXAPEPTIDE. SUBSEQUENT CLEAVAGE AFTER
LYS-145 LEADS TO ALPHA-TRYPSIN. FURTHER CLEAVAGE AFTER LYS-190
YIELDS PSEUDOTRYPSIN. A CLEAVAGE MAY ALSO OCCUR AFTER ARG-119.
CC -- SIMILARITY: Belongs to peptidase family S1.
CC -- DATABASE: NAME=Worthington enzyme manual;
WWW="http://www.worthington-biochem.com/TRY/".

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CC EMBL; D38507; BAA07516.1; -
DR PDB; 1A07; 25-FEB-98.
DR PDB; 1A0J; 14-OCT-98.
DR PDB; 1A28; 13-JAN-99.
DR PDB; 1BJU; 13-JAN-99.
DR PDB; 1BJV; 13-JAN-99.
DR PDB; 1BTP; 29-JAN-96.
DR PDB; 1BFW; 15-OCT-95.
DR PDB; 1BTX; 15-OCT-95.
DR PDB; 1BTY; 15-OCT-95.
DR PDB; 1BTZ; 15-OCT-95.
DR PDB; 1C1N; 30-JAN-02.
DR PDB; 1C1O; 26-SEP-01.
DR PDB; 1C1P; 26-SEP-01.
DR PDB; 1C1Q; 26-SEP-01.
DR PDB; 1C1R; 26-SEP-01.
DR PDB; 1C1S; 26-JUL-00.
DR PDB; 1C1T; 26-SEP-01.
DR PDB; 1C2D; 26-SEP-01.
DR PDB; 1C3E; 26-SEP-01.
DR PDB; 1C3F; 26-SEP-01.
DR PDB; 1C3G; 26-SEP-01.
DR PDB; 1C3H; 26-SEP-01.
DR PDB; 1C3I; 26-SEP-01.
DR PDB; 1C3J; 26-SEP-01.
DR PDB; 1C3K; 26-SEP-01.
DR PDB; 1C3L; 26-SEP-01.
DR PDB; 1C3M; 26-SEP-01.
DR PDB; 1C3P; 26-SEP-01.
DR PDB; 1C5Q; 26-SEP-01.

PDB; IC5R; 26-SEP-01.
PDB; ICSS; 26-SEP-01.
PDB; ICST; 26-SEP-01.
PDB; ICST; 26-SEP-01.
PDB; ICST; 26-SEP-01.
PDB; ICSE; 23-MAR-99.
PDB; ICES; 26-SEP-01.
PDB; ICU8; 26-SEP-01.
PDB; ICU9; 26-SEP-01.
PDB; ID6R; 05-MAY-00.
PDB; IEB2; 11-MAR-02.
PDB; IEZX; 25-OCT-00.
PDB; IFOT; 20-SEP-00.
PDB; IFOU; 20-SEP-00.
PDB; IFZS; 05-JUN-00.
PDB; IG36; 23-OCT-01.
PDB; IG3B; 17-JAN-01.
PDB; IG3C; 17-JAN-01.
PDB; IG3D; 17-JAN-01.
PDB; IG3E; 17-JAN-01.
PDB; IG9I; 11-APR-01.
PDB; IGHT; 31-JAN-94.
PDB; IGHZ; 22-JAN-02.
PDB; IGIO; 22-JAN-02.
PDB; IGII; 22-FEB-02.
PDB; IGJ3; 22-JAN-02.
PDB; IGJ4; 22-JAN-02.
PDB; IGJ5; 22-FEB-02.
PDB; IGJ6; 22-JAN-02.
PDB; IGJ6; 27-APR-02.
PDB; IGJ6; 27-APR-02.
PDB; IGJ8A; 12-SEP-01.
PDB; IGJR; 18-JUL-01.
PDB; IGJS; 14-OCT-96.
PDB; IGJT; 14-OCT-96.
PDB; IKL1; 28-NOV-01.
PDB; IKL1; 28-NOV-01.
PDB; IKL1; 28-NOV-01.
PDB; IKLM; 28-NOV-01.
PDB; IKLN; 28-NOV-01.
PDB; IKLO; 28-NOV-01.
PDB; IKLP; 28-NOV-01.
PDB; IMAX; 14-OCT-96.
PDB; IMAY; 14-OCT-96.
PDB; IMTS; 20-AUG-97.
PDB; IMTU; 12-NOV-97.
PDB; IMTV; 12-NOV-97.
PDB; IMTW; 12-NOV-97.
PDB; IN6X; 04-MAR-03.
PDB; IN6Y; 04-MAR-03.
PDB; INT2; 15-APR-91.
PDB; IOIQ; 29-APR-03.
PDB; IPFC; 31-JAN-94.
PDB; IPPE; 31-JAN-94.
PDB; IPPH; 31-JAN-94.
PDB; IQAO; 10-APR-00.
PDB; IQBI; 29-APR-00.
PDB; IQBE; 29-APR-00.
PDB; IQB9; 30-APR-00.
PDB; IQBN; 03-MAY-00.
PDB; IQBO; 03-MAY-00.
PDB; IQCP; 19-JAN-00.
PDB; IQL7; 25-AUG-00.
PDB; IQL8; 25-AUG-00.
PDB; ISBW; 07-APR-00.
PDB; ISRI; 09-JUL-99.
PDB; ISMF; 31-JUL-94.
PDB; ITAB; 15-JUL-92.
PDB; ITAW; 24-JUN-97.
PDB; ITGB; 14-MAR-85.
PDB; ITGC; 09-APR-85.
PDB; ITGN; 22-OCT-84.
PDB; ITGS; 14-MAR-85.
PDB; ITGT; 15-OCT-90.
PDB; ITIO; 23-SEP-98.

PDB; ITLD; 15-OCT-92.
PDB; ITNG; 30-NOV-94.
PDB; ITNH; 30-NOV-94.
PDB; ITNI; 30-NOV-94.
PDB; ITNJ; 30-NOV-94.
PDB; ITNK; 30-NOV-94.
PDB; ITNL; 30-NOV-94.
PDB; ITPA; 14-MAR-85.
PDB; ITPO; 14-MAR-85.
PDB; ITPP; 16-APR-87.
PDB; IPTS; 26-JAN-95.
PDB; ITYN; 26-JAN-95.
PDB; IXUF; 16-DEC-98.
PDB; IXUG; 16-DEC-98.
PDB; IXUH; 11-NOV-98.
PDB; IXUI; 11-NOV-98.
PDB; IXUJ; 11-NOV-98.
PDB; IXUK; 11-NOV-98.
PDB; IYYK; 08-JUN-99.
PDB; IBTC; 19-JAN-00.

Query Match 17.5%; Score 394.5; DB 1; Length 243;
Best Local Similarity 37.4%; Pred.No.1e-24;
Matches 91; Conservative 41; Mismatches 86; Indels 25; Caps 8;

QY 150 KIIGGEFTTIENQPFAAIYRRHRGSGSVTYVCGLISPCWVISATHCFIDYPKEDYIV 209
||| : : : :
Db 20 KIVGYTCCANTVPYQVSL-----NSCYHFCSGLINSQWVVSAHCY----KSQIQV 68
||| : : : :
QY 210 YLGSRILNSTQGEMKFVENLIHKDYSDATTIAHNNDIALIKRSKEGRCAQPSRTIQ 269
||| : : : :
Db 69 RLGEDNINVEGNEQFASAKSI VHPSYNSNTL--NNDIMLIKLS---AASLNSRVAS 122
||| : : : :
QY 270 ICLPSMYNDPQFGSCITGKGENSETDLYBPQLKMTVVKLISHRECQQPHYVGSEVT 329
||| : : : :
Db 123 ISLETT--SCASAGTQCCLISGWNTKSSGTSYPDVLKCLKAPIUSDSCKSA--YPGGITS 178
||| : : : :
QY 330 KWLCAADPWKTDCSQGDGSGPLVCISLQGRMTLTGVSWRGALDKPGVYTRVSHFLP 389
||| : : : :
Db 179 NMFCAGYLEGGKDSCQDGSGGPVVS--GK--LQGIWSWGCGAQKNKPGETVKCNYS 234
||| : : : :
QY 390 WIR 392
||| : : : :
Db 235 WIK 237

RESULT 49
TMSS HUMAN STANDARD; PRT; 457 AA.
AC Q9H3S3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transmembrane protease, serine 5 (EC 3.4.21.-) (Spinesin).
GN TMPRSS5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RC TISSUE=Brain.
RX PubMed=11741986;
RA Yamaguchi N., Okui A., Yamada T., Nakazato H., Mitsui S.;
RT "Spinesin/TMPRSS5, a novel transmembrane serine protease, cloned from
human spinal cord.";
RL J. Biol. Chem. 277:6806-6812(2002).
CC -|- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
CC -|- TISSUE SPECIFICITY: Brain-specific. Predominantly expressed in
neurons, in their axons, and at the synapses of motoneurons in the
spinal cord.
CC -|- SIMILARITY: Belongs to peptidase family S1.
CC -|- SIMILARITY: Contains 1 SRCR domain.

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EMBL; AB028140; BAB20375.1; ..
HSSP; P00763; LDPO.
Genew; HGNC:14908; TMPRSS5.
MIM; 606751; ..
MEROPS; S01.313; ..
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001190; Srcr_receptor.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SMO020; TRY_SPC; 1.
PROSITE; PS0240; TRYPsin_DOM; 1.
PROSITE; PS00134; TRYPsin_HIS; 1.
PROSITE; PS00135; TRYPsin_SER; 1.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
PROSITE; PS0287; SRCR_2; FALSE_NEG.
Hydrolase; Serine protease; transmembrane; Signal-anchor;
Glycoprotein.
DOMAIN 1 49
TRANSMEM 50 70
CYTOPLASMTIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
EXTRACELLULAR (POTENTIAL).
SRCR.
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CLEAVAGE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC..) (POTENTIAL).
N-LINKED (GLCNAC..) (POTENTIAL).
N-LINKED (GLCNAC..) (POTENTIAL).
N-LINKED (GLCNAC..) (POTENTIAL).
N-LINKED (GLCNAC..) (POTENTIAL).
SEQUENCE 457 AA; 49574 MW; 64406AB4985A2651 CRC64;

seq Watch 17.3%; Score 391; DB 1; Length 457;
st Local Similarity 33.2%; Pred. No. 4e-24;
tches 93; Conservative 51; Mismatches 106; Indels 30; Gaps 9;

QY 129 HDCADGKLGK---FOCGOKTLRPFRFKIIGGEFTTIENQPWFIAIRRHGGSVTVVCCGS 184
DZ :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
DL 194 NKTSGQVSLRCSECGARPLASR--IVGQSVAPEGWPQASVALGFR-----HTCGGS 245
QY 185 LISPCWVISATHCFDIDY--PKEDYIYVLGRSLNNT-----QGEMKEVENILLHKDY 237
DZ :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
DL 247 VLAIPRWVVTAACHMHSFRLARLSWRVHAG---LVSHSAVRPHQGAL---VERIIHPFLY 300
QY 238 SADTLAHENDIALIKRSKEGCRAQPSRTQTICLPSTMYNDPOFGTSCEITCFGKENSTD 297
DZ :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
DL 301 SAQN--HDVDVALLRLQT----ALNFSDTVGAVCLPAKEHPFKGSRVCVSWGHTHFSh 354
QY 298 YLYPQLKWTVKLISHRECOQPHYGVSEVTVMLCNAAPDWKTDSCGDSSGGLVCSLQ 357
DZ :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::
DL 355 TVYSMDMLQDTVVPLFSTLCNSSCVYGALTFRMLCAGYLDGRADACQGDSSGGLVCPDG 414
QY 358 GMTTITGVISWGRCALXDKEGYTRYVSHELFWIRSHKTE 397
DZ :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: :::: ::::

415 DTWRLVGVVSWGRACAEPNHPGVYAKVAEFLDWIHDTAQD 454


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Search completed: May 25, 2004, 14:53:55
Time : 18.5408 secs

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Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A.
MEDLINE=2215945; PubMed=12149463;
Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann R.,
Dichek D.A.;
"Increased expression of urokinase during atherosclerotic lesion
development causes arterial constriction and lumen loss, and
accelerates lesion growth";
Proc. Natl. Acad. Sci. U.S.A. 99:10665-10670(2002).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AY122285; AAM83187.1; -.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR006209; EGF-like.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR008293; Pept_S1A_UPA.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
PROSITE; PS00021; EGF_1; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS0134; TRYPSIN_HIS; 1.
PROSITE; PS0135; TRYPSIN_SER; 1.
PIRSP; PIRSF001144; Urk_plasm_act; 1.
Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SEQUENCE 433 AA; 48375 MW; 65E64F36415549B0 CRC64;
Query Match 83.5%; Score 1885; DB 6; Length 433;
Best Local Similarity 82.8%; Pred. No. 9.5e-170;
Matches 342; Conservative 23; Mismatches 38; Indels 10; Gaps 2;
1 SNEHQV--PNCDCNGTGVSNKYFSNTHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFY 58
21 SHELHGVSDASNCGLNGGTCVTYKFYSNWRNCNPKKFGGQHCCEIDTLTKCYHGDHSY 80
59 RGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVG 118
81 RKGANTDMDRPLCLAWNSANVLTKTYYHAHRPDALQLGLGKHNYCRNPDHQRPPWCYVQVG 140
119 LKPLVQECVHDCAD-----GKLKFCQCGKTLRPRFKIIGGFTTIENQWFAAIYR 170
141 LKLIQECVHDCSSGKKPALPPKLEBFQCGQKALRPRFKIIGGFTTIENQWFAAIYR 200
171 RHRGGSVTVYCGGSLISPCWVISATHCPIDYPKKEDYIVVLGRSLNSNTQGMKPEVEN 230
201 RHRGGSVTVYCGGSLISPCWVVSATHCFINQKEDYIVVLGRSLNSMTPGEMKPEVEQ 260
231 LILKHDYSADTLAHDNDIALKIRSGRCHAPRTTQTCLPSMYNDPFGTSCBITGF 290
261 LILHEGYSADTLAHDNDIALKILSNNGQCAQPSRSITCLPFWNADPNFGTSCBITGF 320
291 GKENSTDLYPEQLKMTVKLISHRECOQPHYGVSEVTTKMLCAADPQWKTDCQGDSSG 350
321 GKENSTDLYPEQLKMTVKLVSVQECQPHYGVSEVTTKMLCAADPQWKTDCQGDSSG 380
351 PLVCSLQGRMTLTGIVSWGRCALKDKPGVTVRVSHFLPWIRSHKENGIAL 403

Db 381 PLVCSLQGRMTLTGIVSWGRCALKDKPGVTVRVSHFLPWIRSHKENGIAL 433
RESULT 2
Q8MHY7
ID Q8MHY7 PRELIMINARY; PRT; 433 AA.
AC Q8MHY7;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Urokinase-type plasminogen activator.
GN UROKINASE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugiki M., Yoshida E., Anai K., Maruyama M.;
Submitted (APR-2001) to the ENBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yano W., Watanabe M.;
"Oryctolagus cuniculus urokinase-type plasminogen activator, mRNA,
complete cds";
Submitted (JUL-2002) to the ENBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AY029517; AAK40239.1; -.
DR EMBL; AB087224; BAC02685.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR008293; Pept_S1A_UPA.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS0134; TRYPSIN_HIS; 1.
DR PROSITE; PS0135; TRYPSIN_SER; 1.
DR PIRSP; PIRSF001144; Urk_plasm_act; 1.
KW Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SEQUENCE 433 AA; 48444 MW; 6DD35A371010A6EE CRC64;
Query Match 83.3%; Score 1880; DB 6; Length 433;
Best Local Similarity 82.6%; Pred. No. 2.8e-169;
Matches 341; Conservative 23; Mismatches 39; Indels 10; Gaps 2;
1 SNEHQV--PNCDCNGTGVSNKYFSNTHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFY 58
21 SHELHGVSDASNCGLNGGTCVTYKFYSNWRNCNPKKFGGQHCCEIDTLTKCYHGDHSY 80
59 RGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVG 118
81 RKGANTDMDRPLCLAWNSANVLTKTYYHAHRPDALQLGLGKHNYCRNPDHQRPPWCYVQVG 140
119 LKPLVQECVHDCAD-----GKLKFCQCGKTLRPRFKIIGGFTTIENQWFAAIYR 170

D 141 LKQLTQCKVHDCSSGKKPALPPGKLEFQCCKQKALRPFRKLIIGGFTTIENQPFPAAIYR 200
 Q 171 RHRGGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGSRSLNSNTGEMKFEVEN 230
 D 201 RHRGGSVTVVCGSLSPCWVVSATHCFINQKKEDYIVYLGSRSLNSMTPEGNKFEVEQ 260
 Q 231 LILHKDYSADTLAHHNDIALLKIRSEKRCQAPSTIOTICLPSMYNDPQFTSCETGTF 290
 D 261 LILHGGYRADTLAHHNDIALLKILSNNGCQAPSRSIOTICLPPWADNPFNGTSCETGTF 320
 Q 291 GKENSTDYLYPQLKXVTVKGLSHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDGG 350
 D 321 GKENSTDYLYPQLKXVTVKGLSVYECQCPHYGVSEVTTKMLCAADPQWKTDSCQDGG 380
 Q 351 PLVCSLOHMTLGTIVSGRGCCALKDKGVYTRVSHFLPWIRSHRSHYKENGAL 403
 D 381 PLVCSVQGRMTLGTIVSGRGCCALKDKGVYTRVSRFLPWIRSHRSHYKENGAL 433
 R ULT 3
 Q I Q9X770 PRELIMINARY; PRT; 214 AA.
 A Q9X770; (TREMBlrel. 12, Created)
 D 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 D 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 D Urokinase-type plasminogen activator (Fragment).
 C Oryctolagus cuniculus (Rabbit).
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 C Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 C NCBI_TaxID=9986;
 K [1]
 K SEQUENCE FROM N.A.
 E TISSUE=Lung;
 F "Partial mRNA of rabbit uPA";
 F "vin J., Idell S.,
 R Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 R -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 C -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 C ENBL; AF097647; AAD39351.1; -
 D HSP; P00749; 1EJN.
 D MER08; S01.231; -
 D GO; GO:0004263; F:chymotrypsin activity; IEA.
 D GO; GO:0016301; F:kinase activity; IEA.
 D GO; GO:0008233; F:peptidase activity; IEA.
 D GO; GO:0004295; F:trypsin activity; IEA.
 D GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 D InterPro; IPR009003; Cys Ser trypsin.
 D InterPro; IPR000001; Kringle.
 D InterPro; IPR001254; Peptidase S1.
 D InterPro; IPR001314; Peptidase_S1A.
 D Pfam; PF00051; kringle; 1.
 D Pfam; PF00089; trypsin; 1.
 D PRINTS; PR00722; CHYMOTRYPSIN.
 D ProDom; PD000395; Kringle; 1.
 D SMART; SM00130; KR; 1.
 D SMART; SM00020; Tryp_SPC; 1.
 D PROSITE; PS00022; EGF_1; 1.
 D PROSITE; PS01186; EGF_2; 1.
 D PROSITE; PS01253; FIBRONECTIN_1; 1.
 D PROSITE; PS00021; KRINGLE_1; 2.
 D PROSITE; PS00070; KRINGLE_2; 2.
 D PROSITE; PS02040; TRYPSIN_DOM; 1.
 D PROSITE; PS00134; TRYPSIN_HIS; 1.
 D PROSITE; PS00135; TRYPSIN_SER; 1.
 F SQ SEQUENCE 214 AA; 24314 MW; 59975C41C32B0D7E CRC64;
 Query Match 42.2%; Score 953.5; DB 6; Length 214;
 Best Local Similarity 81.3%; Pred. No. 5.5e-82;
 Matches 174; Conservative 12; Mismatches 21; Indels 7; Gaps 1;
 Q 67 MGRPCLWNSATVLQOTYHAHRSALQLGLGKHNYCRNPNRRPWCYVQVGLKPLVQSC 126
 D 1 MDRPCLAWNSAVLTKYIHAHRPDALQLGLGKHNYCRNPNRRPWCYVQVGLKQLIQSC 60

QY 127 MYEDCA-----DGKLFQCGCKTLRPRFKLIIGGFTTIENQPFPAAIYRHRGGSVTV 179
 Db 61 KVHDSGKKPALPPGKLEFQCCKQKALRPFRKLIIGGFTTIENQPFPAAIYRHRGGSVTV 120
 QY 180 VCGSLSPCWISATHCFIDYPKKEDYIVYLGSRSLNSNTGEMKFEVENLILHKDYS 239
 Db 121 VCGSLSPCWVVSATHCFINQKKEDYIVYLGSRSLNSMTPEGNKFEVEQLILHEGYRA 180
 QY 240 DTLAHHNDIALLKIRSEKRCQAPSTIOTICLIP 273
 Db 181 DTLAHHNDIALLKILSNNGCQAPSRSIOTICLIP 214
 RESULT 4
 Q66YK8 PRELIMINARY; PRT; 562 AA.
 ID Q66YK8
 AC Q66YK8; (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Tissue plasminogen activator.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RA Liu Y., Xu L., Zeng Y., He X.;
 RT "cDNA of tissue plasminogen activator";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY221101; AAC34406.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000083; Fibrinctn.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00039; fnl; 1.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 F SQ SEQUENCE 562 AA; 62902 MW; 837D98392F6EDD1F CRC64;
 Query Match 38.0%; Score 858.5; DB 4; Length 562;
 Best Local Similarity 37.5%; Pred. No. 1.8e-72;
 Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
 QY 3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWNCNPKKFGGCHCEIDKSKTCYEGNGHFY 58
 Db 77 QCHSVVPKSCSEPRFCFGGTCTQALYFSDP-VCCQPEGPAGKCCBIDTRATCYEDQGISY 135
 QY 59 RGKASTDTMGPRCLPWNASATVLQOTYHAHRSALQLGLGKHNYCRNPNRRPWCYVQVGL 118
 Db 136 RGTWSTAESGECTNWNSSALLAQKPYSGRRPDALRLGLGNHNYCRNPNRRPWCYVFK 195

QY 119 LKPLVQECWVHDCADG----- 134
 DE 196 QKYSSEFCSTPACSEGNDCYFNGSAYRGTHSLTESGASCLPWNMILIGNVTTAQNPS 255
 QY 135 -----KLKQ-----CG-QKTLRPRFKLIGGE 155
 DE 256 AQAALGLKGNHYNCRNPDGDAKPMWCHLVKRRLTWEYCDVPSCSTCGLRQYSQPFRIKGL 315
 QY 156 FTTIENQWPAAYRRH-RGGSVTVYVCGSLISPCWVISATHCFIDYPPKEDYVYVLRGS 214
 DE 316 FADIASHPWOAIPAKHRRSPGGERFLOGGILISSCWILSSAAHCFQERFPFPHLTVLGRT 375
 QY 215 RLNSNTQGEKFEVENILHDKYSDTLAHNDIALKIRSEKGRCAQPSRTIQTICLPS 274
 DE 376 YRVVPGSEBQKEVEKIVHKEFDDDT--YNDIALQLKSSRCAQESSVVRTVCLPP 433
 QY 275 MYNDPQGTSCBITGFGKNSDYLYPEQLKMTVVKLISHRECCQPHYGVSEVTTMLCA 334
 DE 434 ADLQLPDWTCELSGYKHEALSPFYSERLKEAHLVLPSSRCTSQHLLNRTVTDNMLCA 493
 QY 335 AD-----PQWKT--DSCQDGGPLVCSLQGRMTLTGIVSNRGRCALKDKPGVTVRSHL 388
 DE 494 GDRSGGPOANLHDACQDGGPLVCLNDGRMTLVGLIISWGLGCGQDQVPGVTVKVTNYL 553
 QY 389 FWIRSHTK 396
 DE 554 DWIRDNR 561
 RE UT 5
 QY 99 Q9BU99 PRELIMINARY; PRT; 516 AA.
 ID AC Q9BU99;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to plasminogen activator, tissue.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 DE EMBL; BC002795; AA02795.1; --
 DE HSSP; P00750; 1A5H.
 DE GO; GO:0004253; F:chymotrypsin activity; IEA.
 DE GO; GO:0008233; F:peptidase activity; IEA.
 DE GO; GO:0004295; F:trypsin activity; IEA.
 DE GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DE InterPro; IPR009003; Cys_Ser_trypsin.
 DE InterPro; IPR006209; EGF-like.
 DE InterPro; IPR006210; IEGF.
 DE InterPro; IPR000001; Kringle.
 DE InterPro; IPR001254; Peptidase_S1.
 DE InterPro; IPR001314; Peptidase_S1A.
 DE Pfam; PF00008; EGF; 1.
 DE Pfam; PF00051; kringle; 2.
 DE Pfam; PF00089; trypsin; 1.
 DE PRINTS; PR00722; CHYMOTRYPSIN.
 DE PRINTS; PR00018; KRINGLE.
 DE PRODOM; PR000395; Kringle; 2.
 DE SMART; SM00181; EGF; 1.
 DE SMART; SM00130; KR; 2.
 DE SMART; SM00020; Tryp_Spc; 1.
 DE PROSITE; PS00022; EGF_1; 1.
 DE PROSITE; PS01186; EGF_2; 1.
 DE PROSITE; PS00021; KRINGLE_1; 2.
 DE PROSITE; PS00070; KRINGLE_2; 2.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
 KW Serine protease.
 SQ SEQUENCE 516 AA; 57370 MW; BAB31901FDC96800 CRC64;
 Query Match 37.8%; Score 852.5; DB 4; Length 516;
 Best Local Similarity 37.1%; Pred. No. 6e-72;
 Matches 184; Conservative 55; Mismatches 154; Indels 103; Gaps 9;
 QY 1 SNEHL-----QVPSNCDLNGGTCSNKNYFNSHWCNCPKFGGQHCEDKSKTC 50
 DE 23 SGEHARFRGARYQCCSEPCFNGGTCCQALYFSDF-VCCDEGAGKCEIDTRATC 81
 QY 51 YEGNGHFVRGKASTDTMGRPCLPWNSATVLCQTYHAHRSALQGLGKGNHYNCRNPNRR 110
 DE 82 YEDQGISYRGTWSTAESGAECTNNWNSALAQKPYSGRRPDAILRLGLGNHYNCRNPNRDSK 141
 QY 111 PWCYVQVGLKPLVQECWVHDCADG----- 134
 DE 142 PWCYVFKAGKYSSEFCSTPACSEGNDCYFNGSAYRGTHSLTESGASCLPWNMILIGK 201
 QY 135 -----KLKQ-----CG-QKTLRP 147
 DE 202 VYTAQNPSAQAALGLKGNHYNCRNPDGDAKPMWCHLVKRRLTWEYCDVPSCSTCGLRQYSOP 261
 QY 148 RKLIIGGEFTTIENQWPAAYRRH-RGGSVTVYVCGSLISPCWVISATHCFIDYPPKED 206
 DE 262 QFRINGGLFADIASHPWOAIPAKHRRSPGGERFLOGGILISSCWILSSAAHCFQERFPFPHH 321
 QY 207 YIVLGRSLNSNTQGEKFEVENILHDKYSDTLAHNDIALKIRSEKGRCAQPSRT 266
 DE 322 LTVILGRYRVVPGSEBQKEVEKIVHKEFDDDT--YNDIALQLKSSRCAQESSV 379
 QY 267 ICTICLPSMYNDPQGTSCBITGFGKNSDYLYPEQLKMTVVKLISHRECCQPHYGVSE 326
 DE 380 VRTVCLPPADLQLPDWTCELSGYKHEALSPFYSERLKEAHLVLPSSRCTSQHLLNRT 439
 QY 327 VTTKMLCAAD-----PQWKT--DSCQDGGPLVCSLQGRMTLTGIVSNRGRCALKDKPGV 380
 DE 440 VTDNMLCAGDTRSGGPOANLHDACQDGGPLVCLNDGRMTLVGLIISWGLGCGQDQVPGV 499
 QY 381 YRVVSHFLPWIRSHTK 396
 DE 500 YTKVTNYLDWIRDNR 515
 RESULT 6
 ID Q8MKB1 PRELIMINARY; PRT; 564 AA.
 AC Q8MKB1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tissue-type plasminogen activator.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sugiki M., Yoshida E., Anai K., Maruyama M.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 DE EMBL; AY029518; AAK40240.1; --
 DE GO; GO:0005576; C:extracellular; IEA.
 DE GO; GO:0004263; F:chymotrypsin activity; IEA.
 DE GO; GO:0008233; F:peptidase activity; IEA.
 DE GO; GO:0004295; F:trypsin activity; IEA.
 DE GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DE InterPro; IPR009003; Cys_Ser_trypsin.

RESULT 7
C Q23
I Q8SQ23 . PRELIMINARY; PRT; 562 AA.

QY 156 FTTHQNPWPAALY-RRHGGSVYVCGGLSPICWVISAATHCFIDYPPKEDYIVVLGRS 214
DB 316 YADITSHFWAAALFVKNRRSGBRFLCGGLISLSCWLSAAHCFQBRPPHVRVVLGRT 375
QY 215 RLNSNTQGMKFEVENLILHKDYSADTLAHNDIALKIRSKRGCAQPSRTIQTCLPS 274
DB 376 YRLVPGSEEAFAVEKYVHKEFDDDT--YDNDIALQLKSDSLTCAQSSDAVRTVCLPE 433
QY 275 MYNDPQCTSCBTGCGKENSITLYPEQLKMTVVKLISHRECOQPHYGVSEVTTMLCA 334
DB 434 ANQLPDWTECELSGYGVKHSAPFFYSERLUKEAHVRLPYSSRCTSKHLFNKTIINMLCA 493
QY 335 ADPOW-----KTDSCGDSGGPLVCSLQGRMTLTGIVSNGRCALCKDPGVVTVRSHFL 388
DB 494 GDRSGGDNANLHADCGDGGPLVCMKGNHMTLVGVISNGLCGGQKDPGVVTVRSHFL 553
QY 389 PWIRSHTK 396
DB 554 NWIRDNTR 561
RE 28
Q8 22
ID Q8C6L2 PRELIMINARY; PRT; 231 AA.
AC Q8C6L2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasmidogen activator (Fragment).
OE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RF STRAIN=C57BL/6J; TISSUE=Ovary;
RX MEDLINE=22354683; PubMed=12456851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK054349; BAC35743.1; -
DR PIR; PT0534.
DR GO; GO:0004295; P:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00083; trypsin; 1.
DR PRINTS; PR00083; trypsin; 1.
DR Pfam; PF00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00083; trypsin; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR NON TER 231
FT SEQUENCE 231 AA; 25510 MW; 25E8980A682737F2 CRC64;

Query Match 35.8%; Score 808.5; DB 11; Length 231;
Best Local Similarity 69.5%; Pred. No. 3.2e-68;
Matches 139; Conservative 21; Mismatches 31; Indels 9; Gaps 2;
QY 9 SNCDLGGTCVSNKYSNIHWNCNPKFGQHCIDKSKTCYEGNGHFGYRGKASTDTMG 68
DB 30 SNCCQGGVGVSYKYSRIRRCSPKRFQGEHCIDASKTCVHGNGDSYRGKANTDTKG 89
QY 69 RPLPWNATVLOQTYHAHRSALQLGLGKHNYCRNPDNRRPWCYVQVGLKPLVQECMV 128
DB 90 RPLAWNAPAVLQKPYNAHRPDAISLGLGKHNYCRNPDNRRPWCYVQVGLKPLVQECMV 149

QY 129 HDCADGKLGK-----FOCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRHGGSV-VTY 179
DB 150 HDCSLSKKPSVVDQGFQCGQKALRPRFKIVGGFTEVENQWFAAIYQKNGGSPSP 209
QY 180 VCGGLSPICWVISAATHCFI 199
DB 210 KCGGLSPICWVISAATHCFI 229
RESULT 9
Q8BZWI
ID Q8BZWI PRELIMINARY; PRT; 395 AA.
AC Q8BZWI;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neonatal thrombolytic agent alpha-form (Fragment).
OE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RA Dou D.;
RT "A brain-type plasminogen activator";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF260825; AAK11956.1; -
DR HSSP; P00750; 1PK2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004283; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00039; fnl; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 1.
DR SMART; SM00038; FN1; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
FT NON TER 395
FT SEQUENCE 395 AA; 44323 MW; 3FBD4A2F0B7C11C8 CRC64;

Query Match 34.9%; Score 788.5; DB 4; Length 395;
Best Local Similarity 42.9%; Pred. No. 4.9e-66;
Matches 161; Conservative 49; Mismatches 144; Indels 21; Gaps 8;
QY 30 WNCNPKFGQHCIDKSKTCYEGNGHFGYRGKASTDTMGREFCLPWNATVLOQTYHAHRS 89
DB 33 WCNLS---GRAQCS-EGNSDCYFGNGSAYRGTHSLTSGASCLPWNAMILIGKVYTAQNP 87
QY 90 DALQLGLGKHNYCRNPDNRRPWCYVQVGLKPLVQECMVHDCADGKLFQCG-QKTLRPR 148
DB 88 SAQALGLGKHNYCRNPDGDAKFWCHLVKNRRLTWECYCDVPSCS-----TCGLKQYSOPQ 141
QY 149 FKIIIGGEFTTIENQWFAAIYRRH-RGGSVTVVCGGLSPICWVISAATHCFIDYPPKEDY 207

D 142 FRKGLFADIAHPWQAAIFAKHEBSPGERFLCGGILISSCWILSAAHCFQERPPPHL 201
Q 208 IYVGRSLNSNTQGMKEFEVENLILHKDYSADTLAHNDIALKIRSKRGCAQPSRTI 267
D 202 TWLGTIRVVPGEERQKECEKYIVHKEFDDDT--YNDIALQLKSDSSRCACSSVW 259
Q 268 QITCLPSMNDPOFGTSCITGFKENSTDYIYPBOLKTVVVLISHRECQOPHYGSEV 327
D 260 RTVCLPFPADQLPDMTECELSGKGKALSPYSEKLEAHVRLYPSSRCTSQHLLNRTV 319
Q 328 TTKMLCAAD-----POWKT-DSQQDGGGLVCSLQGRMTLTGIVSGRGKALCKPGVY 381
D 320 TDNMLCAGTRSGGPPANLHDACQDGGGLVCLNDGRMTLVGLISWGLGCGQKQVPGVY 379
Q 382 TRVSHLPWIRSHTK 396
D 380 TKVTNYLDWIRDNR 394

R JULT 10
C SE8 PRELIMINARY; PRT; 154 AA.
Q96S28;
Q96S28; 01-DRC-2001 (TrEMBLrel. 19, Created)
D 01-DRC-2001 (TrEMBLrel. 19, Last sequence update)
D 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
D Urokinase-type plasminogen activator amino-terminal fragment.
C XTF.
C Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
C NCBI_TaxID=9606;
R R SEQUENCE FROM N.A.
F Fu J., Bai X., Ruan C.;
F "Cloning and expression of the amino-terminal fragment of human
F urokinase-type plasminogen activator."
F Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
R [2]
R SEQUENCE FROM N.A.
R Bai X., Fu J., Wang W., Xi X., Ruan C.;
R "Overexpression of the amino-terminal fragment of human urokinase-type
R plasminogen activator in breast cancer cells results in decreased
R tumor invasion, growth and angiogenesis."
R Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
R -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
C EMBL; AY029537; AAK38734.1; --
D GO: GO:0016301; F-kinase activity; IEA.
D InterPro; IPR006209; EGF-like.
D InterPro; IPR006210; EGF.
D Pfam; PF00051; kringle; 1.
D PRINTS; PR00018; KRINGLE.
D ProDom; PD000395; Kringle; 1.
D SMART; SM00181; EGF; 1.
D SMART; SM00130; KR; 1.
D PROSITE; PS00022; EGF_1; 1.
D PROSITE; PS00021; KRINGLE 1; 1.
D PROSITE; PS00070; KRINGLE 2; 1.
D Glycoprotein; Kinase; Kringle.
R SEQUENCE 154 AA; 17305 MW; A3CCF2FCFF505572 CRC64;

Very Match 34.5%; Score 778; DB 4; Length 154;
Best Local Similarity 99.3%; Pred. No. 1.5e-85;
atches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Q 1 SNELHVPNSNCDCLNGTCTVSNKYFNSNIHWCNCFKFGQHQHCEIDKSKTCYEGNGHFYRG 60
D 21 SNELHVPNSNCDCLNGTCTVSNKYFNSNIHWCNCFKFGQHQHCEIDKSKTCYEGNGHFYRG 80
Q 61 KASTDTMGRCLPWNATVLOQTYHAHRSALQGLGKKNYCNPNRNRPRWCYQVGLK 120
D 61 KASTDTMGRCLPWNATVLOQTYHAHRSALQGLGKKNYCNPNRNRPRWCYQVGLK 140

QY 121 PLVQECNVHDCADG 134
DB 141 LLVQECNVHDCADG 154

RESULT 11
Q800Y7
ID Q800Y7 PRELIMINARY; PRT; 540 AA.
AC Q800Y7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hepatocyte growth factor activator (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2212796; PubMed=12128063;
RA Holsinger D.R., Becker A.E., Thurston R.J., Rice C.D.;
RT "Expression of a hepatocyte growth factor activator protein in turkey
RT (Meleagris gallopavo) deferent duct epithelial cells."
RL Comp. Biochem. Physiol. 132:769-777(2002).
R [2]
RP SEQUENCE FROM N.A.
RA Holsinger D.R., Becker A.E., Thurston R.J., Rice C.D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216598; AAO46038.1; --
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0004263; F:chymotrypsin activity; IEA.
DR GO: GO:0004295; F:trypsin activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_cryptin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000562; FN Type II.
DR InterPro; IPR006210; tBGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00020; Tryp_spc; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN 1; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
DR PROSITE; PS00240; TRYPsin_DOM; 1.
DR PROSITE; PS00134; TRYPsin_HIS; 1.
DR PROSITE; PS00135; TRYPsin_SER; 1.
FT NON_TER 1
FT NON_TER 540 540
SQ SEQUENCE 540 AA; 61159 MW; 0BB3B4A89C0B577F CRC64;

Query Match 32.0%; Score 722.5; DB 13; Length 540;
Best Local Similarity 38.3%; Pred. No. 1.3e-59;
Matches 155; Conservative 60; Mismatches 147; Indels 43; Gaps 11;

QY 13 CLNGGTC-----VSNKYFNSNIHWCNCFKFGQHQHCEIDKSKTCYEGNGHFYRGKASTDTMG 68
DB 143 CMNGGECMIASSGKTV-----CDCKGPFVKGKCNVFNHHCYRGNGTEYRGTAKTISG 197

QY 69 RPCLPWNSTVLOQTHAHRSALQLGLGKHNCRNPNRRRPPWCYVQVGLKELVQCMV 128
 DB 198 HSCLPWNSTVLOQTHAHRSALQLGLGKHNCRNPNRRRPPWCYVQVGLKELVQCMV 257
 QY 129 HDCAAGKL-----KFCQCK-----TLRPFKIIIGBFTTIENQWPAAY 169
 DB 258 TSCASRRRPPVLEIDITFAVPRRPPCGRRHKRSFVRP--IIGGSSLPSSHPTAAIV 315
 QY 170 RRHGGGVTVCGSLSPCWISATCFDYPKEDYIVYLCRSLNSNTQCEMKFEVE 229
 DB 316 ---IGES---FCAGTLTQTCWVSAHCFANSQKSIKVLVQCHFNRTTDTVQTFEIE 369
 QY 230 NLILHKDYSADTLAHNDIALKIRSKGRCAPSRITQICLP-----SMYNDPQFQTSCE 286
 DB 370 KYILYPOYSVRPTEH-DIALIKLKGQRCAVKSQVQICLPESNTVFPD-QF--KCQ 425
 QY 287 ITGSGKNSDYLPEOLKMTVKVLSHRECOQPHYVGSVTTKMLCAADPQWKTDSGCG 346
 DB 426 ISGWHKHENITGYSDVLQETLPIIPEEKCRSPFIYGTSEISNMFAGYFDSKSDACQ 485
 QY 347 DSGGFLVCSLQGRMTLTGIVSWRGCCALDKPKGYVTRVSHFLPWI 391
 DB 486 DSGGFLACENNEISYLGVISWGDGCRVKNPKGYVTRVSNVNI 530

UT 12
 RE 34 QYCS4 PRELIMINARY; PRT; 653 AA.
 ID QYCS4 PRELIMINARY; PRT; 653 AA.
 AC QYCS4 PRELIMINARY; PRT; 653 AA.
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strauberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR HSSP; P00761; 1AN1.
 DE GO; GO:0005576; C:extracellular; IEA.
 DE GO; GO:0004283; F:chymotrypsin activity; IEA.
 DE GO; GO:0008233; F:peptidase activity; IEA.
 DE GO; GO:0004295; F:trypsin activity; IEA.
 DE GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DE InterPro; IPR000742; EGF_2.
 DE InterPro; IPR006209; EGF_like.
 DE InterPro; IPR000083; Fibrinctnl.
 DE InterPro; IPR000562; FN_Type_II.
 DE InterPro; IPR006210; IEGF.
 DE InterPro; IPR000001; Kringle.
 DE InterPro; IPR001254; Peptidase S1.
 DE InterPro; IPR001314; Peptidase_S1A.
 DE Pfam; PF00008; EGF; 2.
 DE Pfam; PF00039; fn1; 1.
 DE Pfam; PF00040; fn2; 1.
 DE Pfam; PF00051; kringle; 1.
 DE Pfam; PF00089; trypsin; 1.
 DE PRINTS; PR00722; CHYMOTRYPSIN.
 DE PRINTS; PR00013; ENTYPSEII.
 DE PRINTS; PR00018; KRINGLE.
 DE ProDom; PD000895; FN_Type_II; 1.
 DE ProDom; PD000395; Kringle; 1.
 DR SMART; SM00181; EGF; 2.
 DR SMART; SM00059; FN2; 1.

DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN 1; 1.
 DR PROSITE; PS00023; FIBRONECTIN 2; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS00070; KRINGLE 2; 1.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hypothetical protein; EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 653 AA; 70553 MW; F818D90174ED6FDD CRC64;

Query Match 31.7%; Score 716; DB 11; Length 653;
 Best Local Similarity 36.3%; Pred. No. 6,6e-59;
 Matches 154; Conservative 58; Mismatches 162; Indels 50; Gaps 8;

QY 5 HQVPSNCDLNGGTCVSNKYFSNIHW-----CNCPKKFGGQHCIDKSKTCYENGH 56
 DB 239 HTACLSSPLNGGTC-----HLIVGTGTVCTCPLGVAGRFNIVPTEHCFNGT 289
 QY 57 FYRGKASTDTMGRPCLPWNSTVLOQTHAHRSALQLGLGKHNCRNPNRRRPPWCYVQ 116
 DB 290 EYRGVASTAASGLSCLAWNSDLLYQELHVDVSAARVLLGLGPHAYCRNPKDERPWCYV 349
 QY 117 VGLKPLVQECMVHDC-----ADGKLKFCQCK-----TLRPFKII 152
 DB 350 KDNALSWEYCRLTACESLARVHSQSPEILAAPEAPAVRPTCGKRHKRTFLRPR--II 407
 QY 153 GGEFTIENQWPAAYRHRHGGSVTVCGSLSPCWISATCFDYPKEDYIVYLG 212
 DB 408 GSSSLPGSHFWLAAIY---IGNS---FCAGSLVHTCWVWSAAHCFANSPPRDSITVVLG 461
 QY 213 RSLNSNTQCEMKFEVENLILHKDYSADTLAHNDIALKIRSKGRCAPSRITQICLP 272
 DB 462 QHFFNRRTDVTQTGIEKYVFTLYSVFNPNNH-DLVILRLKXKGERCAVESQFVPICL 520
 QY 273 PSYNDPQFQTSCEITGSGKNSDYLPEOLKMTVKVLSHRECOQPHYVGSVTTKML 332
 DB 521 PEAGSFPTGHHKQIAGHGHNDENVSSYNSLLBALPVLVADHKCSPEVYGAISPNNML 580
 QY 333 CAADPQWKTDSGCGFLVCSLQGRMTLTGIVSWRGCCALDKPKGYVTRVSHFLPWI 392
 DB 581 CAGYFDCSKDACQDGGGFLVCKNGVAYLYGIISWGDGCRVKNPKGYVTRVSNVNI 640
 QY 393 SHTK 396
 DB 641 DRIR 644

RESULT 13
 ID 097507 PRELIMINARY; PRT; 616 AA.
 AC 097507;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE FXII.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Takahashi T.; Kihara T.;
 RT "porcine liver factor XII".
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; AB022426; BAA37148.1; -.

D HSP; P00763; LDPO.
D MEROPS; S01.211; .
D GO; GO:0005576; C:extracellular; IEA.
D GO; GO:0004363; F:chymotrypsin activity; IEA.
D GO; GO:0008233; F:peptidase activity; IEA.
D GO; GO:0004395; F:trypsin activity; IEA.
D GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
D InterPro; IPR009003; Cys_Ser_trypsin.
D InterPro; IPR000742; EGF_2.
D InterPro; IPR006209; EGF_like.
D InterPro; IPR000083; Fibronectin.
D InterPro; IPR000562; FN_Type_II.
D InterPro; IPR006210; IEGF.
D InterPro; IPR000001; Kringle.
D InterPro; IPR001254; Peptidase_S1.
D InterPro; IPR001314; Peptidase_S1A.
D Pfam; PF00008; EGF_2.
D Pfam; PF00039; fn1; 1.
D Pfam; PF00040; fn2; 1.
D Pfam; PF00051; kringle; 1.
D Pfam; PF00089; trypsin; 1.
D PRINTS; PR00089; trypsin; 1.
D PRINTS; PR00013; FNYPEII.
D PRINTS; PR00018; KRINGLE.
D ProDom; PD000995; FN_Type_II; 1.
D ProDom; PD000395; Kringle; 1.
D SMART; SM00181; EGF_2.
D SMART; SM00059; FN2; 1.
D SMART; SM00130; KR; 1.
D SMART; SM00020; Tryp_Spc; 1.
D SMART; SM00022; EGF_1; 2.
D PROSITE; PS01186; EGF_2; 1.
D PROSITE; PS01253; FIBRONECTIN_1; 1.
D PROSITE; PS01253; FIBRONECTIN_2; 1.
D PROSITE; PS00023; FIBRONECTIN_2; 1.
D PROSITE; PS00021; KRINGLE_1; 1.
D PROSITE; PS00070; KRINGLE_2; 1.
D PROSITE; PS00240; TRYPSIN_DOM; 1.
D PROSITE; PS00134; TRYPSIN_HIS; 1.
D PROSITE; PS00135; TRYPSIN_SER; 1.
D EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
D Serine protease.
D SEQUENCE 616 AA; 68012 MW; 4C5FE3D71EBBD1A9 CRC64;

Query Match 30.2%; Score 680.5; DB 6; Length 616;
Best Local Similarity 34.6%; Pred. No. 1.4e-55;
atches 158; Conservative 59; Mismatches 156; Indels 83; Gaps 13;

C 6 QVPSNCCLNGGTCVSNKYFSNIHWNCNPKFGQHCCEIDKSKTCYEGNGHFGYRGASTD 65
D 176 QVCSNPNLNGGSCLOTE---GHLRCPCPTGYAGRLCDVLDKERCYSDRGLSTRGAQTT 232
C 66 TMGRFCLPWSATVLOQTY-HAHRSDALQLGLGKHNYCRPNDRRPWCYVQVGLKPLVQ 124
D 233 LSGAPCQFWAS---EATYWNMTAEQALNGLGDHAFCRNFDNDRPWCYVWRGDLSWQ 288
C 125 ECMVHDC-----ADGKLXFQ----- 139
D 289 YCLARCAQFGEAPPILTPQSFSEHQDSPLLSREPQPTPTPSNLTSAMCAPPEQRG 348
C 140 -----CGQKTLRPF---KIIGGEPTTIENQFWFAIYRRHGGSVTVVCGSLI 186
D 349 PLPSAGLVGGQR-LRKLSSLNRIVGLVALPCAHPYIAALYWGQN-----FCAGSLI 401
C 187 SPQWISATHCIDFDYPKEDYIVYVLSRLNSNTQGMKEFEVENLIHKDYSADTLAHNN 246
D 402 APCWLTAAHCLQRPAPELTVVLGQDRHQCEQCTTLAVRSYRLHESYSPTQYQH-- 459
C 247 DIALLLKIR-SKEGRCAQSFRTIOTICLP---SMYNDPQFGTSCIEITFGKENSTDLYPE 302
D 460 DLALVRLKETADGCAAPSPFVQVCLPRSVASAAPE-GALCEVAGWGHQFPGEAYES 518
C 303 QLRMTVVLISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDGGGLVLC---SLQGR 359

Db 519 FLQEAQVPLISPERCSAADVHGAAFTPGMLCAGLEGGTACQGDGGPLVCEDETAERQ 578
QY 360 MTLTGIVSWGRGKALKDKPKGVYTRVSHFLPWIRSH 395
Db 579 LVLRGIVSWGSGCGDLKPKGVYTDVANYLAWIQEHT 614

RESULT 14
Q81Z25
ID Q81Z25 PRELIMINARY; PRT; 615 AA.
AC Q81Z25;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Coagulation factor XII-Mie.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada H., Nishioka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;
RT "Molecular characterization of coagulation factor XII-Mie.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB095845; BAC23095.1; .
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004283; F:chymotrypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; Fibronctn.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF_2.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00013; FNYPEII.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000995; FN_Type_II; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF_2.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00059; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 615 AA; 67735 MW; 030508870A0C7EDB CRC64;

Query Match 30.0%; Score 678; DB 4; Length 615;
Best Local Similarity 34.1%; Pred. No. 2.4e-55;
Matches 152; Conservative 57; Mismatches 159; Indels 78; Gaps 10;

QY 13 CLNGTGVSNKYFSNIHWNCNPKFGQHCCEIDKSKTCYEGNGHFGYRGASTD 72

DE 183 CLHGRCLC-----VEGRLCHCFVGTGTFCDVDTKASCYDGRGLSYRGLARTLTSLGAPCQ 239
QY 73 PWSATVLOQTY-HAHRSDALQGLGKHNCRNPNDRRRPWCYVQVGLKPLVQECMVHDC 131
DE 240 PWAS-----EATYRNVTAEQARWGLGGAFCRNPDNDIRPWCFFVLRDRLSWYCDLAQC 295
QY 132 -----ADGKL----- 136
DE 296 QTPTQAAPPTVSPRLHVLMPAAPPKPOPTTRTPPQSGTQPGALPAKEQPPSLTRNG 355
QY 137 KFQCGQ---KTLRPRFKIIGEFTTIENQPFALYRHRGGSVTVYVCGSLISPCWVIS 193
DE 356 PLSCGQRLKLSLWTRVVGGLVLRGANPIALYWGHS-----FCAGSLIAPCWLT 409
QY 194 ATHCFIDYPKKEDYVYLGRSLRNTQGMKFEVENLILHKDYSADTLAHDNDIALKI 253
DE 410 AAHLQDRPAPEDLTVLVQGRNHSCEPCQTLAVRSYRLHEAFS--PVSQYQHDALLRL 467
QY 254 R-SKEGRCAQPSRTIOTICLSMYNDPQFGSCITGFKENSIDYLYPEQLXMTVYKLI 312
DE 468 QEDADGSCALLSPYQVPLSGAARSETTLCQVAGCGHQFEGAEBYASFLQEAQVFL 527
QY 313 SHRECOQPHYGYSEVTTKMLCAADPQWKTDSCQDSGGPLVCSLQG---RMTLTGIVSWG 369
DE 528 SLERCSAPDVHGSILPGMLCAGFLEGDTACQDSGGPLVCEQQAARLTLQGIISWG 587
QY 370 PGCAKDKGYNTRYSHLPWIRSH 395
DE 588 SGCGDRNKPQYTVDAVYLAWIREHT 613
RE LT 15
O3 27
IE O35727 PRELIMINARY; PRT; 597 AA.
AC O35727;
DT 01-JAN-1998 (TREMELrel. 05, Created)
DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Factor XII.
GF F12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RE TISSUE=Liver;
RC Schloesser M., Schwager S., Engel W.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DE EMBL; X99571; CAA67891.1; -;
DE HSSP; P00760; IAO7.
DE MEROPS; S01.211; -;
DE MGD; MGI:1891012; F12.
DE GO; GO:0005575; C:extracellular; IEA.
DE GO; GO:0004263; F:chymotrypsin activity; IEA.
DE GO; GO:0008233; F:peptidase activity; IEA.
DE GO; GO:0004295; F:trypsin activity; IEA.
DE GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DE InterPro; IPR009003; Cys Ser trypsin.
DE InterPro; IPR006209; EGF-like.
DE InterPro; IPR000083; Fibinctnl.
DE InterPro; IPR000562; FN Type_II.
DE InterPro; IPR006210; IEGF.
DE InterPro; IPR000001; Kringle.
DE InterPro; IPR001254; Peptidase S1.
DE InterPro; IPR001314; Peptidase_S1A.
DE Pfam; PF00008; EGF; 2.
DE Pfam; PF00039; fn1; 1.
DE Pfam; PF00040; fn2; 1.
DE Pfam; PF00051; kringle; 1.
DE Pfam; PF00089; trypsin; 1.

DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0013; ENTPEI1.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; FN Type_II; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
KW Serine protease.
SQ SEQUENCE 597 AA; 65638 MW; F3AC07C37D0C0FBA CRC64;
Query Match 29.6%; Score 668; DB 11; Length 597;
Best Local Similarity 35.6%; Pred. No. 2.1e-54;
Matches 152; Conservative 61; Mismatches 154; Indels 60; Gaps 13;
QY 13 CLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNHFYRGKASTDTYGRPCL 72
DB 183 CLNGGSL---LVEDHPLCRCPSTGYTFCDLDLWATCYEGRLSYRQAGTTQSGAPCQ 239
QY 73 PWSATVLOQTY-HAHRSDALQGLGKHNCRNPNDRRRPWCYVQV----- 118
DB 240 RM-----TVEATYRNTEKQALSWGLGHAFCEPNPDNTPWCFVWSGDELSDYDGLBQC 295
QY 119 -----LKPLV-----QE-----CMVH---DCADGKLKFG-----CGQ---KTLRPRFKI 151
DB 296 QTPTFAPLVPSQESPSQAPSLSHAPNDSTDHQTSLSKTNTMCGQGRFRKGLSSPMRV 355
QY 152 IGGEFTTIENQPFALYRHRGGSVTVYVCGSLISPCWISATHCIFDYPKEDYIVVL 211
DB 356 VGLVALPQSHFYIALYGNM-----FCAGSLIAPCWLTAAHCLNRPAPELTVVL 409
QY 212 GSRSLNNTQGMKFEVENLILHKDYSADTLAHDNDIALKIR-SKEGRCAQPSRTIQT 270
DB 410 GQDRHNQSCWCQTLAVRSYRLHEGFSITYGH--DLALLRQESKTNSCATLSPHVQPV 467
QY 271 CLPSMYNDPQFGTSCETGFGKENSTDYLYPEQLXMTVYKLIHRECCQPHYGVSEVTK 330
DB 468 CLPSGAAPSETVLCVAGWHQLEGAEYSTFLQEAQVFFIALDRCSNNSNVHGDAILPG 527
QY 331 MLCAADPQWKTDSCQDSGGPLVC---SLQGRMTLTGIVSWGRGALCKPKGVYTRVSHF 387
DB 528 MLCAGFLEGDTACQDSGGPLVCEGTAEGTAHQLTLRGVISWGGCGDRNKPQYTVDAVY 587
QY 388 LPMIRSH 394
DB 588 LAWIQKH 594
RESULT 16
Q80YC5 PRELIMINARY; PRT; 609 AA.
ID Q80YC5
AC Q80YC5
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to coagulation factor XII (Hageman factor) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Liver;
Strausberg R.; to the EMBL/GenBank/DBJ databases.
Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC049867; AA49867.1; -
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR01881; EGF_Ca.
InterPro; IPR006209; EGF-like.
InterPro; IPR000083; Fibinectn1.
InterPro; IPR000562; FN_Type_II.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 2.
Pfam; PF00039; fn1; 1.
Pfam; PF00040; fn2; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00018; KRINGLE.
ProDom; PD000995; FN_Type_II; 1.
ProDom; PD000395; Kringle; 1.
SMART; SM00181; EGF; 2.
SMART; SM00179; EGF_Ca; 2.
SMART; SM00058; FN1; 1.
SMART; SM00059; FN2; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01195; EGF_2; 1.
PROSITE; PS01253; FIBRONECTIN_1; 1.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
NON_TER.
SEQUENCE 609 AA; 6768 MW; DF97D4D2B369B6D2 CRC64;
Query Match 29.6%; Score 668; DB 11; Length 609;
Best Local Similarity 35.6%; Pred. No. 2.le-54;
Matches 152; Conservative 61; Mismatches 154; Indels 60; Gaps 13;
13 CLNGGTCVSKYFSNIHWCNCPKFGGQHCEIDKSKTCYEGNGHFRGKASTDTMGRPL 72
195 CLNGGSL-----LVEDHPLCRPTGYTGFCDDLWATCYEGRGLSYRGAGTTQSGAPCQ 251
73 PWSATVLCQTY-HAHRSDALQLGLGKHNCRPNRRRRCVYVQV-----118
252 RW-----LKEPLV-----QEV-----CDAGKLFQ-----CGQ---KTLRPRFKI 151
308 QTPTFAFLVVPESOEPSOAPSLSHAPNDSTDHQTSKNTWGGCGQFRKGLSFMFV 367
152 IGGFTTIENQPAFYRHRGSSVTVYCGGSLISPCWVISATHCFIDYPKKEDIVYL 211
368 VGGUVALPGSHPIYALYWN-----FCAGSLIAPCWVILAHCLQRPAPELTVVL 421
212 GRSLNLTQGEKMFVENILHKYSGADTLAHHNDIALKIR-SKEGRCAQPSRTIQT 270
422 QDRHNSCEWCQTLAVRSYRLHEGFSSITVQH-DLALLRLQESKNTSCAILSPHVQV 479
271 CLPSMYNDPQGTSCETIGKSTNDYLYPEQLKMTVVKLISHRECOQPHYVGSVYTK 330
Db Qy 480 CLPSGAAPPSETVLCVAGNGHQPEGAEEYSTFLQEAQVFIALDRCSNVHGDAILPG 539
331 MLCADPQWTDSCQSGSGPLVC---SLQGRMTLTGIVNGRCALKDKPGVYTRVSHF 387
540 MLCAGFEGGTDAQCGSGGGLVCEGTAEHQLTLRGVSWGSGCGDRNKPVGVTDVANY 599
388 LPWIRSH 394
600 LAMIKQH 606
RESULT 17
Q8K0D2 PRELIMINARY; PRT; 517 AA.
ID Q8K0D2
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; BC031775; AAH31775.1; -
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein; EGF-like domain; Glycoprotein; Hydrolase;
KW Kringle; Protease; Serine protease.
SQ SEQUENCE 517 AA; 57326 MW; 3855A42035A5EA59 CRC64;
Query Match 29.4%; Score 664.5; DB 11; Length 517;
Best Local Similarity 36.9%; Pred. No. 3.7e-54;
Matches 154; Conservative 57; Mismatches 163; Indels 43; Gaps 14;
13 CLNGGTCVSKYFSNIHWCNCPKFGGQHCEIDKSKTCYEGNGHFRGKASTDTMGRPL 72
116 CQNGVCVSRHRRSRF-TCACPDYKGFCEIGPD-DCYVGDGYSYRGKSKTVNQNPCL 173
73 PWSATVLCQTY-HAHRSDALQLGLGKHNCRPNRRRRCVYVQVGLKPL-----VQEC 126

DB 174 YWNSHLLQTYNMFEDASTHGIABHFNCPDGHKPCWCFVKVNSEKVKWEYCDVTVC 233
QY 127 MVDCADCKLKF-----CCQOKTLRPF--KIIGBETTIENQFWFAIY---- 169
DE 234 PVPTDTPNVSLELPEVWELFGFSCGTEVAEHAHVKRIYGGFKSTAGKHPQVLSQTSUP 293
QY 170 ---RRHGGGVTVYVCGSLISPCWVTSATCFIDYPKKEDIYVYLGSRSLNSNTQGEKPF 226
DB 294 LTTSMPQG---HFCGGLIHPQWVLTAAHC-TDINTKHLKV-LGDQDLKKTESHEQTF 347
QY 227 EVENLILHKYSADTLAHNDIALLKRSKGRCAQPSRIOTICLPSMYNDP-QFGTSC 285
DE 348 RVEKILKYSQNERDEIPHNDIALLKLPVGGHCALESRYKTVCLPS---DFPPSGTEC 404
QY 286 EITGFGKENSVDLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPQW-KTDC 344
DE 405 HISGNGVTEGE--GSRQLLDAKVKLIANPLNSRQLYDHTIDDSMICAGNLQKPGSDTC 462
QY 345 QGDSGGPLVCSLQGRMTLTGIVSGRCALKDPGVTVRVSHFLPWIRSHTKENG 401
DB 463 QGDSGGPLTCEKDTGVYVGVSVGLECG--KPGVYTVQTKFLNWKITMTHREAGL 517
RE 1T 18
Q1 20
ID Q14520 PRELIMINARY; PRT; 560 AA.
AC Q14520; O00663;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE HGF activator like protein (Hyaluronan binding protein 2).
OE Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitamura N.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RF SEQUENCE FROM N.A.
RX MEDLINE=96425001; PubMed=8927452;
RA Chai-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
RA Tomita M.;
RT "Purification and characterization of a novel hyaluronan-binding
RT protein (PHBP) from human plasma: it has three EGF, a kringle and a
RT serine protease domain, similar to hepatocyte growth factor
RT activator.",
RL J. Biochem. 119:1157-1165(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Kidney;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -|- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DE EMBL; D49742; BAA08576.1; -;
DE EMBL; S83182; AAB46909.1; -;
DE EMBL; BC031412; AAH31412.1; -;
DE PIR; JC4795; JC4795.
DE HSSP; P00763; LDPO.
DE MEROPS; S01.033; -;
DE Genew; HGNC:4798; HARP2.
DE GO; GO:0005615; C:extracellular space; TAS.
DE GO; GO:0005539; F:glycosaminoglycan binding; TAS.
DE GO; GO:0007155; P:cell adhesion; TAS.
DE InterPro; IPR009003; Cys Ser trypsin.
DE InterPro; IPR006209; EGF-like.
DE InterPro; IPR000001; Kringle.
DE InterPro; IPR001234; Peptidase_S1.
DE InterPro; IPR001314; Peptidase_S1A.
DE Pfam; PF00008; EGF; 3.

DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
KW Serine protease.
SQ SEQUENCE 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;
Query Match 28.9%; Score 651.5; DB 4; Length 560;
Best Local Similarity 36.4%; Pred. No. 6.9e-53;
Matches 152; Conservative 58; Mismatches 161; Indels 47; Gaps 14;
QY 13 CLNGSTCVSNKYFNIHWCNCPKKGGOHCEIDKSKTCYEGNGHFYRGKASTDTWGRPCL 72
DB 159 CQNGATCSRHRKRSKP-TCACPDQFKGFCFEG-SDDCYVGGYSGYRGKMRVTNQHACL 216
QY 73 PWSATVLTQTYHAHRSDALQLGLGKHNCRPNRRPWCYVQVGLKPLVOE-CWVHDC 131
DB 217 YWNSHLLQENYVNMFMEDASTHGIABHFNCPDGHKPCWCFVKVNSEKVKWEYCDVSAC 276
QY 132 ADGKLKF-----CCQOKTLRPF--KIIGBETTIENQFWFAIYRHR 173
DB 277 SAQDVAYPEESTPSTKLPGFDSGKTEIAERIKRIYGGFKSTAGKHPQWASLQ---- 332
QY 174 GGSVTF-----YVCGSLISPCWVTSATCFIDYPKKEDIYVYLGSRSLNSNTQGEK 225
DB 333 -SSLPTTISMPQGHFCGGLIHPQWVLTAAHC-TDI-NTRHLKVGLDQDLKKEEFHQS 389
QY 226 FEVENLILHKYSADTLAHNDIALLKRSKGRCAQPSRIOTICLPSMYNDP--GT 283
DB 390 FRVEKIFKYSHYNERDEIPHNDIALLKLPVGGHCALESRYKTVCLP---DGSFPFSGS 445
QY 284 SCEITGFGKENSVDLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPQW-KT 342
DB 446 ECHISGNGVTEGE--GSRQLLDAKVKLIANPLNSRQLYDHTIDDSMICAGNLQKPGD 503
QY 343 SCQDSGGPLVCSLQGRMTLTGIVSGRCALKDPGVTVRVSHFLPWIRSHTKENG 400
DB 504 TCQDSGGPLTCEKDTGVYVGVSVGLECG--KPGVYTVQTKFLNWKITKESG 559
RESULT 19
Q9TVAS PRELIMINARY; PRT; 157 AA.
AC Q9TVAS;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Urokinase plasminogen activator (Fragment).
OS Bos taurus (Bovine);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=21071388; PubMed=11204721;
RA Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.;
RT "Coordinate expression of matrix-degrading proteinases and their
RT activators and inhibitors in bovine skeletal muscle.",
RL J. Anim. Sci. 79:94-107(2001).
CC -|- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DE EMBL; AF144761; AAD30301.1; -;
DE HSSP; P00749; IURK.

GO; GO:0016301; F:kinase activity; IEA.
InterPro; IPR006209; EGF-like.
InterPro; IPR000001; Kringle.
Pfam; PF00051; kringle; 1.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
Glycoprotein; Kinase; Kringle.
NON_TER 157 157
NON_TER 157 157
SEQUENCE 157 AA; 17858 MW; A768D6C72C1FBB7 CRC64;

Query Match 28.3%; Score 638; DB 6; Length 157;
Best Local Similarity 70.7%; Pred. No. 2.7e-52;
atches 111; Conservative 14; Mismatches 24; Indels 8; Gaps 1;

13 CLANGTCVSNKYFNHWCNCPKFGGQHCEIDKSKTCYBGNHGFYRGKASTDTMGRPCL 72
1 CLANGKCVTVKYNFNIQRCSPKFGQEHCEIDTSKTCYQNGHSGVGRKANRDLSPCL 60

73 PWSATVLQOTYHAHRSDALQLGLGKHYCRNPDNRPRMPCYVQVGLKPLVQECMYHDC 132
61 AWPSTVLLKMYHAHRSDAIQLGLGKHYCRNPDNRPRMPCYVQVGLKPLVQECMYHDC 120

133 DGKL-----KFQCGKTLRPREKLIIGFEFTIEN 161
121 VGKSPSPSPEKKEPFQCGKALRFRKIVGQVTNAEN 157

ULT 20
587 PRELIMINARY; PRT; 128 AA.
097587;
097587;
01-MAY-1999 (TRENBLrel. 10, Created)
01-MAY-1999 (TRENBLrel. 10, Last sequence update)
01-OCT-2003 (TRENBLrel. 25, Last annotation update)
Urokinase (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
[1]
SEQUENCE FROM N.A.
STRAIN=New Zealand White;
MEDLINE=95057575; PubMed=9837780;
Reno C.; Boykiw R.; Martinez M.L.; Hart D.A.;
"Temporal alterations in mRNA levels for proteinases and inhibitors
and their potential regulators in the healing medial collateral
ligament."
Biochem. Biophys. Res. Commun. 252:757-763(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; AF069711; AAC95003.1; -.
HSP; P00749; IEJN.
MEROPS; S01.231; -.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys.Ser trypsin.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; TRYP_SPC; 1.
PROSITE; PS00240; TRYPIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
Hydrolase; Kinase; Protease; Serine protease.
NON_TER 1 1
NON_TER 128 128

SQ SEQUENCE 128 AA; 14328 MW; 1BC7ED305071A06D CRC64;

Query Match 25.9%; Score 585; DB 6; Length 128;
Best Local Similarity 84.4%; Pred. No. 2.1e-47;
Matches 108; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 164 WFAALYRRHRCGVSYYVCGSLISPCWVISAHGFIDYPKKEDYIVLGRSLNSNTQGE 223
Db 1 WFAALYRRHRCGVSYYVCGSLISPCWVISAHGFIDYPKKEDYIVLGRSLNSMTTGE 60

QY 224 MKFEVENILHKDYSADTLAHNDIALIKIRSKGRCQAQPSRTIQTICLPSMYNDPQFGT 283
Db 61 MKFEVEQLILHEGYRADTLAHNDIALIKILSNNGCAQPSRSIQTICLPPWADPNFGT 120

QY 284 SCEITGFG 291
Db 121 SCEITGFG 128

RESULT 21
Q9ROW3 PRELIMINARY; PRT; 812 AA.
AC Q9ROW3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Plasminogen protein precursor (EC 3.4.21.7).
GN PLASMINOGEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bangert K.; Johnsen A.H.; Thorsen S.;
RT "Rat plasminogen: cDNA and gene structure."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanalas J.J.; Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
receptor site for plasminogen."
RL J. Biol. Chem. 266:10825-10829(1991).
CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; AJ242649; CAB46014.1; -.
DR HSP; P00747; 1PMK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys.Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.


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GO: GO:0008333; F:peptidase activity; IEA.
GO: GO:0003809; F:thrombin activity; IEA.
GO: GO:0004295; F:trypsin activity; IEA.
GO: GO:0007596; P:blood coagulation; IEA.
GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro: IPR009003; Cys Ser trypsin.
InterPro: IPR000001; Kringle.
InterPro: IPR003014; PAN.
InterPro: IPR003609; Pan_app.
InterPro: IPR001254; Peptidase_S1.
InterPro: IPR001314; Peptidase_S1A.
InterPro: IPR003966; Peptidase_S1A_pr.
Pfam: PF00051; kringle; 5.
Pfam: PF00024; PAN; 1.
Pfam: PF00089; trypsin; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
PRINTS: PR00018; KRINGLE.
PRINTS: PR00505; PROTHROMBIN.
ProDom: PD000395; Kringle; 5.
SMART: SM00130; KR; 5.
SMART: SM00473; PAN_AP; 1.
SMART: SM00020; TRYD_SPC; 1.
PROSITE: PS00021; KRINGLE_1; 5.
PROSITE: PS00070; KRINGLE_2; 5.
PROSITE: PS00240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; 1.
PROSITE: PS00135; TRYPSIN_SER; 1.
Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.
CHAIN
SIGNAL
1 19
20 810
SEQUENCE 810 AA; 90555 MW; R05C7D4B0D020B3C CRC64;
try Match 22.1%; Score 498; DB 4; Length 810;
t:Local similarity 33.4%; Pred. No. 3,7e-38;
ches 136; Conservative 45; Mismatches 170; Indels 56; Gaps 15;

10 NCDCLNGGTCVSNKYFNIHWCNCPKKGQ-----HCIDKSKTCYEGNGH 56
428 NPDADKGFWCFTTDPSPVRWEYCNLKCSGTEASVAPPVLLPDVETPSEEDCMFGNGK 487
57 FYRGKAGSTDTMGRCPLPNWASATVLLQYTAHR---SDALQLGLGKHNYCRNPD-NRRRP 111
488 GYRKGRATTVTGTPCQDWA-----QEPHHSFTPTNFRAGLEK-NYCRNPDGVDVGP 541
112 WCYYVQVGLKPLVQECWYHDCADGKLKQCQKTLRPR---FKIIGSEFTTIENQWFAAI 168
542 WCYTF-TNPKRLDYCDYPPQCA--APSPDCGKQPVEPKKCFGRVVGVCVAHPHSPWQVSL 598
169 YRRHRGGSVTVCGGSLTSPCOWISATHCTIDYPKXEDYIVLGRSLNMTQCEMKFEV 228
599 --RTRFG--MHEFCGTTLSPEWVLTAAHLEKSPRPSYKVLGAHQEVNLEPHVQIEV 654
229 ENLILHKDYADTLAHNDIALKIRKEGRCAQPSRTIOTICLPMSYNDPQF-----GTS 284
655 SRLFEPT-----RKDIALKLSP-----AVITDKVIPACLPS-----PNYVVADRT 698
285 CEITGFGKENSVDLYPEQLKMTVVKLISHRECOQPHYGVSEVTKMLCAADPQWKDSC 344
699 CFVTGWGETQGT--FGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSC 756
345 QDSSGGLPVCSLQGRWTLTGIVSGRCALKDKRPGVTVTRVSHFLPWI 391
757 QDSSGGLPVCFEKDKYILQGVTSNGLGCARPKNKPGVTVRVSFRFTWI 803

JT 23
99
Q95M89 PRELIMINARY; PRT; 103 AA.
Q95M89;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Plasminogen activator urokinase (Fragment).

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PLAU.
C Equus caballus (Horse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
C NCBI_TaxID=9796;
C [1]
F SEQUENCE FROM N.A.
F MEDLINE=21314992; PubMed=11421942;
F Shubtowski D.M., Venta P.J., Douglass C.L., Zhou R.-X., Ewart S.L.;
F "Polymorphism identification within 50 equine gene-specific sequence
F tagged sites.";
F Anim. Genet. 32:78-78(2001).
C -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
D EMBL; AY008806; AA114840.1;
D GO; GO:0004263; F:chymotrypsin activity; IEA.
D GO; GO:0016301; F:kinase activity; IEA.
D GO; GO:0008233; F:peptidase activity; IEA.
D GO; GO:0004295; F:trypsin activity; IEA.
D GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
D InterPro; IPR009003; Cys Ser trypsin.
D InterPro; IPR001254; Peptidase_S1.
D Pfam; PF00089; trypsin; 1.
D PRINTS; PR00722; CHYMOTRYPSIN.
D SMART; SMO020; Tryp_Spc; 1.
D PROSITE; PS0240; TRYPSIN_DOM; 1.
D PROSITE; PS00134; TRYPSIN_HIS; 1.
D Hypothetical protein; Kinase; Protease; Serine protease.
D NON_TER 1 103
D SEQUENCE 103 AA; 11525 MW; 05739514F6331180 CRC64;

Query Match 21.9%; Score 495; DB 6; Length 103;
Best Local Similarity 87.4%; Pred. No. 5.4e-39;
atches 90; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

164 WFAIYRRHGGSVYVCGSLSPCWVLSATHCFIDYPKEDYIVYVGLSRSLNSTQGE 223
1 WFAIYRRHGGSVYVCGSLSPCWVLSATHCFIDYPKEDYIVYVGLSRSLNSTQGE 60

224 MKEFEVNLILHKOYSADTLAHNDIALLKIRSKEGRCQAQPSRT 266
61 MKEFEVNLILHKOYSADTLAHNDIALLKIRSKEGRCQAQPSRS 103

JLT 24
EF3
Q96EF3 PRELIMINARY; PRT; 300 AA.
Q96EF3
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Coagulation factor XII) (Hageman factor).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUE=Lung;
Straussberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
Kalinine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
Koundinya M., Raphael J., Moreira D., Kelley T., Labaer J., Lin Y.,
Phelan M., Farmer A.;
Cloning of human full-length cDNAs in BD Creator(TM) System Donor
vector.";
Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL; BC012330; AA112330.1; -

DR EMBL; BT007350; AAP36014.1; -
DR HSSP; P00761; IAN1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SMO020; Tryp_Spc; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hypothetical protein; Hydrolase; Protease; Serine protease.
KW SEQUENCE 300 AA; 32216 MW; PFC2BDF9382F638A CRC64;

Query Match 21.9%; Score 493.5; DB 4; Length 300;
Best Local Similarity 37.3%; Pred. No. 2.8e-38;
Matches 112; Conservative 46; Mismatches 119; Indels 23; Gaps 7;

QY 103 RNDNRARPWCYVQVGLKPLVQECWHDGADGKLKFCGQ--KTLAPRPKLIIGERTTI 159
Db 15 RTTPSQSTP-----GALPAKREQPPSLTRNGPL--SCQRLRSLSSMTRVVGLVALR 66

QY 160 ENQPFWFAIYRRHGGSVYVCGSLSPCWVLSATHCFIDYPKEDYIVYVGLSRSLNSN 219
Db 67 GAHFVIAALYNGHS-----FCAGSLIAPCWVLTAAHCLQDRPAPEDLTIVVGLQERRNHS 120

QY 220 TQCEKKEVENLILHKOYSADTLAHNDIALLKIR-SKEGRCAQPSRTIQTICLPSMYND 278
Db 121 CEPQOTLAVRSYRLHEAFS--PVSYQHDLLALRIQEDADGSCALLSPYVQVCLPSGAAR 178

QY 279 PQFTSCBITGFKENSTDYLPQLKMTVVKLISHRECCQPHYVGGSEVITKMLCAADPQ 338
Db 179 PSEITLCQVAGHQFEGAEYASFLQEAQVPPFSLERCSAPDVHGSILFGMLCAGFLE 238

QY 339 WKTSCQDSDGGLVCSLQG---RMTLTGVSWGRGKALDKPKGVYTRVSHFLPWIRSH 395
Db 239 GGTDACQDSDGGLVCSLQG---RMTLTGVSWGRGKALDKPKGVYTRVSHFLPWIRSH 298

RESULT 25
Q46506 PRELIMINARY; PRT; 454 AA.
AC Q46506
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Apolipoprotein a (Fragment).
GN B4BAP0A.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RA Cox L.A., Jett C., Hixson J.E.;
RT "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
RT Site Mutation is Associated with Deletion of a Single Exon in a Null
RT Allele."
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DR EMBL; AF029691; AAB97886.1; -
DR HSSP; P00747; 2PK4.
DR MEROPS; S01.999; -
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR009003; Cys Ser trypsin.
 DR InterPro: IPR000001; Kringle_1.
 DR InterPro: IPR001254; Peptidase S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00051; Kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 2.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00021; KRINGLE_1; 2.
 DR PROSITE: PS00070; KRINGLE_2; 2.
 DR PROSITE: PS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydrolase; Kringle; Lipoprotein; Protease;
 FT Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;
 37y Match 21.8%; Score 493; DB 6; Length 454;
 st Local Similarity 33.8%; Pred. No. 5.3e-38;
 tches 127; Conservative 51; Mismatches 134; Indels 64; Gaps 14;
 QY 50 CYEGNGHFYRGKASTDTMGRCPLPWSATVLQ--QTYHAHRS DALQLGLGKHNYCRPN 107
 DE 102 CYHGDGSGYRGSFSTVTGRTCCQSSWMTPHQKRTPEHPDGLTV-----NYCRNPD 156
 QY 108 RRRPWCYVQVGLKPLV--QECMVHDCAD-----GKLPQCGQ 342
 DB 157 DTGFWCFI---MDPSVAWEYCNLFRCSDTEGTVVTLVPIPSLEARSQASSPDCGK 213
 QY 143 KTLRPR---FKLIGETTTNQWFAIYRHRGGSVTVVCGSLSPCWVLSATHCFI 199
 DB 214 PQVEFKCPGVRGVGCAHAHWSQVSL--RTRFGK--HFCGGLTLPSPWVLTARCLE 269
 QY 200 DYPKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSADTLAHNDIALKIRSKGR 259
 DE 270 MSPSPSSKVLG-----AHQEVNLESHVQIEVSKLFSBPTGA---DIALKL-----SR 317
 QY 260 CAQPSRTIQTCLSMYNDPQF-----GTSCEITGFKENSTDIYLPQLKMTVVKLISHR 315
 DB 318 PAITDKVIPACLPFS---PNYITAMTECVITGWTGQTF--FGAGLLREARLPVIENT 371
 QY 316 ECQPHYVYGVSEVTKMLCAADPQWKTDSCQDSCGSLVCSLQGRMTLTGIVSWGRCALK 375
 DE 372 VCNRYEPLNGRVKSTELCAGHLAGTDSQDSCGSGPVVCFDKKYLIRGITSNGPGCARP 431
 QY 376 DKPGYVTVSHFLPMI 391
 DE 432 NKPGYVTVSVSFTWTI 447

RE Q8 6T 26
 ID Q8AVB0 PRELIMINARY; PRT; 429 AA.
 AC Q8AVB0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Plasminogen precursor (Fragment).
 DE Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RE SEQUENCE FROM N.A.
 RA Hanumanthaiah R., Day K., Jagadeeswaran P.;
 RI "Comprehensive analysis of blood coagulation pathways in teleostei:
 RI Evolution of coagulation factor genes and identification of zebrafish
 RI factor VIII";
 RI Blood Cells Mol. Dis. 0:0-0(2002).

DR EMBL: AF515276; AAN71006.1;
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR009003; Cys_Ser_trypsin.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Peptidase S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00051; Kringle; 2.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 2.
 DR SMART: SM00130; KR; 2.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00070; KRINGLE_2; 2.
 DR PROSITE: PS0240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 FT NON_TER 1
 SQ SEQUENCE 429 AA; 47556 MW; 9A580A214A549C12 CRC64;
 Query Match 21.8%; Score 491.5; DB 13; Length 429;
 Best Local Similarity 35.3%; Pred. No. 6.8e-38;
 Matches 127; Conservative 37; Mismatches 155; Indels 41; Gaps 13;
 QY 48 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQ---TYHAHRS DALQLGLGKHNYCRN 104
 DB 100 KDCXNGNGAEYRGSTMTVMGTTCQAMRSMTPHQAHSFTPTHDPKGLG-----SNQCRN 154
 QY 105 PDNR--RRPWCYVQVGLKPLVQECMVHDCADKGLKFCQCGKTLRPR---FKLIGSEFTTIE 160
 DB 155 PDSVDVNGPWCYVTDPSKKW--DYCQIPDCE---SLKCGPATKPKRCFGRIVGCVSKPH 209
 QY 161 NOPWFAIYRHRGGSVTVVCGSLSPCWVLSATHCFIDYPKKEDIYVILGRSLNSNT 220
 DB 210 SWPW--QISLTRG--KIHFCGGLTLPQWVVTAAHLERSDSSPAVKMLGITERATE 265
 QY 221 QCEMKFEVENLILHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPQ 280
 DB 266 SSKQERDVKII---KGPAQT-----DIALKL-----DRPALINDKVPCLPEKDYIVP 313
 QY 281 FQTSCEITGFKENST---DYLPEQLKMTVVKLISHRECOOPHYGVSEVTKMLCAADP 337
 DB 314 SNTCEYVTVGWTGQDTQDGEGY-----LKEITGFVIVENVCNRPFLNGRVKHENCAINI 368
 QY 338 QMKTDSCQDSCGSLVCSLQGRMTLTGIVSWGRCALKDKPGYVTVRSHFLPWIRSHTK 397
 DB 369 EGGNDSQDSCGSLVCSLQGRMTLTGIVSWGRCALKDKPGYVTVRSHFLPWIRSHTK 428

RESULT 27
 O46507 PRELIMINARY; PRT; 334 AA.
 ID O46507
 AC O46507;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Plasminogen (Fragment).
 GN BABPEPSG.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheciinae; Papio.
 OC NCBI_TaxID=9557;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Cox L.A., Jett C., Hixson J.E.;
 RI "Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice
 RI Site Mutation is Associated with Deletion of a Single Exon in a Null
 RI Allele";
 RI Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

C -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 D EMBL; AF029692; AAB97887.1; -.
 D HSP; P00747; SHPG.
 D MEROPS; S01.233; -.
 D GO; GO:0005509; F:calcium ion binding; IEA.
 D GO; GO:0004263; F:chymotrypsin activity; IEA.
 D GO; GO:0008233; F:peptidase activity; IEA.
 D GO; GO:0003809; F:thrombin activity; IEA.
 D GO; GO:0004295; F:trypsin activity; IEA.
 D GO; GO:0007596; P:blood coagulation; IEA.
 D GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 D InterPro; IPR009003; Cys_Ser_trypsin.
 D InterPro; IPR001254; Peptidase_S1.
 D InterPro; IPR001314; Peptidase_S1A.
 D InterPro; IPR003966; Peptidase_S1A_pr.
 D Pfam; PF00051; kringle; 1.
 D Pfam; PF00089; trypsin; 1.
 D PRINTS; PR00722; CHYMOTRYPSIN.
 D PRINTS; PR0018; KRINGLE.
 D PROSITE; PS00135; TRYPSIN_SER; 1.
 D Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
 D NON_TER; 1.
 F SEQUENCE 334 AA; 36791 MW; C7DC06E03B965286 CRC64;
 E
 Query Match 21.6%; Score 486.5; DB 6; Length 334;
 Best Local Similarity 36.2%; Pred. No. 1.5e-37;
 Matches 129; Conservative 46; Mismatches 134; Indels 47; Gaps 16;
 C 50 CYENGHFYKASTDWMGRPLPNSATVLQTYHAH----RSDALQLGLGKHNYCRNP 105
 D 5 CMFNGKRYKKAATVTGTPQEWAA-----KEPHSLIFTETTPRAGLEK-NYCRNP 59
 C 106 D-NRRRPWCYVQVGLKPLVQECMVHDCADGKLKFCQCKTLRPR---FKIIGGFTTIE 161
 D 59 DGDVGGFWCYT-TNPRKLYDCVDPQCASS--SFDGKPKQVPEKPKGRVVGCVAAH 115
 C 162 QPWFAAYRRHSGSVYVCGSLISPCWISATHCFIDYPKEDYIVLGRSLNSNTQ 221
 D 116 WPMQVSL--RTRFG--MHFCGGTLISPEWVLTAAHCLKSPRPSFYKVLGAHQ----- 165
 C 222 GEMKFE--VENLILHKDYSADTLAHHNDIALLKIRSEKGRCAOPSRITQICLPSMYNDP 279
 D 166 -EYLEPHVQIEIVSKMFSEPA--DIALKLSP-----AITDKVIPACLPSP---P 213
 C 280 QF-----GTSCEITGFGKENSTDYLPQLKMTVVKLISHRECQOPHYGSEVTTKMLCAA 335
 D 214 NYVVADRETCFTGWGTQGT--YGAGLLKEARLPVIEVNCNRYEFLNGRVKSTELCAG 271
 C 336 DPQKNTSCQDGGPLVCSLQGRMTLTGIVSGRGCAKDKGQVYTRVSHFLPWI 391
 D 272 HLAGTDSQDGGPLVCEKQKYLQGVTSNGLGCAKPKGVYVYVSRFTWI 327
 R ILT 28
 C 783
 I 018783 PRELIMINARY; PRT; 806 AA.
 A 018783;
 D 01-JAN-1998 (TRENBLrel. 05, Created)
 D 01-JAN-1998 (TRENBLrel. 05, last sequence update)
 D 01-OCT-2003 (TRENBLrel. 25, last annotation update)
 D Plasminogen.
 C Macropus eugenii (Tamar wallaby).
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 C Mammalia; Metatheria; Diprotodontia; Macroplidae; Macropodidae; Macropus.

OX NCBI_TaxID=9315;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98004511; PubMed=9342350;
 RA Lawn R.M., Schwartz K., Patthy L.;
 RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
 CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 D EMBL; AF012297; AAB65760.1; -.
 D HSP; P00747; SHPG.
 D MEROPS; S01.233; -.
 D GO; GO:0005509; F:calcium ion binding; IEA.
 D GO; GO:0004263; F:chymotrypsin activity; IEA.
 D GO; GO:0008233; F:peptidase activity; IEA.
 D GO; GO:0003809; F:thrombin activity; IEA.
 D GO; GO:0004295; F:trypsin activity; IEA.
 D GO; GO:0007596; P:blood coagulation; IEA.
 D GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 D InterPro; IPR009003; Cys_Ser_trypsin.
 D InterPro; IPR001254; Peptidase_S1.
 D InterPro; IPR001314; Peptidase_S1A.
 D InterPro; IPR003966; Peptidase_S1A_pr.
 D Pfam; PF00051; kringle; 1.
 D Pfam; PF00089; trypsin; 1.
 D PRINTS; PR00722; CHYMOTRYPSIN.
 D PRINTS; PR0018; KRINGLE.
 D PROSITE; PS00135; TRYPSIN_SER; 1.
 D Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
 D NON_TER; 1.
 F SEQUENCE 806 AA; 90981 MW; 95FAA86DC2064D5 CRC64;
 E
 Query Match 20.8%; Score 469.5; DB 6; Length 806;
 Best Local Similarity 31.9%; Pred. No. 1.8e-35;
 Matches 129; Conservative 43; Mismatches 165; Indels 67; Gaps 15;
 QY 13 CLNGGTCVSNKYFNSIHCNCPKFKGQHCIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
 DB 448 CSGTGSTVLNAQTTRV-----PSVDTTSHPSD---CMYSGKDYRKGRSTTVTGLCQ 498
 QY 73 PWSATVLTQTYHAH---RSDALQLGLGKHNYCRNP-NRRRPWCYVQVGLKPLVQECMV 128
 DB 499 AWTA-----QEPHRTITFTPDYPRAGLEENYCRNPDGDPNGWCYT-TNPKLFDYCDI 552
 QY 129 HDCADGKLKFCQCKTLRPR---FKIIGGFTTIEQWFAAYRRHSGSVYVCGSL 185
 DB 553 PCQVSPS-SFDGKPRVEPKQPCGRIVGCVAPHSNEM--QISLRTFGE--HFCGGL 607
 QY 186 ISPCWISATHCFIDYPKEDYIVLGRSLNSNTQEMKFEVENLILHKDYSADTLAHH 245
 DB 608 IAPQWVLTAAHCLERSQWPGAYKVLG-----LHREVNPEYSQGE 647
 QY 246 -----NDIALLKIRSEKGRCAOPSRITQICLPSMYNDPQGTGTCETGFGKE 293
 DB 648 IGVSLFKGPLAADIALLKL-----NRPAAINDKVIPACLPQDFWVDPRTICHVTGWGDT 703
 QY 294 NSTDYLYPE-QLKMTVVKLISHRECQOPHYGSEVTTKMLCAADPQWKTSCQDGGPL 352
 DB 704 QGTS---PRGLLKQASLEFVINDNRVNCNRYEFLNGRVKSTELCAGHLVGRGSCQDGGPL 760
 QY 353 VCSLQGRMTLTGIVSGRGCAKDKGQVYTRVSHFLPWI 396

761 ICEDDDKVLQGVTSWGLGCRPNKPGYVYVRSYISWIEDVMK 804

RE UT 29
Q9 V3
AC Q9V1V3 PRELIMINARY; PRT; 868 AA.
DT 01-NOV-1999 (TremBLrel. 12, Created)
DT 01-NOV-1999 (TremBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Tunicate retinoic acid-inducible modular protease precursor.
GN TRAMP.

OE Polyandrocarpa misakiensis.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Styelidae; Polyandrocarpa.
OX NCBI_TaxID=7723;
RN (1)
RE SEQUENCE FROM N.A.
RC STRAIN=white spot;
RX MEDLINE=99423646; PubMed=10491255;
RA Ohashi M., Kawamura K., Fujii N., Yubisui T., Fujiwara S.;
RT "A retinoic acid-inducible modular protease in budding ascidians."
RI Dev. Biol. 214:38-45(1999).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AB030007; BAA8252.1; -.
DR HSP; P00763; IDPO.

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0005044; F:scavenger receptor activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006503; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00057; ldl_recept_ar; 3.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00530; SRCR; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00261; LDLRECEPTOR.
DR PRINTS; PR00258; SPREACTRCPTR.
DR SMART; SM00122; LDLr; 3.
DR SMART; SM00473; PAN_AP; 1.

DR SMART; SM00202; SR; 2.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01209; LDLRA_1; 3.
DR PROSITE; PS00668; LDLRA_2; 3.
DR PROSITE; PS0287; SRCR_2; 2.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease; Signal.
FT SIGNAL
SC SEQUENCE 868 AA; 97660 MW; F71462865F36A6CA CRC64;

ary Match 20.2%; Score 457; DB 5; Length 868;
st Local Similarity 39.2%; Pred. No. 3e-34;
ches 104; Conservative 43; Mismatches 100; Indels 18; Gaps 9;

QY 139 CCGOKTL----RPRFKIIGGFTTIENQWPAAYRRHRGSGVTVYCGGSLISPCWISA 194
DE 608 ECGRXPVIEAPLPTARIYVGGSTPEHPWQAGIWL-----PWYWCYGGSLIHPCWLT 662
QY 195 THCFI-DYPKEDYIVLGRSLNSNTQGMKFEVENILHKDYSAADTLAHNDIALKI 253
DE 663 AHCFVREYPIR-DYIRLGDHITGVDDTEQLFKIAEIKH-DYNTVT--KENDIALLI 718

QY 254 RSKEGRCAQPSRTIOTICLPSMYNDPQFGTSCITGFGKENSTDY-LYPEOLKMTVVKLI 312
DB 719 ENDARECATIPEVOTVCLPKSSSQFDAKTICEVTGWKDSATAVRAVVPVQAEIPLI 778
QY 313 SHRECOQPHYGYSEVTTXMLCAADPQWKTDCQSGSGGFLVCSLQG--RMILTIGVSWGR 370
DB 779 ANKKCLRDSEY-TQLGPTMFCAGYLTGGKDSQSGSGGFLSCRDQSDDRYVYVWGVSMGN 837
QY 371 GCALKDKPGVYTRVSHFLPWRISHT 395
DB 838 GCAKPKAFGVYAKVAVFDWIEQMT 862

RESULT 30

Q8N171
ID Q8N171 PRELIMINARY; PRT; 327 AA.
AC Q8N171;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Similar to protease, serine, 8 (Prostasin) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RE SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; BC036846; AH36845.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT NON_TER
SC SEQUENCE 327 AA; 35106 MW; 60458ED817AC1CF3 CRC64;

Query Match 19.7%; Score 445.5; DB 4; Length 327;
Best Local Similarity 38.3%; Pred. No. 1.1e-33;
Matches 105; Conservative 36; Mismatches 100; Indels 33; Gaps 8;

QY 134 GKLPCCGOKTLRPRFKIIGGFTTIENQWPAAYRRHRGSGVTVYCGGSLISPCWIS 193
DB 69 GRKSAACQGFPMSSR--IVGDRDGRDGEWFOAS1--QHRG---AHVCGGSLIAFQWVLT 121
QY 194 ATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENILHKDYSAADTLAHNDIALKI 253
DB 122 AAHCPRRALPAEYRVRLGALRLGSTSPRTLSVPVRRVLLPDPYSED--GARGDLALLQL 179
QY 254 RSKEGRCAQPSRTIOTICLPSMYNDPQFGTSCITGFGKENSTDYLYP-----EQLKM 306
DB 180 R-----RPVLSARVQVCLPVEGARPPFTGTCRVTVGWS-----LRFGVLPPEWRPQQ 229
QY 307 TVVKLISHRECOQPHYGYSEVTTK-----MLCAADPQWKTDCQSGSGGFLVCSLQGR 359
DB 230 VRVPLDSDTCDGLYHVGADVPQAEIRIVLPGSLCAGYQGHKDACQSGSGGFLVCSLQSGS 289
QY 360 MTLTIGVSWGRCAKDXRPGVYTRVSHFLPWRIS 393
DB 290 WVLGVYVSWGRKCALPNRPGVYTSVATYSPWIIQA 323

Kim D.R., Sharmin S., Inoue M., Kido H.;
"Cloning and expression of novel mosaic serine proteases with and
without a transmembrane domain from human lung.";
Biochim. Biophys. Acta 1518:204-209 (2001).
EMBL; AB048796; BAB39741.1; -;
HSP; P00763; LDPO.
MEROPS; S01.087; -;
GO; GO:0016021; C: integral to membrane; NAS.
GO; GO:0006508; P: proteolysis and peptidolysis; NAS.
GO; GO:0004263; F: chymotrypsin activity; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR002172; LBL_receptor_A.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001190; Sscr_receptor.
Pfam; PF00057; ldl_recept_a; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00192; LDua; 1.
SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_Spc; 1.
PROSITE; PS0287; SRCR_2; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Protease, Serine protease.
SEQUENCE 581 AA; 62689 MW; 4DABE24D7D5B4M44 CRC64;

try Match 18.8%; Score 424; DB 4; Length 581;
st Local Similarity 23.8%; Pred. No. 2.4e-31;
tches 119; Conservative 53; Mismatches 145; Indels 82; Gaps 14;

32 NCPK-----KFGQHCEDKS-KTCYEGNGHYRGKASDTDTWGRCLPW 74
198 SCPHAVRCGVDCVKLSDELGCVRFDWDRKLLKIYSGSHQWLPICSSN-----W 249
75 NSA-----TVLQOTYHAHRSDALQGLGKINYCRNPNRRRPPWCYVQVGLKPL 122
250 NDSYSEKTCRQLGPFSAHRTTEVAHRDFANSFSILRYN-----ST 289
123 VQECW--VHDCADGKLFQCGQKTLRPF-KIIGGETTIENQFPAALYRRHGGSVIY 179
290 IQESLHRSHCPQSYRIQLQCHGCLRAMTGRIYVGLASAKSWFQVSL---HFG--TH 344
180 VCGSGLISPCWVISATHCFFIDYPKK--EDYIVYLGSRSLNSNTQGENKFVEVNLHKOY 237
345 ICGGTLIDAQWVLTAAHCFVTVREKLGKWKYAGTSLNLHQLPEAA---SIAEIIINSY 401
238 SADTLAHNDIALKIRSKGRCAOP---SRTIQTICLPSMYNDPQFGTSCETITGFG 291
402 TDE--EDDYDIALM-----RLSKPLTSLAHHPACLPMHGQTFSLNETCWITGFG 452
295 STDVLYPEQLKMTVVKLISHRECQPHYGVSEVTTKMLCAADPQWKTDCQGDGSGPLVC 354
453 ETDKTSFPLREVQNLIDFKKNDYLVYDSYLTPTMWCAGDLHGRDSCQGDGSGPLVC 512
355 SLOGRMTLTGIVSGRGKALDKPKGVYTRVSHFLPWIRSHKEE 398
513 EQNNRWYLAGVTSGTGCGQKPKGVYTKVTEVLPWIRSHKEE 551

RE IT 38
Q8 E0
ID Q8CFE0 PRELIMINARY; PRT; 471 AA.
AC Q8CFE0;
DT 01-MAR-2003 (TremBLrel. 23, Created)
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Similar to mosaic serine protease (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Breast tumor;
Strasbourg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC042878; AAH42878.1; -;
GO; GO:0016020; C: membrane; IEA.
GO; GO:0004263; F: chymotrypsin activity; IEA.
GO; GO:0008233; F: peptidase activity; IEA.
GO; GO:0005044; F: scavenger receptor activity; IEA.
GO; GO:0004295; F: trypsin activity; IEA.
GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR002172; LBL_receptor_A.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001190; Sscr_receptor.
Pfam; PF00057; ldl_recept_a; 1.
Pfam; PF00530; SRCR_1; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00202; SR; 1.
SMART; SM00202; Tryp_Spc; 1.
PROSITE; PS0287; SRCR_2; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
FT NON TER 1
SQ SEQUENCE 471 AA; 52535 MW; ED58CFE657C3BCC4 CRC64;

Query Match 18.7%; Score 423; DB 11; Length 471;
Best Local Similarity 32.9%; Pred. No. 2.3e-31;
Matches 114; Conservative 46; Mismatches 133; Indels 54; Gaps 13;

QY 64 TDTMGRCLPNNSATVLCQTYHAHRSDALQGLGKHN-----YCRNPNRRRPPWCYVQ 116
DB 161 TDSK-RTCCQLGDFSAVYRTTEVAHRDITSSFLSEYNTTIOESLYRSCPSRR----YVS 215
QY 117 VGLKPLVQECWVHDCADGKLFQCGQKTLRPF-KIIGGETTIENQFPAALYRRHGG 176
DB 216 L-----QCS-----HGLRAMTGR--IVGGALTSEKWPQVSL---HFG-- 250
QY 177 VTYVCGSLISPCWVISATHCFFIDYPKK--EDYIVYLGSRSLNSNTQGENKFVEVNLH 234
DB 251 TTHICGGTLIDAQWVLTAAHCFVTVREKLGKWKYAGTSLNLHQLPEAA---SISQIIIN 307
QY 235 KDYSADTLAHNDIALKIRSKGRCAOP---SRTIQTICLPSMYNDPQFGTSCETITGFG 291
DB 308 GNYTDE--ODDYDIALI-----RLSKPLTSLAHHPACLPMHGQTFGLNETCWITGFG 358
QY 292 KENSTDVLYPEQLKMTVVKLISHRECQPHYGVSEVTTKMLCAADPQWKTDCQGDGSGP 351
DB 359 KTKETDKTSFPLREVQNLIDFKKNDYLVYDSYLTPTMWCAGDLHGRDSCQGDGSGP 418
QY 352 LVCSLQGRMTLTGIVSGRGKALDKPKGVYTRVSHFLPWIRSHKEE 398
DB 419 LVCEQNNRWYLAGVTSGTGCGQKPKGVYTKVTEVLPWIRSHKEE 465

RESULT 39
Q8QW7 PRELIMINARY; PRT; 277 AA.
ID Q8QW7;
AC Q8QW7;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Trypsase-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

R STRAIN=BALB/c; TISSUE=Testis;
 F Wong G.W., Yasuda S., Li L., Stevens R.L.;
 F "Cloning and characterization of mouse trypsin-6 (mt6).";
 F Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 F EMBL: AY262280; AAB20885.1; -
 F GO: 0004263; F:chymotrypsin activity; IEA.
 F GO: 0004295; F:trypsin activity; IEA.
 F GO: 0004298; F:proteolysis and peptidolysis; IEA.
 F GO: 0006508; P:proteolysis and peptidolysis; IEA.
 F InterPro: IPR009003; Cys_Ser_trypsin.
 F InterPro: IPR001254; Peptidase_S1.
 F InterPro: IPR001314; Peptidase_S1A.
 F Pfam: PF00089; trypsin; 1.
 F PRINTS: PR00722; CHYMOTRYPSIN.
 F SMART: SM0020; Tryp_Src; 1.
 F PROSITE: PS00240; TRYPSIN_DOM; 1.
 F PROSITE: PS00134; TRYPSIN_HIS; 1.
 F PROSITE: PS00135; TRYPSIN_SER; 1.
 F SEQUENCE 277 AA; 29887 MW; 3310C067573E5E74 CRC64;
 Query Match 18.7%; Score 422.5; DB 11; Length 277;
 Best Local Similarity 36.0%; Pred. No. 1.3e-31;
 Matches 104; Conservative 43; Mismatches 97; Indels 45; Gaps 11;
 C 122 LVQCMVHDCADGKLFQCCQKTLRPFKIIGFEFTTIENQWPFAIYRRHGGSVTVYC 181
 D 13 LVLTGRMQECA-----ACGPRMSSR--IVGGRDAQDGEWPQTSI--QHRG--AHVC 59
 C 182 GGSLSFCWISATHCIDPKK---EDYIVLGRSLNLSNTQGMKFEVENILHKDYS 238
 D 60 GGSIIAPQVLTAGHCP---PRRWPESEYVLLGALSIVRSSHELLVPLVRLPPDYS 116
 C 239 ADTLAHNDIALKIRSKGRCAPSRITQICLPSMYNDPQFGTSCIEITGFGKENSTDY 298
 F 117 EDEA--RGDALLQLRHP-----VSLSTRIQVCLPAPGSHPPGSPCWVTGWS----- 164
 C 299 LYP-----EQLKQVTVKVLISHRECQPHYGS-----VTTKMLCAADPQWTKDSC 344
 F 165 LSPGVPLPKRQLOGVRVPLDLSRACDLRYHGAVNPQGERIVLPGLCAGYRGRHKDAC 224
 C 345 QGDSGGPLVCSLQGRMTLTGVSMGRGKALKDKPGVTVRYSHLPMRS 393
 F 225 QGDSGGPLTQMSHGWVGVSMGKGCALPNRPGVTNVAKYSPVIOA 273
 F ULT 40
 C 4X7
 F Q804X7 PRELIMINARY; PRT; 425 AA.
 A Q804X7;
 D 01-JUN-2003 (TrEMBLrel. 24, Created)
 D 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 D 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 C Coagulation factor VII precursor (EC 3.4.21.21).
 C F7.
 C Gallus gallus (Chicken).
 C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 C Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 C Gallus.
 C NCBI_TaxID=9031;
 F [1]
 F SEQUENCE FROM N.A.
 F Davidson C.J., Hirt R.P., Lal K., Snell P., Elgar G.,
 F Tuddenham E.G.D., McVey J.H.;
 F "Comparative sequence analysis and molecular evolution of blood
 F coagulation genes from gallus gallus and fugu rubripes";
 F Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 F EMBL: AF465268; AAO33363.1; -
 F GO: 0005576; C:extracellular; IEA.
 F GO: 0003802; F:blood coagulation factor VII activity; IEA.
 F GO: 0005509; F:calcium ion binding; IEA.
 F GO: 0004263; F:chymotrypsin activity; IEA.
 F GO: 0004678; F:hydrolase activity; IEA.
 F GO: 0004295; F:trypsin activity; IEA.
 F GO: 0006508; F:proteolysis and peptidolysis; IEA.

DR InterPro: IPR000152; Asx_hydroxy¹_S.
 DR InterPro: IPR009003; Cys_Ser_trypsin.
 DR InterPro: IPR000742; EGF_2.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR001438; EGF-II.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR002383; GLA_blood.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR InterPro: IPR000294; VitK_dep_GLA.
 DR Pfam: PF00008; EGF; 2.
 DR Pfam: PF00594; gla; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00010; EGFLOOD.
 DR PRINTS: PR00001; GLABLOOD.
 DR SMART: SM00181; EGF; 2.
 DR SMART: SM00179; EGF_Ca; 1.
 DR SMART: SM00069; GLA; 1.
 DR SMART: SM00020; Tryp_Src; 1.
 DR PROSITE: PS00010; ASX_HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_Ca; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; 1.
 DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 SW HYDROLASE.
 QY SEQUENCE 425 AA; 47626 MW; 36A69BFD8B6CDAC CRC64;
 Query Match 18.5%; Score 417; DB 13; Length 425;
 Best Local Similarity 27.1%; Pred. No. 7.6e-31;
 Matches 114; Conservative 68; Mismatches 130; Indels 108; Gaps 18;
 QY 4 LHQVSNCD---CLNGGTCVSNKYFSNIHMCNCKFKGGQHCE--IDSKTKCYGNGHFY 58
 DB 83 IYSDPNQCDSSPCQNGGSC--DDQFQD-YVCRCPFEYEGSKCETAVAENLKCIVDNG--- 136
 QY 59 RGKASTDTMGPRCLPWNNSATVLQYTHAHRSDALQLGLGKHNYCRNPDRRPPWCYVQVG 118
 DB 137 -----GCEQYCADEQSEKRV-CF----- 153
 QY 119 LKPLVQECVWHDCADG-----KLKPGQG-----OKTLRPFKIIIGFEFTTIE 160
 DB 154 -----CAGYALASDGVSCIPQVKYPCGTIPVLARKNTTAQGRIVGGVTCPPG 201
 QY 161 NQWFAALYRRHGGSVTVYCGSSLSIPCWVISATHCFIDYPKKEDYIVLGRSLNLSNT 220
 DB 202 ECPWQALLIQDQKG-----KCGSLLSPWVVTAAHC-LDYAHSKQLRVLRGEYSVKVAE 255
 QY 221 QGEMKFEVENILHKDYSADTLAHENDIALKIRSKGRCAPSRITQICLP-----SMY 276
 DB 256 KTEQSSGVSKIIRHEEYITGVNH--DIALLKLETP---VNLTDVVPVLCIPKRFAYV 309
 QY 277 NDPQGTSCIEITGFGK--ENSTDYLPQLKMTVTVKLISHRECQPHYGSVETKMLCA 334
 DB 310 ELSSIKFSN-VSGWGRLLDGGATSTFLMRVHLPRVKT---QCECK--QANLNITENMFCA 363
 QY 335 ADPQWTKDSCQDGGPLVCSLQGRMTLTGVSMGRGKALKDKPGVTVRYSHLPMRS 394
 DB 364 GLTGTGKDSCKGDSGGPHATKYKNTWFLTGIVSMGKGCAGVSGYGVYTVRYSHLPMRS 423
 RESULT 41
 Q8CGR6
 ID Q8CGR6 PRELIMINARY; PRT; 276 AA.
 AC Q8CGR6;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Glandular kallikrein K1K13.

GN KX13.
 OE Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RX MEDLINE=22325484; PubMed=12437987;
 RA Olsson A.F., Lundwall A.;
 R1 "Organization and evolution of the glandular kallikrein locus in Mus
 RT musculus";
 RI Biochem. Biophys. Res. Commun. 299:305-311(2002).
 RN [2]
 RE SEQUENCE FROM N.A.
 RA Adams M., Mural R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY152432; AA078420.1; -.
 DR MGD; MG1:95292; KX13.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:000508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR001254; Peptidase_S1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM0020; TRYP_SPC; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR KW Hydroxylase; Protease; Serine protease.
 SQ SEQUENCE 276 AA; 30360 MW; 33E189C67492FDCA CRC64;
 Query Match 18.2%; Score 411.5; DB 11; Length 276;
 Best Local Similarity 38.0%; Pred. No. 1.5e-30;
 Matches 98; Conservative 40; Mismatches 81; Indels 39; Gaps 11;
 QY 153 GGEFTTNPQWPAIYRRHGGSVTVVCGSLISPCWVISAATHCFIDYPKKEDYIVYLG 212
 DE 39 GGYTCLPHSOPWQAALIRG-----LTCGGVLPKWLTAHC-----RKDGYTVHLG 88
 QY 213 RSLRNSNTQGMKEFEVENLIHKDYSADT--LAHNDIALKIRSKRGCAQPSRTIQT 270
 DE 89 KHALGRVENCEQAMEVRSIPHPPEYQVTPHLNHDHIMLELKSP-----VOLSSHVRTL 144
 QY 271 -----CLPSMYNDPQGTSCETIGFGKENSVDLYPEQLKMTVKLISHRECCQPHYVG 324
 DE 145 KLSADDCCLPT-----GTCRVSGWGTTSPPQVNYNPKTIQOCANIELRDEECRQ--VYP 195
 QY 325 SEVTTKMLCAADPQWKTDSCGDSGGPLVCSLQGRMTLTIGIVSWGR-GCALKDKPGVYTR 383
 DE 196 GKITANMLCAGTKGGKDCSGDSGGPLICN--GK--LYGIISWGDPPCQGNRPQVYTR 251
 QY 384 VSHFLPWIRS---HTKEE 398
 DE 252 VSKYLRIWRIIRNTPEQ 269
 RE LT 42
 QY Q8R0P5 PRELIMINARY; PRT; 638 AA.
 AC Q8R0P5;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Kallikrein B. plasma 1.
 GN KX13.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Kidney;

RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC026555; AA026555.1; -.
 DR HSPF; P00761; IAN1.
 DR MGD; MG1:102849; KX13.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001177; Apple.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00024; PAN; 4.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00005; APPLEDOMAIN.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR SMART; SM00223; APPLE; 4.
 DR SMART; SM0020; TRYP_SPC; 1.
 DR PROSITE; PS00495; APPLE; 4.
 DR PROSITE; PS02040; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR KW Hydroxylase; Protease; Serine protease.
 SQ SEQUENCE 638 AA; 71382 MW; CC27C93F4B57C599 CRC64;
 Query Match 18.2%; Score 411.5; DB 11; Length 638;
 Best Local Similarity 33.5%; Pred. No. 4.2e-30;
 Matches 94; Conservative 56; Mismatches 106; Indels 25; Gaps 8;
 QY 126 CMVHDCADGKLKFCGGKTLRPFKIIGGFTTNPQWPAIYRRHGGSVTVVCGSL 185
 DE 375 CKLVDSPD-----C--TTKINARIVGGTNASLGWEPQVSL--QVKLVSTHLGSGSI 423
 QY 186 ISPCWVISAATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKEFEVENLIHKDYSADTLAH 245
 DE 424 IGRQWLVTAACHFCGIPYDPVVRVYIGLLSEITKETPSSRIKELIHQYKVS--EGN 481
 QY 246 NDIALKIRSKRGCAQPSRTIQTICLPSMYNDPQGTSCETIGFG--KENSTDYLYPE 302
 DE 482 YDIALIKLQTP-----LNYTEFQKPLCLPSKADTNTVTCWVTGWYTKQGETONI--- 534
 QY 303 QLKMTVVKLISHRECCQPHYGVSEVTTKMLCAADPQWKTDSCGDSGGPLVCSLQGRMTL 362
 DE 535 -LQKATIFLVNFECCQK-KYRDYVINKQMICAGYKEGGTDACKGDSGGPLVCKHSGRWQL 592
 QY 363 TGIVSWGRGCAKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
 DE 593 VGITSMGEGCARKDQPGVYTKVSEYMDWILEKTQSSDVRL 633
 RESULT 43
 Q8CJ16 PRELIMINARY; PRT; 371 AA.
 AC Q8CJ16;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Adrenal mitochondrial protease short variant.
 GN AMP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC STRAIN=NEDH;
 RA Omer S., Bicknell A.B., Lowry P.J.;
 RT "Identification of a rat adrenal mitochondrial protease";
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

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EMBL; AF537099; AAN06758.1; ..
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0005044; F:scavenger receptor activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001190; Srcr receptor.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS0287; SRCR 2; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
K Protease.
KW SEQUENCE.
SQ SEQUENCE 371 AA; 40694 MW; 89A64081D9A1FE26 CRC64;

Query Match 18.2%; Score 411; DB 11; Length 371;
Best Local Similarity 31.7%; Pred. No. 2.4e-30;
Matches 115; Conservative 57; Mismatches 121; Indels 70; Gaps 17;

Q 50 CYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLG---LGKHNVCNRPD 106
D :|||:-----WNPALGM-----HICQS-----LGYFRLTQHKAVNLS 82
Q 107 ---NRRPWCYVQGLKP---LVQECM---VHDCADGKLK---FQCQKTLRPRFKIIGGE 155
D :|||:-----FAQLSARPGSLVEAWQPSNCPGSRIVSLKCECGARPLASR--LVGQQ 138
Q 156 FTTIENQPFALYYRRHGGSVTVCGSLISPCWISATHCFIDY--PKKEDYIVYGLR 213
D :|||:-----HTCGSVLAPYVWVTAACHMYSPRLSRLSSWRVHAG-- 192
Q 214 SRLNSNT-----QCEMKFEVENLILHKDYSADTLAHNDIALIKIRSKEGRCQAQPSRTIQ 268
D :|||:---LVSHSAVQHOGTM---VEKIIPHLYSAQN---HDYDVALQLRTP-----INSDTVS 241
Q 269 TICLPSPNDPQGTSCETITFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYGSEVT 328
D :|||:-----AVCLPAKEHQFPQGSQWVGWGHDPSTHSSDTLQDTWVPLLSTDLNCSSCMYSGALT 301
Q 329 TKMLCAADPWKMTDSCQSGSGPLVCSLQGRMTLTGIVSWGRGCALKDKPQVTVVSHFL 388
D :|||:-----HMLCAGYLDGRADACQSGSGPLVCPSGDTHLVGVVSWGRGCAPNRPFGYAKVAEFL 361
Q 389 FWI 391
D :|||
D 362 DWI 364

RESULT 44
Q8CUI7 PRELIMINARY; PRT; 445 AA.
AC Q8CUI7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Adrenal mitochondrial protease long variant.
GN AMP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEDH.
RA Omer S.; Bicknell A.B.; Lowry P.J.;
RA "Identification of a rat adrenal mitochondrial protease.";
RA Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
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EMBL; AF537098; AAN06757.1; ..
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0005044; F:scavenger receptor activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR001190; Srcr receptor.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS0287; SRCR 2; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
KW Protease.
SQ SEQUENCE.
SQ SEQUENCE 445 AA; 48440 MW; BE3F56D8372ED988 CRC64;

Query Match 18.2%; Score 411; DB 11; Length 445;
Best Local Similarity 31.7%; Pred. No. 3e-30;
Matches 115; Conservative 57; Mismatches 121; Indels 70; Gaps 17;

Q 50 CYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLG---LGKHNVCNRPD 106
D :|||:-----WNPALGM-----HICQS-----LGYFRLTQHKAVNLS 156
Q 125 CHEG-----
D :|||:-----VHDCADGKLK---FQCQKTLRPRFKIIGGE 155
Q 107 ---NRRPWCYVQGLKP---LVQECM---VHDCADGKLK---FQCQKTLRPRFKIIGGE 155
D :|||:-----FAQLSARPGSLVEAWQPSNCPGSRIVSLKCECGARPLASR--LVGQQ 212
Q 156 FTTIENQPFALYYRRHGGSVTVCGSLISPCWISATHCFIDY--PKKEDYIVYGLR 213
D :|||:-----HTCGSVLAPYVWVTAACHMYSPRLSRLSSWRVHAG-- 266
Q 213 AVASGRWFOASVMLGSR-----HTCGSVLAPYVWVTAACHMYSPRLSRLSSWRVHAG-- 266
Q 214 SRLNSNT-----QCEMKFEVENLILHKDYSADTLAHNDIALIKIRSKEGRCQAQPSRTIQ 268
D :|||:---LVSHSAVQHOGTM---VEKIIPHLYSAQN---HDYDVALQLRTP-----INSDTVS 315
Q 269 TICLPSPNDPQGTSCETITFGKENSTDYLYPEQLKMTVVKLISHRECQQPHYGSEVT 328
D :|||:-----AVCLPAKEHQFPQGSQWVGWGHDPSTHSSDTLQDTWVPLLSTDLNCSSCMYSGALT 375
Q 329 TKMLCAADPWKMTDSCQSGSGPLVCSLQGRMTLTGIVSWGRGCALKDKPQVTVVSHFL 388
D :|||:-----HMLCAGYLDGRADACQSGSGPLVCPSGDTHLVGVVSWGRGCAPNRPFGYAKVAEFL 435
Q 389 FWI 391
D :|||
D 436 DWI 438

RESULT 45
Q8CDRO PRELIMINARY; PRT; 455 AA.
AC Q8CDRO;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane protease.
GN TMPSR85.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
```

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs"; Nature 420:563-573 (2002).

EMBL; AK029714; BAC26577.1; --

MED; MGI:1933407; Tmpres5.

GO; GO:0016020; C-membrane; IEA.

GO; GO:0004263; F:chymotrypsin activity; IEA.

GO; GO:0005044; F:scavenger receptor activity; IEA.

GO; GO:0004295; F:trypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR009003; Cys Ser trypsin.

InterPro; IPR001254; Peptidase S1.

InterPro; IPR001314; Peptidase S1.

InterPro; IPR001190; Srcr_receptor.

Pfam; PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS0287; SRCR_2; 1.

PROSITE; PS0240; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

SEQUENCE 455 AA; 49669 MW; BE22EB2E7503C74B CRC64;

Query Match 17.9%; Score 404; DB 11; Length 455;

Best Local Similarity 33.0%; Pred. No. 1.4e-29;

Matches 99; Conservative 46; Mismatches 105; Indels 50; Gaps 9;

QY 110 RPYCVQVGLKPLVQECMWHDCADGLK-----FQCGOKTLRPFKLIIGGEFTTIEQWPF 165

DE 181 RPKGLVEESWKPRA-----NCFSGRIVSLKCECGARPLASR--IVGQAVASGRWPWQ 232

QY 166 AALYRRHRRGGSVTVYCGSLISPCWVISATHCFIDYPKKEDYIVYLRSLNS-----218

DE 233 ASVNLGSR-----HTCGASVLAPHVVVTAACHMYSP-----RLSRLSSWRVHAGL 277

QY 219 -----NTGEMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIQTIC 271

DE 278 VSHGAVRQHGTM---VEKLIPLPLSAQN--HDYDVALLQLRTP----INFSDTVGAVC 328

QY 272 LPMSYNDPQPGTSCIEITGFGKNSDYLYPEQLKMTVVKLISHRECOQPHYGYSEVTTKM 331

DE 329 LPAKEQHPGWSOCWVGWGTDPSTHSSDTLQDTWVLLSTYLCNSSOMYSYGALTHRM 388

QY 332 LCAADPQWKTSCQDGGSLVCSLQGRWTLTGIVSWGRGCAKDKPGVTVRVSHPLPWI 391

DE 389 LCAGYLDGRADACQDGGSLVCSLQGRWTLVHGVSWGRGCAEPNPGVYAKVAEFLDWI 448

RE 46

QY 1 Q8WVC1 PRELIMINARY; PRT; 422 AA.

AC Q8WVC1

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RE 1

SEQUENCE FROM N.A.

TISSUE=Colon;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

CC 1-5 SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; BC018146; AA018146.1; --

DR HSP; P00761; IAN1.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR009003; Cys_Ser_trypsin.

DR InterPro; IPR001272; LDL_receptor_A.

DR InterPro; IPR001254; Peptidase S1.

DR InterPro; IPR001314; Peptidase S1A.

DR Pfam; PF00057; ldl_recept_a; 4.

DR Pfam; PF00089; tryptsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00261; LDLRECEPTOR.

DR SMART; SM00192; LDla; 4.

DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS01209; LDLRA_1; 2.

DR PROSITE; PS00668; LDLRA_2; 4.

DR PROSITE; PS0240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Hypothetical protein; Hydrolase; Protease; Serine protease.

FT NON TER 1

SQ SEQUENCE 422 AA; 46257 MW; 2C99875D1B58B319 CRC64;

Query Match 17.8%; Score 401.5; DB 4; Length 422;

Best Local Similarity 28.1%; Pred. No. 2.2e-29;

Matches 119; Conservative 65; Mismatches 157; Indels 83; Gaps 20;

QY 5 HQVPSNCDCLNGG--TCVSNKYFSNIHW-----CNCPK---KFGGQHCE 43

DB 47 HSDLNLCSDAGHQFTC-KNKFCKPLFWCDVNDGDSDEQSCFACQTFRCNKGK- 104

QY 44 IDKSKTCVEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCR 103

DB 105 LSKSQCC---NGKDDCGDGEA---SCPKNVVTCTKHYRCLNGLCLSKG-----150

QY 104 NPDNRRPWCYVQVGLKPLVQEC-MWHDCADG--KLKPCQCGKTLRPRFKIIGGEFTTIE 160

DB 151 NP-----ECDKEDCSGDEKDCDGLRSFTTQARVVGTDADG 191

QY 161 NQWFAALYRRHRRGGSVTVYCGSLISPCWVISATHCFID-----YPKEDYIVYLG-RS 214

DB 192 EWPQVQVSLHALGQG-----HICGASLISFNLVLSAAHCYIDDRGPRYSDPTQWTAFLGLHD 247

QY 215 RLNNTQEMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIQTICLPS 274

DB 248 QSQASAPGVQERLKRLIISHPFFNDFTFDY--DIALLELE---KPAEYSSMWVRPICLPD 301

QY 275 MYNDPQPGTSCIEITGFG--KENSTDYLYPEQLKMTVVKLISHRECOQPHYGYSEVTTKM 332

DB 302 ASHVFPAGKAIVTWGWTQYGGTGALI---LQGEIRVINQTTCE--NLLPQGITPRRM 356

QY 333 CAADPQWKTSCQDGGSLVCSLQGRWTLTGIVSWGRGCAKDKPGVTVRVSHPLPWI 391

DB 357 CVGFLSGGVDSQDGGSLVCSLQGRWTLVHGVSWGRGCAQNRKPGVTVRLPLFRDWI 416

QY 392 RSHT 395

DB 417 KENT 420

RESULT 47

Q9DAT3

ID Q9DAT3 PRELIMINARY; PRT; 624 AA.

AC Q9DAT3

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 1600027G01Rik protein (RIKEN cDNA 1600027G01 gene).

GN F11 OR 1600027G01Rik.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RE 1

SEQUENCE FROM N.A.

TISSUE=Placenta;

RC STRAIN=C57BL/6J; PubMed=11217851;

EX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

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R Arakawa T., Hata A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
R Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
R Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
R Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
R Fleischmann W., Gaasterland T., Gissi C., King B., Kouchiwa H.,
R Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
R Schmi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
R Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
R Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
R Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
R Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
R Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
R Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
R Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
R Wynukel H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
R Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
R Hayaishizaki Y.,
R "Functional annotation of a full-length mouse cDNA collection.";
R Nature 409:685-690(2001).
R [2]
R SEQUENCE FROM N.A.
R TISSUE=Liver;
R Strausberg R.;
R Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
R -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
R EMBL; AK005346; BAB2411.1; -.
R EMBL; BC019485; AAH19485.1; -.
R HSSP; P00750; INTF.
R MEROPS; S01.213; -.
R MGD; MGI:99481; F11.
R GO; GO:0005576; C:extracellular; IEA.
R GO; GO:0004263; F:chymotrypsin activity; IEA.
R GO; GO:0008233; F:peptidase activity; IEA.
R GO; GO:0004295; F:trypsin activity; IEA.
R GO; GO:0007596; F:blood coagulation; IEA.
R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
R InterPro; IPR001177; Apple.
R InterPro; IPR009003; Cys_Ser_trypsin.
R InterPro; IPR003014; PAN_
R InterPro; IPR001254; Peptidase S1.
R InterPro; IPR001314; Peptidase_S1A.
R Pfam; PF00024; PAN; 4.
R Pfam; PF00089; trypsin; 1.
R PRINTS; PR00005; APPLEDOMAIN.
R PRINTS; PR00722; CHYMOTRYPSIN.
R SMART; SM00223; APPLE; 4.
R SMART; SM00020; Tryp_SPC; 1.
R PROSITE; PS00495; APPLE; 3.
R PROSITE; PS00240; TRYPSIN_DOM; 1.
R PROSITE; PS00134; TRYPSIN_HIS; 1.
R PROSITE; PS00135; TRYPSIN_SER; 1.
R Hydrolase; Protease; Serine protease.
R SEQUENCE 624 AA; 69788 MW; 0EEDDEBC5600B97 CRC64;
R Query Match 17.7%; Score 400.5; DB 11; Length 624;
R Best Local Similarity 27.9%; Pred. No. 4.5e-29;
R Matches 126; Conservative 55; Mismatches 144; Indels 127; Gaps 21;
R 13 CLNGGTCVSNKYFSNI-----HWC-----NCPKFGGQHCIDKSK 48
R 230 CTHPTCLPTFFSQWPKESQRLCLKTSGLSPSTRITKSHALSGSLQCHRSPV 289
R 49 TCVEGNHGYRGKASTDMG-----RPLPMNSATVLTQTYHAHRSALQ 93
R 290 FCHPS---FYN---DTDFLGEELDIVDKQETCQKTCT--NNARQCFPTYF----- 334
R 94 LGLGKNYCRPNRRPWCVQVGLKPLVQECNWDHDCADG----- 134
R 335 -----SHLCLN--ENRRGRCYLKLS-----SNGSPTRILHGGTSGVSLRL 375
R 135 -KLKFCQCKTLPRFRKIIIGFEFTTIENQFWFAAIYRRHGGSVTYCGGSLISPCWVIS 193
R 376 CKMDNVCTTK-INPR--VVGGAASVHGEWFWQVTLHI-----SQGLHCGGSIIGNQWILT 427

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QY 194 ATHCF--IDYPKKEDYIVYLGRSLNNTGEMKFEVENLILHKDYSDTLAHNDIAL 251
Db 428 AAHCFSGIEPKK--LAVYGVIVNOSINEGTAFRRVQEMIIHDQYT--TAESYDIALL 483
QY 252 KIRSKGRCQAQPSRTIQ-TICLPSMYNDPOFGTSCETGTF-----GKENSTDYLYPEQL 304
Db 484 KLES-----AMNYTDFQRPICLPSKGRNNAVHTCEWVTGWYGTALRGVEGST-----L 531
QY 305 KMTVVVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDCQGGSGGFLVCSLQGRWTLTG 364
Db 532 QKAKVPLVSNEEC-QTRYRRHKITNMICAGYEGGKDTCKGDSGGFLSKYNGVWHLVG 590
QY 365 IVSWGRGCAKDKPGVTVYRSHFLPWRSHTK 396
Db 591 ITSNGEGCGQKRPDGVTVNAKYVDWMLEKTQ 622
RESULT 48
Q72410 PRELIMINARY; PRT; 855 AA.
AC Q72410;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polysomase 1B protein.
GS POLYSERASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22784742; PubMed=12886014;
RA Cal S., Lopez-Ortin C.;
RT "An alternative splicing of human polysomase lacking the last serine
RT protease domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:9185-9190(2003).
DR EMBL; AJ488947; CAD35759.1; -.
KW Alternative splicing.
SQ SEQUENCE 855 AA; 91352 MW; 8AF2759D9740CF3F CRC64;
Query Match 17.7%; Score 400; DB 4; Length 855;
Best Local Similarity 34.9%; Pred. No. 7.4e-29;
Matches 98; Conservative 49; Mismatches 110; Indels 24; Gaps 10;
QY 130 DCADG--KLKFCQCG-QKTLPRFRKIIIGFEFTTIENQFWFAAIYRRHGGSVTYCGGSLI 186
Db 179 DCSGDSFAHCEGCLQFAWRMAGRIVGGMEASPGEPFQASL-RENK----EHFCGAII 233
QY 187 SPCVVISATHCFIDYPKKEDYIVYLGRSLNNTGEMKFEVENLILHKDYSDTLAHN 246
Db 234 NARWLVSAAHCFNEFPQPTKVAIVGATYLSGSEASTVRAQVQIVKFLYNADTADF-- 291
QY 247 DIALKIRSKGRCQAQ---SRTIQTICLPSMYNDPOFGTSCETGFGKENSTDYLYPEQ 303
Db 252 DVAVLELTS-----PLPFGRIHQVCLPAAHTFPFKKCLISGMYLKEDFLVKDEV 344
QY 304 LKMTVVVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDCQGGSGGFLVCSLQGRWTLTG 362
Db 345 LQKATVELLDQALCAS--LYGHSITDRMVCAGYLDGKVDSCQGGSGGFLVCEBFSGRFL 402
QY 363 TGIVSWGRGCAKDKPGVTVYRSHFLPMI-RSHTKEENGLA 402
Db 403 AGIVSWGIGCAARRPGVYARVTRLDWILEATTKASMPLEA 443
RESULT 49
Q72411 PRELIMINARY; PRT; 1059 AA.
AC Q72411;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

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DI 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polysaccharide 1A protein.
GN POLYSACCHARIDE
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22784742; PubMed=12886014;
RA Cal S., Lopez-Otin C.;
RI "An alternative splicing of human polysaccharide lacking the last serine
RT protease domain."
RL Proc. Natl. Acad. Sci. U.S.A. 100:9185-9190(2003).
DR EMBL; AJ488946; CAB35758.1;
KW Alternative splicing.
SQ SEQUENCE 1059 AA; 114020 MW; 17D27A2D99F2A264 CRC64;

ary Match 17.7%; Score 400; DB 4; Length 1059;
ary Local Similarity 34.9%; Pred. No. 9.6e-29;
atches 98; Conservative 49; Mismatches 110; Indels 24; Gaps 10;

Qy 130 DCADG--KLKPCQG-QXTLPRFKLIGETTTIENQWPAIYRRHGGSTVYVCGSLI 186
Db 179 DCSGDSDEAHCECEGLOPAWMAGRIVGMEASPEFPWQASL-RENK-----EHFCGAII 233
Qy 187 SPQWVIGATHCFIDYPKKEDYIVYGRSLNSNTQGMKPEVENLILHKDYSADTLAHN 246
Db 234 NARLVSAHCFNEFQPTKVAIVGATYLSGSEASTVAQVIVKHPLYNADTF-- 291
Qy 247 DIALLKTRSEKGRCAQP---SRTQITCLPSMYNDPOFGTSCEITGPKENSTDIYLPQ 303
Db 292 DVAVLETS-----PLPFGRIQVCLPAATHIFPPSKKCIISGMGYLKEDFLVKPEV 344
Qy 304 LKMTWVWLKSHRECCQPHYGVSEVTTKMLCAADPQWKTDSQDGGSGPLVC-SLQGRMTL 362
Db 345 LKATVELLDALCAS--LYGHSITDMVCAGYLDGVDSQDGGSGPLVCSEPSGRFFL 402
Qy 363 TGIVSWRGCGKALKDKPGVYTVVSHFLPMI-RSHYKEENGIA 402
Db 403 AGIVSWGIGCAEARPPGVYARVTRLDWILEATTAKSMPLA 443

RE 50
IT 17 PRELIMINARY; PRT; 855 AA.
AC Q9JUI7;
DI 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DF 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Membrane bound serine protease (Membrane bound arginine specific
DE serine protease).
GN MBSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Jejunum;
RA Tsuzuki S.;
RI "A membrane bound serine protease expressed in rat small intestine."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Ductenium;
RA Inoue H., Takahashi K., Kishi K.;
RI "membrane-bound arginine specific serine protease."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
DR EMBL; AB037898; BAB03502.1;

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DR EMBL; AB049189; BAB13765.1;
DR PIR; JC7731; JC7731.
DR HSSP; P00763; LDPO.
DR MEROPS; S01.302; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0002233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000859; CUB; 2.
DR InterPro; IPR003003; Cys_Ser_trypsin.
DR InterPro; IPR002172; Ldl_receptor_A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00431; CUB; 2.
DR Pfam; PF00057; Ldl_receptor_a; 4.
DR Pfam; PF00089; trypsin_1; 2.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00261; LDRECEPTOR.
DR SMART; SM00042; CUB; 2.
DR SMART; SM00192; Ldla; 3.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS01180; CUB; 2.
DR PROSITE; PS01209; LDLRA_1; 2.
DR PROSITE; PS00068; LDLRA_2; 4.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Protease; Serine protease.
FT VARIANT 665 665 K -> N.
SQ SEQUENCE 855 AA; 94955 MW; 35806B7ECF6CF03D CRC64;

Query Match 17.6%; Score 397; DB 11; Length 855;
Best Local Similarity 28.2%; Pred. No. 1.4e-28;
Matches 120; Conservative 69; Mismatches 153; Indels 84; Gaps 22;

Qy 1 SNELHQVPSNCDCLNGGTCVSNKYPSNIHW-----CNCPRKFGQHCE- 43
Db 481 SDEH--CRCNATHQFMC-KNQCKPLFWVCDSDVNDGCGSDEEGSCPA--GSFKCSN 534
Qy 44 ----IDSKTCYEGNGHYRFGKASTDTMGRPCLPWNSATVLOQTYAHRSDALQGLGKH 100
Db 535 GKCLPQSOQC---NGKDCGDSDEA---SCDNVNAVSTKYTYRC-----QNGL---- 578
Qy 101 YCRNPDRRRPWCYVQVGLKPLVQECMVHDCADG--KLKFCQCGKTLRPRFKIIGBFTT 158
Db 579 -CLNKGK---PEC---DGKK-----DCSDGSDKNCDCGLRSFTKQARVVGGTNAD 622
Qy 159 IENQWPAIYRRHGGSTVYVCGSLISPCWVISATHCFID-----YPKEDYIVYLG- 212
Db 623 EGGEWPMQVSLHALGQG---HLCGASLSPDWLWSAAHCFQDETIFKYSDDHMTAFGL 678
Qy 213 RSLNSNTQGMKPEVENLILHKDYSADTLAHNDIALKIRSKBGRCAQPSRTIQTICL 272
Db 679 LQSKRSASGVQEHKXLIITHPSFNDFDY--DIALLELE---KPAEYSTVVRPCL 732
Qy 273 PSMYNDPQGTSCETGFG--KENSTDYVYLPOLKQVTVVVKLISHRECOOPHYGSEVTK 330
Db 733 PNTHTVFPAGKAIWVTGHTKEGGTGALI---LQKEIRVINQTTCE--LLPQOITPR 787
Qy 331 MLCADPQWKTDSQDGGPL--VCSLOGRMTLTGIVSMGRGKALKDKPGVYTVVSHFLP 389
Db 788 MMCVGLSGVDSQDGGPLSSVEKGRIFQAGVSWGEGCAQRNPGVYTVRIPEDV 847
Qy 390 WIRSHS 395
Db 848 WIKET 853

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Job time : 69.7546 secs

GenCore version 5.1.6
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protein - protein search, using sw model

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1155,508 Million cell updates/sec

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al number of hits satisfying chosen parameters: 1586107

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imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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1: Genesep1980s:*

2: Genesep1990s:*

3: Genesep2000s:*

4: Genesep2001s:*

5: Genesep2002s:*

6: Genesep2003as:*

7: Genesep2003bs:*

8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2257	100.0	403	5	AAE16547 Human uro
2	2243	99.4	411	1	AAP50871 Sequence
3	2243	99.4	411	2	AAR06244 Urokinase
4	2243	99.4	411	2	AAR62991 Pro-uroki
5	2243	99.4	411	3	AAU92836 Urokinase
6	2243	99.4	411	5	AAE16544 Human uro
7	2243	99.4	431	1	AAP50114 Sequence
8	2243	99.4	431	1	AAP60783 Human uro
9	2243	99.4	431	1	AAP70258 Sequence
10	2243	99.4	431	1	AAP80430 Deduced A
11	2243	99.4	431	1	AAP81204 Pro-uroki
12	2243	99.4	431	1	AAP92119 Natural h
13	2243	99.4	431	2	AAR07112 Human pro
14	2243	99.4	431	2	AAR04253 Human pro
15	2243	99.4	431	2	AAR63141 Full leng
16	2243	99.4	431	2	AAR47903 Pro-uroki
17	2243	99.4	431	3	AAU50869 Human uro
18	2243	99.4	431	3	AAU99591 Human pla
19	2243	99.4	431	4	AAE16545 Amino aci
20	2243	99.4	431	5	AAE17128 Human uro
21	2243	99.4	431	5	AAU92228 Human pla
22	2243	99.4	431	5	AAU92460 sc-UPA. 1
23	2243	99.4	431	6	ABR55855 Human uro
24	2243	99.4	431	6	ABU56547 Lung canc
25	2243	99.4	431	6	ABU56708 Lung canc

26	2243	99.4	431	6	ABU11076	Abu11076 Human uro
27	2243	99.4	431	6	ABR92137	ABR92137 Human cer
28	2243	99.4	434	2	AAR20537	AAR20537 Amidated
29	2243	99.4	434	2	AAR20538	AAR20538 Amidated
30	2243	99.4	436	2	AAR20536	AAR20536 Amidated
31	2241	99.3	431	7	AAE25745	AAE25745 Human pro
32	2240	99.2	430	2	AAW24578	AAW24578 Inhibitor
33	2240	99.2	431	1	AAU91886	AAU91886 Sequence
34	2240	99.2	431	1	AAU94764	AAU94764 Non-glyco
35	2240	99.2	431	6	AAE37128	AAE37128 Human uro
36	2240	99.2	431	7	ADD46429	ADD46429 Human pro
37	2239	99.2	411	2	AAU34584	AAU34584 Mutant hu
38	2239	99.2	431	5	AAU92330	AAU92330 Human pla
39	2238	99.2	411	1	AAU96146	AAU96146 Sequence
40	2238	99.2	411	2	AAU92926	AAU92926 Pro-uroki
41	2238	99.2	411	4	AAU74797	AAU74797 Prourokin
42	2238	99.2	431	5	AAU99229	AAU99229 Human pla
43	2237	99.1	411	2	AAU62999	AAU62999 Pro-uroki
44	2237	99.1	411	2	AAU62992	AAU62992 Pro-uroki
45	2237	99.1	411	2	AAU62998	AAU62998 Pro-uroki
46	2237	99.1	411	2	AAU62993	AAU62993 Pro-uroki
47	2235	99.0	411	2	AAU63000	AAU63000 Pro-uroki
48	2235	99.0	411	2	AAU39343	AAU39343 Human pro
49	2235	99.0	411	2	AAU42284	AAU42284 Human pro
50	2235	99.0	411	4	AAU20489	AAU20489 Human pro
51	2235	99.0	412	2	AAU10334	AAU10334 Recombina
52	2235	99.0	431	5	AAU99236	AAU99236 Human pla
53	2234	99.0	411	2	AAU07904	AAU07904 Human pro
54	2234	99.0	411	2	AAU07902	AAU07902 Human pro
55	2234	99.0	411	2	AAU07903	AAU07903 Human pro
56	2234	99.0	411	2	AAU40225	AAU40225 PUK. 2/19
57	2234	99.0	431	1	AAU30041	AAU30041 Sequence
58	2234	99.0	431	5	AAU99231	AAU99231 Human pla
59	2233	98.9	411	2	AAU62997	AAU62997 Pro-uroki
60	2233	98.9	411	7	AAU85977	AAU85977 Human sin
61	2233	98.9	431	5	AAU99232	AAU99232 Human pla
62	2232	98.9	431	1	AAU70250	AAU70250 Sequence
63	2231	98.8	411	2	AAU13634	AAU13634 Human rat
64	2231	98.8	411	2	AAU47958	AAU47958 PUK S26T.
65	2231	98.8	411	2	AAU62995	AAU62995 Pro-uroki
66	2231	98.8	411	2	AAU62996	AAU62996 Pro-uroki
67	2231	98.8	431	5	AAU99238	AAU99238 Human pla
68	2230	98.8	411	1	AAU91684	AAU91684 Sequence
69	2230	98.8	411	2	AAU10056	AAU10056 Pro-uroki
70	2230	98.8	411	5	AAU13269	AAU13269 Human pro
71	2230	98.8	431	5	AAU99237	AAU99237 Human pla
72	2229	98.8	411	2	AAU10057	AAU10057 Pro-uroki
73	2229	98.8	411	2	AAU62994	AAU62994 Pro-uroki
74	2229	98.8	411	2	AAU63003	AAU63003 Pro-uroki
75	2229	98.8	411	2	AAU63001	AAU63001 Pro-uroki

ALIGNMENTS

RESULT 1

AAE16547
ID AAE16547 standard; protein; 403 AA.

XX

AC AAE16547;

XX 09-APR-2002 (first entry)

DT Human urokinase-type plasminogen activator scuPA delta136-143 mutant.

XX Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
clotting disorder; uterine contraction disorder; respiratory disease;
male impotence; adult respiratory distress syndrome; scuPA delta136-143;
single chain urokinase; mutant; mutein.

XX

Oe Homo sapiens.
 Oe Synthetic.
 Xf WO200197752-A2.
 Xf 27-DEC-2001.
 Xf 13-JUN-2001; 2001WO-US018976.
 Xf 20-JUN-2000; 2000US-0212874P.
 Xf (UYPE-) UNIV PENNSYLVANIA.
 Xf Cines DB, Higazi RA;
 Xf WPI; 2002-122240/16.
 Xf N-PSDB; RAD27080.
 Xf Composition for modulating muscle cell and tissue contractility for
 P1 treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 P2 comprising domains from urokinase-type plasminogen activator.
 P3
 P4
 P5 Claim 22; Fig 1F; 117pp; English.
 Xf The invention relates to a composition comprising one or more domains of
 CC urokinase-type plasminogen activator (uPA). The composition is used to
 CC modulate the contractility and angiogenic activity of a mammalian muscle,
 CC endothelial cell or tissue. The composition is used for treating stroke,
 CC hypotension, hypertension, atherosclerosis, heart attack, microvascular
 CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
 CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 CC such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC invention is human urokinase-type plasminogen activator (uPA) single chain
 CC urokinase (scuPA) deletion mutant designated as scuPA delta136-143
 Xf Sequence 403 AA;
 S5
 ary Match 100.0%; Score 2257; DB 5; Length 403;
 st Local Similarity 100.0%; Pred. No. 7.8e-176;
 ches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 Df 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 Qy 61 KASTDTMGEPCLPWSNATVLOQTYHAHRS DALQLGLGKHNCRPNDRRRPWCYVQVGLK 120
 Df 61 KASTDTMGEPCLPWSNATVLOQTYHAHRS DALQLGLGKHNCRPNDRRRPWCYVQVGLK 120
 Qy 121 PLVQCMVHDCADGKLFQCGGOKTLPRFKIIGGFTTINQPMFAIYRHRGSGVTYV 180
 Df 121 PLVQCMVHDCADGKLFQCGGOKTLPRFKIIGGFTTINQPMFAIYRHRGSGVTYV 180
 Qy 181 CGGSLISPCWVISA THCFIDYVKKEDYVYLGSRSLNNTGEMKFEVENILILKDYASD 240
 Df 181 CGGSLISPCWVISA THCFIDYVKKEDYVYLGSRSLNNTGEMKFEVENILILKDYASD 240
 Qy 241 TLAHNDIALKIRSKGRCAPQRTIQTICLPMSYNDPQFQTSCEITGFGKENSTDYLY 300
 Df 241 TLAHNDIALKIRSKGRCAPQRTIQTICLPMSYNDPQFQTSCEITGFGKENSTDYLY 300
 Qy 301 PQLQKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGGLVCSLOGRM 360
 Df 301 PQLQKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGGLVCSLOGRM 360
 Qy 361 TLITGIVSWRGCCALXDKPGVYTRVSHFLPWRSHRTKEENGLAL 403
 Df 361 TLITGIVSWRGCCALXDKPGVYTRVSHFLPWRSHRTKEENGLAL 403

RESULT 2
 AAP50871
 ID AAP50871 standard; protein; 411 AA.
 XX
 AC AAP50871;
 XX
 DT 30-NOV-1991 (first entry)
 XX
 DE Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese
 DE Patent Application No.37119/84).
 XX
 KW Thrombolytic agent; plasminogen activator activity; fibrin affinity;
 KW enzyme.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..279
 FT Cleavage-site 158..159
 FT /note="potential cleavage site which generates the two-
 FT chain form from the zymogen"
 FT Disulfide-bond 189..205
 FT Disulfide-bond 197..268
 FT Disulfide-bond 293..362
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380
 XX
 PN EPI39447-A.
 XX
 XX 02-MAY-1985.
 PD
 XX 07-SEP-1984; 84EP-00306117.
 PF
 XX 13-SEP-1983; 83JP-00170354.
 PR
 XX 17-OCT-1983; 83JP-00195051.
 XX
 XX (GRC) GREEN CROSS CORP.
 PA
 XX Kasai S, Arimura H, Mori K, Suyama T;
 PI WPI; 1985-106530/18.
 XX
 XX New urokinase zymogen - useful as thrombolytic agent.
 PT
 XX Disclosure; Page 12; 30pp; English.
 PS
 XX Zymogen AAP50871 is the inactive precursor form of human urokinase.
 CC Urokinase zymogen is cleaved into the two-chain form composed of
 CC characteristic urokinase H (molecular wt.of 30,000) and L (molecular
 CC wt.of 20,000) chains when treated with catalytic amounts of plasmin. The
 CC patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a
 CC single chain molecular structure, and selective affinity for fibrin. It
 CC is a thrombolytic agent which manifests its plasminogen activator
 CC activity on cleavage by proteolytic enzymes (e.g. plasmin) and has higher
 CC affinity for fibrin than known forms of urokinase
 XX
 XX Sequence 411 AA;
 SQ
 Query Match 99.4%; Score 2243; DB 1; Length 411;
 Best Local Similarity 98.1%; Pred. No. 1.1e-174;
 Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 Qy 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 Df 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 Qy 61 KASTDTMGEPCLPWSNATVLOQTYHAHRS DALQLGLGKHNCRPNDRRRPWCYVQVGLK 120

1 61 KASDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
(121 PLVQECMVHDCADGK-----LKFCGQOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
) 121 PLVQECMVHDCADGKSPPEELKFCGQOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 180
(173 RGGSVTVVCGSLISPCWVISA THCFIDYPKKEDYIVYLGSRSLNNTQGMKFEVENLI 232
) 181 RGGSVTVVCGSLISPCWVISA THCFIDYPKKEDYIVYLGSRSLNNTQGMKFEVENLI 240
(233 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 292
) 241 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 300
(293 ENSTDYLYPEOLKMTVVVKLISHRECOQPHYVYGVSEVTTKMLCAADPQWKTDSCQDSDGGPL 352
) 301 ENSTDYLYPEOLKMTVVVKLISHRECOQPHYVYGVSEVTTKMLCAADPQWKTDSCQDSDGGPL 360
(353 VCSLQGRMTLTGIVSWGRGCALCKKPGVYTRVSHFLPWIRSHTKENGLAL 403
) 361 VCSLQGRMTLTGIVSWGRGCALCKKPGVYTRVSHFLPWIRSHTKENGLAL 411
F ULT 3
P 06244
X AAR06244 standard; protein; 411 AA.
X AAR06244;
X 07-DEC-1990 (first entry)
X Urokinase precursor protein.
X Urokinase precursor; fibrinolysis; thrombolytic; cerebral thrombosis;
X myocardial infarction.
X Homo sapiens.
X EP380334-A.
X 01-AUG-1990.
X 25-JAN-1990; 90EP-00300772.
X 27-JAN-1989; 89JP-00016406.
X 17-MAY-1989; 89JP-00121405.
X (GREG) GREEN CROSS CORP.
X Matsuda H, Ueda Y, Tamanouchi K;
X WPI; 1990-233117/31.
X Urokinase precursor-lipid composite - used as thrombolytic agent, having
X prolonged half-life in the blood, enhanced bioavailability and improved
X activity.
X Claim 3; Fig 1; 11pp; English.
X By forming a precursor-lipid composite, the half-life of this
X thrombolytic agent in the blood may be increased, exhibiting improved
X activity without abnormal acceleration of fibrinolytic activity. Compound
X is useful as a thrombolytic agent in treatment of cerebral thrombosis,
X myocardial infarction etc
X Sequence 411 AA;
X Query Match 99.4%; Score 2243; DB 2; Length 411;
X Best Local Similarity 99.1%; Pred. No. 1.1e-174;
X Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
(1 SNEHQVPSNCDLNGTCTVSNKYFSNIHMCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
)

Db 1 SNEHQVPSNCDLNGTCTVSNKYFSNIHMCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
QY 61 KASDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
Db 61 KASDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK-----LKFCGQOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
Db 121 PLVQECMVHDCADGKSPPEELKFCGQOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 180
QY 173 RGGSVTVVCGSLISPCWVISA THCFIDYPKKEDYIVYLGSRSLNNTQGMKFEVENLI 232
Db 181 RGGSVTVVCGSLISPCWVISA THCFIDYPKKEDYIVYLGSRSLNNTQGMKFEVENLI 240
QY 233 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 292
Db 241 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 300
QY 293 ENSTDYLYPEOLKMTVVVKLISHRECOQPHYVYGVSEVTTKMLCAADPQWKTDSCQDSDGGPL 352
Db 301 ENSTDYLYPEOLKMTVVVKLISHRECOQPHYVYGVSEVTTKMLCAADPQWKTDSCQDSDGGPL 360
QY 353 VCSLQGRMTLTGIVSWGRGCALCKKPGVYTRVSHFLPWIRSHTKENGLAL 403
Db 361 VCSLQGRMTLTGIVSWGRGCALCKKPGVYTRVSHFLPWIRSHTKENGLAL 411
RESULT 4
AAR62991
ID AAR62991 standard; protein; 411 AA.
XX AC AAR62991;
XX DT 25-MAR-2003 (revised)
XX DT 21-SEP-1995 (first entry)
XX DE Pro-urokinase.
XX KW Pro-urokinase; thrombolysis; fibrin clot lysis.
XX OS Homo sapiens.
XX Key Location/Qualifiers
FT Disulfide-bond 11..19
FT Disulfide-bond 13..31
FT Disulfide-bond 33..42
FT Disulfide-bond 50..131
FT Disulfide-bond 71..113
FT Disulfide-bond 102..126
FT Disulfide-bond 148..279
FT Disulfide-bond 169..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
FT Domain 297..313
FT /note= "flexible loop"
FT Disulfide-bond 325..341
FT Disulfide-bond 352..380
XX WO9501427-A1.
XX 12-JAN-1995.
XX 28-JUN-1994; 94WO-US007278.
XX 02-JUL-1993; 93US-00087163.
XX (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX Liu J, Gurewich V;
XX WPI; 1995-060991/08.
XX Pro-urokinase mutants - have thrombolytic activity but reduced
FT

fibrinogenolysis activity and non-specific plasminogen activation.
Disclosure; Fig 1; 46pp; English.
AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
Sequence 411 AA;
ery Match 99.4%; Score 2243; DB 2; Length 411;
st Local Similarity 98.1%; Pred. No. 1.1e-174;
tches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHFGYR 60
Df 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHFGYR 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLX 120
Df 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLX 120
QY 121 PLVQECMWHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQFPFAAIYRRH 172
Df 121 PLVQECMWHDCADGKPPSPPEELKFGQKTLRPRFKIIGGEFTTIENQFPFAAIYRRH 180
QY 173 RGGSVTYVCGGSLISPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGEKFEVENLI 232
Df 181 RGGSVTYVCGGSLISPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGEKFEVENLI 240
QY 233 LHKDYSADTLAHNDIALKIRSKRGCAQPSRTIQTCLPSWYNDPQFGTSCBITGFGK 292
Df 241 LHKDYSADTLAHNDIALKIRSKRGCAQPSRTIQTCLPSWYNDPQFGTSCBITGFGK 300
QY 293 ENSTDYLYPEQLKMTVVKLISHRECOQPHYTGSEVTTKMLCAADPQWKTDSQCGDSGGPL 352
Df 301 ENSTDYLYPEQLKMTVVKLISHRECOQPHYTGSEVTTKMLCAADPQWKTDSQCGDSGGPL 360
QY 353 VCSLQGRMTLTGIVSGRGCAKDKPGVYTVSHFLPWIRSHTEENGLAL 403
Df 361 VCSLQGRMTLTGIVSGRGCAKDKPGVYTVSHFLPWIRSHTEENGLAL 411
RI LT 5
AY 2836
II AAY92836 standard; protein; 411 AA.
AC AAY92836;
XZ 29-AUG-2000 (first entry)
XZ Urokinase plasminogen activator (uPA).
DE N-terminal; pro-uPA; urokinase plasminogen activator; receptor; uPAR;
KV anti-cancer; anti-metastatic; anti-proliferative; anti-atherosclerotic;
KV anti-thrombotic; anti-angiogenic; anti-inflammatory; anti-arthritis;
KV anti-fibrotic; apoptotic; vasotropic; anti-diabetic; ophthalmological;
KV thrombolytic.
XZ Homo sapiens.
XZ Key Location/Qualifiers
Ff Disulfide-bond 11..19
Ff Disulfide-bond 13..31
Ff Disulfide-bond 33..42
Ff Disulfide-bond 50..131
Ff Disulfide-bond 71..113
Ff Disulfide-bond 102..126

FT Disulfide-bond 148..279
FT Disulfide-bond 189..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
FT Disulfide-bond 325..341
FT Disulfide-bond 352..380
PN WO200026353-A1.
XX 11-MAY-2000.
PD 28-OCT-1999; 99WO-US025210.
XX 29-OCT-1999; 98US-00181816.
XX (ANGS-) ANGSTROM PHARM INC.
PA Mazar AP, Jones TR;
PI
XX
XX MPI; 2000-365605/31.
XX New cyclic peptide, useful for treatment or diagnosis of e.g. tumors and other diseases involving cell proliferation or migration, targets the urokinase plasminogen activator receptor.
PT Disclosure; Fig 1; 93pp; English.
XX
CC The present sequence shows the wild-type urokinase plasminogen activator (uPA). Cyclic peptides based on the amino acids residues 20-30 (the receptor-binding region) of uPA are claimed. These cyclic peptides target the uPA receptor (uPAR), allowing therapeutic or diagnostic agents to be delivered to uPAR-expressing cells. The cyclic peptides are used, optionally when linked to a therapeutic agent, to inhibit migration, invasion and proliferation of cells, or angiogenesis, or to induce apoptosis. Particularly they are used, in human or veterinary medicine, to treat diseases characterized by these processes, e.g. solid tumors, leukaemia or lymphoma (or their metastases); benign hyperplasia; atherosclerosis; restenosis; ischaemia; deep vein thrombosis; neovascular glaucoma; diabetic retinopathy; arthritis; fibrosis; bone fracture etc., most particularly growth, invasion and metastasis of tumors. When labeled, the cyclic peptides can be used for diagnostic detection of uPAR (a marker of metastasis) on cells, tissues etc., in vivo or in vitro, and when immobilized they are used to isolate uPAR or cells that express them. The cyclic peptides are stable, soluble in water, bind strongly to uPAR. Are relatively inexpensive to produce and may be derivatized by attachment of therapeutic or diagnostic agents without significantly affecting their binding. Since they target uPAR, they should have relatively low systemic toxicity and only low doses are required
XX Sequence 411 AA;
SQ
Query Match 99.4%; Score 2243; DB 3; Length 411;
Best Local Similarity 98.1%; Pred. No. 1.1e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHFGYR 60
Df 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHFGYR 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLX 120
Df 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLX 120
QY 121 PLVQECMWHDCADGK-----LKFQCGQKTLRPRFKIIGGEFTTIENQFPFAAIYRRH 172
Df 121 PLVQECMWHDCADGKPPSPPEELKFGQKTLRPRFKIIGGEFTTIENQFPFAAIYRRH 180
QY 173 RGGSVTYVCGGSLISPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGEKFEVENLI 232
Df 181 RGGSVTYVCGGSLISPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGEKFEVENLI 240
QY 233 LHKDYSADTLAHNDIALKIRSKRGCAQPSRTIQTCLPSWYNDPQFGTSCBITGFGK 292

D 241 LHKDYSADTLAHHNDIALALKIRSKGRCAPQPSRTIQTICLPSPMYNDPQFTSCIEITGFGK 300
C 293 ENSTDYLYPEOLKMTVVKLISHRECOQPHYVGVSEVTTKMLCAADPOWKTDSCQDGGGGL 352
F 301 ENSTDYLYPEOLKMTVVKLISHRECOQPHYVGVSEVTTKMLCAADPOWKTDSCQDGGGGL 360
C 353 VCSLQGRMTLTGIVSWRGCGALCKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
D 361 VCSLQGRMTLTGIVSWRGCGALCKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 411
F ULT 6
F 16544
F AAEL16544 standard; protein; 411 AA.
F AAE16544;
F 09-APR-2002 (first entry)
F Human urokinase-type plasminogen activator tcuPA and scuPA protein.
F Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
F stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
F microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
F tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
F clotting disorder; uterine contraction disorder; respiratory disease;
F male impotence; adult respiratory distress syndrome; tcuPA; scuPA;
F two chain urokinase; single chain urokinase.
C Homo sapiens;
C WO2001:97752-A2.
F 27-DEC-2001.
F 13-JUN-2001; 2001WO-US018976.
F 20-JUN-2000; 2000US-0212874P.
F (UYPE-) UNIV PENNSYLVANIA.
F Cines DB, Higazi AA;
F WPI; 2002-122240/16.
F N-PSDB; AAD27077.
F Composition for modulating muscle cell and tissue contractility for
F treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
F comprising domains from urokinase-type plasminogen activator.
F Claim 9; Fig 1C; 117pp; English.
F The invention relates to a composition comprising one or more domains of
F urokinase-type plasminogen activator (uPA). The composition is used to
F modulate the contractility and angiogenic activity of a mammalian muscle,
F endothelial cell or tissue. The composition is used for treating stroke,
F hypotension, hypertension, atherosclerosis, heart attack, microvascular
F occlusions, thrombotic microangiopathies, surgically induced thrombotic
F disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
F invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
F diabetic retinopathy, wound healing, clotting disorder, uterine
F contraction disorder, male impotence, respiratory disease or condition
F such as asthma, adult respiratory distress syndrome, primary pulmonary
F hypertension, microvascular thrombotic occlusion, and a disorder
F associated with chronic intrapulmonary fibrin formation. The present
F sequence is human urokinase-type plasminogen activator (uPA) two chain
F urokinase (tcuPA) and single chain urokinase (scuPA) protein
F Sequence 411 AA;
F Query Match 99.4%; Score 2243; DB 5; Length 411;
F Local Similarity 98.1%; Pred. No. 1.1e-174;
F atches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNPKFGQGHCEIDKSKTCYEGNGHFYRG 60
DB 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNPKFGQGHCEIDKSKTCYEGNGHFYRG 60
QY 61 KASDTMGRCPLPNSATVLOOTYHAHRS DALQLGLGKHNYCRNPDNERRRWCYVQVGLK 120
DB 61 KASDTMGRCPLPNSATVLOOTYHAHRS DALQLGLGKHNYCRNPDNERRRWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK-----LKFCQGGKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
DB 121 PLVQECMVHDCADGKPPSPPEELKFCQGGKTLRPRFKIIGGEFTTIENQWFAAIYRRH 180
QY 173 RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDIYVWLGSRNSNTQGMKEVENLI 232
DB 181 RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDIYVWLGSRNSNTQGMKEVENLI 240
QY 233 LHKDYSADTLAHHNDIALALKIRSKGRCAPQPSRTIQTICLPSPMYNDPQFTSCIEITGFGK 292
DB 241 LHKDYSADTLAHHNDIALALKIRSKGRCAPQPSRTIQTICLPSPMYNDPQFTSCIEITGFGK 300
QY 293 ENSTDYLYPEOLKMTVVKLISHRECOQPHYVGVSEVTTKMLCAADPOWKTDSCQDGGGGL 352
DB 301 ENSTDYLYPEOLKMTVVKLISHRECOQPHYVGVSEVTTKMLCAADPOWKTDSCQDGGGGL 360
QY 353 VCSLQGRMTLTGIVSWRGCGALCKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
DB 361 VCSLQGRMTLTGIVSWRGCGALCKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 411
RESULT 7
AAP50114
ID AAP50114 standard; protein; 431 AA.
XX AC AAP50114;
XX DT 27-SEP-1991 (first entry)
XX DE Sequence encoded by the signal sequence and noncoding region of the pro-
XX UK structural gene (Sequence II).
XX Enzyme; thrombosis therapy; embolic disease; single-chain pro-urokinase.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..20
XX Domain 21..177 /label= signal peptide
XX Domain /label= A chain
XX Domain 179..431 /label= B chain
XX EP154272-A.
XX PN 11-SEP-1985.
XX PD 23-FEB-1985; 85EP-00102031.
XX PF 27-FEB-1984; 84JP-00037119.
XX PR 31-JAN-1985; 85JP-00017969.
XX (GREC) GREEN CROSS CORP.
XX Hiramatsu R, Kaneda T, Nagai M, Rimura H, Nishida M, Suyama T;
XX WPI; 1985-224693/37.
XX DR N-PSDB; AAN50138.
XX PT Glycosylated single-chain pro-urokinase - prepd. by cultivating animal
XX cells transformed by DNA prepd. from m RNA.
XX Disclosure; Page 8-10; 64pp; English.

XX The inventors claim a method of producing single-chain pro-urokinase by
CC using as template, mRNA obtd. from cells of an established human kidney-
CC derived cell line. The urokinase is used to treat thrombosis and embolic
CC diseases as well as in the treatment of diseases in combination with
CC anticancer agents
XX
XX Sequence 431 AA;

Query Match 99.4%; Score 2243; DB 1; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174; Indels 8; Gaps 1;
Matches 403; Conservative 0; Mismatches 0;
QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
DB 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 80
QY 61 KASDTMTGRPCLPNNSATVLOQTHAHSRDLQGLGKHNYCRNPDNRPRPCVVOVGLK 120
DB 81 KASDTMTGRPCLPNNSATVLOQTHAHSRDLQGLGKHNYCRNPDNRPRPCVVOVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFCQGTLPFRFKIIGGEFTTIENQFWFAAIYRRH 172
DB 141 PLVQECMVHDCADGKPPPEELKFCQGTLPFRFKIIGGEFTTIENQFWFAAIYRRH 200
QY 173 RGSVTVYCGSLISPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 232
DB 201 RGSVTVYCGSLISPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHDNDIALKIRSEGRCAQPSRTIQTICLPSMYNDPQFSGTCEITGFGK 292
DB 261 LHKDYSADTLAHDNDIALKIRSEGRCAQPSRTIQTICLPSMYNDPQFSGTCEITGFGK 320
QY 293 ENSTDYLYPEQIKMTVVKLIISHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDSCGGL 352
DB 321 ENSTDYLYPEQIKMTVVKLIISHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDSCGGL 380
QY 353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVRVSHFLPWIRSHTEENGLAL 403
DB 381 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVRVSHFLPWIRSHTEENGLAL 431

LT 8
AP 0783
II AAP60783 standard; protein; 431 AA.
XX
AC AAP60783;
XX
DI 25-MAR-2003 (revised)
XX
XX 23-OCT-1991 (first entry)
XX
DE Human urokinase.
XX
XX B.colli; high molecular urokinase.
XX
XX Homo sapiens.
XX
FE Key Location/Qualifiers
XX Protein 21..431
XX
XX JP61181377-A.
XX
XX 14-AUG-1986.
XX
XX 25-JAN-1985; 85JP-00011032.
XX
XX 25-JAN-1985; 85JP-00011032.
XX
XX (NISC) NISSAN CHEM IND LTD.
XX (HODO) HODOGAYA CHEM IND CO LTD.
XX (SAGA) SAGAMI CHEM RES CENTRE.
XX (CENG) CENTRAL GLASS CO LTD.
XX (NIPS) NIPPON SODA CO.

PA (TOYU) TOYO SODA MFG CO LTD.
XX
DR WPI; 1986-254744/39.
DR N-PSDB; AAN60703.
XX
PT Human urokinase gene - has N-end of aminoacid sequence coded by codon
PT used in Escherichia coli.
XX
PS Disclosure; Fig 2; 19pp; Japanese.
XX
CC The claimed gene product may be expressed in a transformed E.coli host,
CC for the efficient production of high molecular human urokinase. The N-
CC terminal of the protein expressed by the transforming plasmid is replaced
CC with a codon frequently used in E.coli. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 431 AA;

Query Match 99.4%; Score 2243; DB 1; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174; Indels 8; Gaps 1;
Matches 403; Conservative 0; Mismatches 0;
QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
DB 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 80
QY 61 KASDTMTGRPCLPNNSATVLOQTHAHSRDLQGLGKHNYCRNPDNRPRPCVVOVGLK 120
DB 81 KASDTMTGRPCLPNNSATVLOQTHAHSRDLQGLGKHNYCRNPDNRPRPCVVOVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFCQGTLPFRFKIIGGEFTTIENQFWFAAIYRRH 172
DB 141 PLVQECMVHDCADGKPPPEELKFCQGTLPFRFKIIGGEFTTIENQFWFAAIYRRH 200
QY 173 RGSVTVYCGSLISPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 232
DB 201 RGSVTVYCGSLISPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHDNDIALKIRSEGRCAQPSRTIQTICLPSMYNDPQFSGTCEITGFGK 292
DB 261 LHKDYSADTLAHDNDIALKIRSEGRCAQPSRTIQTICLPSMYNDPQFSGTCEITGFGK 320
QY 293 ENSTDYLYPEQIKMTVVKLIISHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDSCGGL 352
DB 321 ENSTDYLYPEQIKMTVVKLIISHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDSCGGL 380
QY 353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVRVSHFLPWIRSHTEENGLAL 403
DB 381 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVRVSHFLPWIRSHTEENGLAL 431

RESULT 9
AAP70258
ID AAP70258 standard; protein; 431 AA.
XX
AC AAP70258;
XX
DT 25-MAR-2003 (revised)
XX
DT 19-MAY-1991 (first entry)
XX
DE Sequence of human prourokinase and leader.
XX
XX Cardiovascular disease treatment; fibrin affinity; thrombolytic; enzyme;
XX protease.
XX
XX Homo sapiens.
XX
OS Key Location/Qualifiers
XX Peptide 1..20
XX FT /label= leader
XX FT Protein 21..431
XX FT /label= prourokinase
XX

EP231883-A.
12-AUG-1987.
29-JAN-1987; 87EP-00101209.
31-JAN-1986; 86JP-00017734.
30-JAN-1987; 87JP-00018626.
(SAGA) SAGAMI CHEM RES CENTRE.
(NIPS) NIPPON SODA CO.
(CENG) CENTRAL GLASS CO LTD.
(TOYO) TOYO SODA MFG CO LTD.
(NISC) NISSAN CHEM IND LTD.
(NISC) NISSAN CHEMICAL INDS KK.
Tagawa M, Wada M, Yamada M, Yokoyama M, Numao N;
WPI; 1987-222882/32.
N-PSDB; AAN70390.
Hybrid plasminogen activator-like polypeptide - having a region for
affinity to fibrin from tissue plasminogen activator and a region from
prourokinase.
Disclosure; Fig 2(1-5); 64pp; English.
The tPA portion of the claimed hybrid polypeptide (see PT) may consist of
2 kringles from N-terminal first serine to 219th glycine of human tPA, 1
kringle from 128th serine to 219th glycine of human tPA or half a kring
from 161st methionine to 219th glycine (see AAP70257). The C-terminal
half of the hybrid polypeptide may contain an AA sequence from 150th
glutamine to C-terminal 411th leucine of pro-urokinase (see AAP70258).
(Updated on 25-MAR-2003 to correct PA field.)
Sequence 431 AA;
Query Match 99.4%; Score 2243; DB 1; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFRG 60
21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFRG 80
61 KASDTWGRPCLPNSATVLTQTVHRSALQLGLGKHNCRPNDRPPWCYVQVGLK 120
81 KASDTWGRPCLPNSATVLTQTVHRSALQLGLGKHNCRPNDRPPWCYVQVGLK 140
121 PLVQECMVHDCADGK-----LKFGQGTLPFRPKIIGGFTTIENQWFAAIYRRH 172
141 PLVQECMVHDCADGKSPPEELKFGQGTLPFRPKIIGGFTTIENQWFAAIYRRH 200
173 RGSVTVVCGSLISPCWVISATHCFIDYPKEDYIVLGRSLNSNTQEMKFEVENLI 232
201 RGSVTVVCGSLISPCWVISATHCFIDYPKEDYIVLGRSLNSNTQEMKFEVENLI 260
233 LHKDYSADTLAHNDIALLKIRSEGRCAQPSRTIQTICLPSMYNDPQGTSCITGFGK 292
261 LHKDYSADTLAHNDIALLKIRSEGRCAQPSRTIQTICLPSMYNDPQGTSCITGFGK 320
293 ENSTDYLPQGLKMTVVKLISHRCQPHYGVSEVTTKMLCAADPQWKTSCQDGGPL 352
321 ENSTDYLPQGLKMTVVKLISHRCQPHYGVSEVTTKMLCAADPQWKTSCQDGGPL 380
353 VCSLQGRMTLTGIVSWRGCAKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
381 VCSLQGRMTLTGIVSWRGCAKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 431

XX AAP80430;
AC 25-MAR-2003 (revised)
DT 14-SEP-1990 (first entry)
XX Deduced AA sequence of the single chain urokinase plasminogen activator
DE (SCU-PA) cDNA insert prepared from human Hep3 cells.
XX Single chain urokinase plasminogen activator (SCU-PA); human Hep3 cells;
KW glyceraldehyde-3-phosphate dehydrogenase gene; thrombosis prevention;
KW thrombosis treatment.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Peptide 1..20
FT Protein 21..411
XX EP288435-A.
XX 26-OCT-1988.
XX 11-APR-1988; 88EP-00810234.
XX 15-APR-1987; 87GB-00009081.
PR 16-JUN-1987; 87GB-00014059.
PR 04-DEC-1987; 87IE-00003239.
XX (CIBA) CIBA GEIGY AG.
PI Meyhack B, Heim J, Burgi R;
XX WPI; 1988-301440/43.
DR N-PSDB; AAN80981.
XX Prodn. of human single chain urokinase-type plasminogen activator - by
culturing yeast strain transformed with hybrid vector contg. yeast
expression control sequences.
XX Example 1; Fig 2; 48pp; English.
XX The patent is for the prodn. of human single chain urokinase-type
plasminogen activator (UTPA). Mutants of scu-PA are especially those
which render the protein protease resistant. Such scu-PA mutants are
covalently modified at sites of proteolysis by proteases occurring in
blood such as thrombin or plasmin, so that they are no longer susceptible
to protease hydrolysis at these locations. The target sites include
Lys135 to Lys136 (cleavage at this site generates the so-called low
molecular weight form of scu-PA or LOK), Arg156 to Phe157 (susceptible to
thrombin attack) and Lys158 to Ile159 (cleavage at this site by plasmin
generates tuc-PA). Suitable scu-PA mutants have site specific
substitutions, insertions or deletions of residues at one or more of
these target sites. Especially preferred are those mutants in which one
amino acid residue or both amino acid residues forming the target sites
are deleted or in which at least one of these amino acid residues is
replaced by another amino acid residue so that the resulting mutants are
resistant to proteolytic attack. The UTPA proteins exhibit the biological
activity of natural human UTPA without any refolding procedure being
necessary. They can be used as for known PAs in humans for the prevention
or treatment of thrombosis or other conditions where it is desired to
produce local fibrinolytic or proteolytic activity. (Updated on 25-MAR-
2003 to correct PR field.)
XX Sequence 431 AA;
SQ Query Match 99.4%; Score 2243; DB 1; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFRG 60
DB 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFRG 80

QY 61 KASTDTMGRPCLPWNSATVLTQTYHAHRSDALQLGLGKHNKYNCRNPNRRRPPKCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLTQTYHAHRSDALQLGLGKHNKYNCRNPNRRRPPKCYVQVGLK 140
QY 121 PLVQECWVHDCADGK-----LKFCQCGOKTLRPRFKIIGGEFTTIENQPFWFAAIYRRH 172
DB 141 PLVQECWVHDCADGKPPSPBELKFCQCGOKTLRPRFKIIGGEFTTIENQPFWFAAIYRRH 200
QY 173 RGGSVTVVCGGSLISPCWVISATHCFIDYPPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
DB 201 RGGSVTVVCGGSLISPCWVISATHCFIDYPPKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHDNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPQFGTSCITGFGK 292
DB 261 LHKDYSADTLAHDNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPQFGTSCITGFGK 320
QY 293 ENSTDYLYPEOLKMTVVKLIISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGL 352
DB 321 ENSTDYLYPEOLKMTVVKLIISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGL 380
QY 353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
DB 381 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431

RE LT 11
AA 1204
ID AAF81204 standard; protein; 431 AA.
XX AAF81204;
XX AAF81204;
XX 25-MAR-2003 (revised)
DT 03-DEC-1990 (first entry)
XX Pro-urokinase with signal sequence.
XX pro-urokinase (pro-UK); plasminogen activator; PUK33; ss.
XX Homo sapiens.

Key : Location/Qualifiers
FH Peptide : 1..20
FT /label= signal peptide
FT Protein : 21..431
FT /label= pro-urokinase
XX EP265874-A.
XX 04-MAY-1988.
XX 23-OCT-1987; 87EP-00115600.
XX 23-OCT-1986; 86JP-00253078.
XX (GREC) GREEN' CROSS CORP.
XX Amatsuji Y, Okabayashi K, Nagai M, Arimura H, Suyama T;
XX WPI: 1988-121000/18.
XX N-PSDB; AN81558.
XX Glycosylated single-chain pro-urokinase prodn. - by cultivating DHFR gene
XX -deficient CHO-K1 cells transformed with a plasmid contg. CDNA, SV40
XX promoter and DHFR gene.
XX Disclosure; Page ?; 19pp; English.

XX The Arg at position 2 is encoded by TGA(sic). Possible error in the
XX specification. Should read CGA ? The pro-UK gene was derived from plasmid
XX PUK33. The cDNA was synthesised using urokinase mRNA isolated from a
XX human kidney cell line. Pro-UK was cloned into a SV40 promoter-contg.
XX plasmid, down- stream of the promoter. This plasmid was then ligated to

CC a DHFR- gene contg. plasmid so that pro-UK and DHFR are inserted in
CC opposite directions. The recombinant plasmid was used to transform CHO-K1
CC cell derived DHFR gene-deficient host cells to produce glycosylated
CC single-chain pro-UK. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 431 AA;
Query Match 99.4%; Score 2243; DB 1; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 SNEHQVPSNCDCLNGCTCVSNKYFSNIHWCNCPKFGGQHCIDSKTCYEGNGHYRG 60
DB 21 SNEHQVPSNCDCLNGCTCVSNKYFSNIHWCNCPKFGGQHCIDSKTCYEGNGHYRG 80
QY 61 KASTDTMGRPCLPWNSATVLTQTYHAHRSDALQLGLGKHNKYNCRNPNRRRPPKCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLTQTYHAHRSDALQLGLGKHNKYNCRNPNRRRPPKCYVQVGLK 140
QY 121 PLVQECWVHDCADGK-----LKFCQCGOKTLRPRFKIIGGEFTTIENQPFWFAAIYRRH 172
DB 141 PLVQECWVHDCADGKPPSPBELKFCQCGOKTLRPRFKIIGGEFTTIENQPFWFAAIYRRH 200
QY 173 RGGSVTVVCGGSLISPCWVISATHCFIDYPPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
DB 201 RGGSVTVVCGGSLISPCWVISATHCFIDYPPKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHDNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPQFGTSCITGFGK 292
DB 261 LHKDYSADTLAHDNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPQFGTSCITGFGK 320
QY 293 ENSTDYLYPEOLKMTVVKLIISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGL 352
DB 321 ENSTDYLYPEOLKMTVVKLIISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDGGGGL 380
QY 353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
DB 381 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431

RESULT 12
AAF92119
ID AAF92119 standard; protein; 431 AA.
XX
XX AAF92119;
XX 25-MAR-2003 (revised)
DT 29-JUN-1990 (first entry)
XX
XX Natural human prourokinase.
XX Human prourokinase; antithrombotic; derivative.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "Optional in new deriv."
FT Misc-difference 2..155 /note= "Incorporated into new deriv."
FT Misc-difference 135 /note= "May be replaced by a non-basic AA in new deriv."
FT Misc-difference 156 /note= "Undefined residue in new deriv."
FT Misc-difference 157 /note= "Pro, Gly, Ala or Val in new deriv."
FT Misc-difference 158 /note= "Lys or Arg in new deriv."
XX
XX W08901513-A.
XX
XX 23-FEB-1989.
XX

XX	OS	Synthetic.
XX	PN	EP390592-A.
XX	PD	03-OCT-1990.
XX	PF	30-MAR-1990; 90EP-00303445.
XX	PR	31-MAR-1989; 89JP-00078574.
XX	PA	(KYOW) KYOWA HAKKO KOGYO KK.
XX	PA	(EXPE-) CENT INST EXPT ANIMALS.
XX	XX	(JIKK-) JIKKEN DOBUTSU CHUO KENK.
PI	XX	Sekine S, Ito S, Katsuki M;
DR	XX	WPI; 1990-299492/40.
DR	DR	N-PSDB; AAQ06049.
XX	PT	Prodn. of recombinant protein, esp. human pro-urokinase - from milk of transgenic animals using promoter of bovine alpha S1 casein chromosomal gene.
XX	PS	Example; Table 1; 55pp; English.
XX	CC	E.coli strain C600SP8 was transformed with recombinant plasmid containing ds DNA derived from human pharynx cancer cell strain Detroit 562. 10000 colonies were screened and one positive clone was identified. Plasmid pUK1 was isolated and found to contain the coding region and 3' non-coding region of pro-UK downstream of Cys(41). Four silent substitutions were identified c.f. Holmes et al., Biotechnology, vol.3, p.923 (1985) as follows: (sic) Asn(254), AAC to AAT; Leu(340), CTA to CTG; Pro(345), CCC to CCA; Gln(346), CAA to CAG. See also AAQ06045-Q06048 and AAQ06392. (Updated on 25-MAR-2003 to correct PA field.)
XX	SQ	Sequence 431 AA;
		Query Match 99.4%; Score 2243; DB 2; Length 431;
		Best Local Similarity 98.1%; Pred. No. 1.2e-174;
		Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY	1	SNELHQVPSNCCLNGGTCSVNKFYSNIHWCNPKKFGQGHCEDKSKTCYEGNGHFVRG 60
DB	21	SNELHQVPSNCCLNGGTCSVNKFYSNIHWCNPKKFGQGHCEDKSKTCYEGNGHFVRG 80
QY	61	KASTDTMGSPCLPWNASATVLQOTYHAHRSDALQLGLGXNYCRNPDRRRRRCVYQVGLK 120
DB	81	KASTDTMGSPCLPWNASATVLQOTYHAHRSDALQLGLGXNYCRNPDRRRRRCVYQVGLK 140
QY	121	PLVQECMVHDCADGK-----LKFCQOKTLRPFKIIGGEFTTIENQFWFAAIYRRH 172
DB	141	PLVQECMVHDCADGKKPPSPPELXFCQOKTLRPFKIIGGEFTTIENQFWFAAIYRRH 200
QY	173	RGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSLNSNTQGMKEVENLI 232
DB	201	RGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRSLNSNTQGMKEVENLI 260
QY	233	LHKDYSADTLAHNDIALKIRSKRGCAQPSRTTQTICLPWMYNDPOFGTSCEITGFVK 292
DB	261	LHKDYSADTLAHNDIALKIRSKRGCAQPSRTTQTICLPWMYNDPOFGTSCEITGFVK 320
QY	293	ENSTDLYPEQLKMVTVKLISHRECOQPHYGVSEVTTMCLCAADPWMTDSQQDGGPL 352
DB	321	ENSTDLYPEQLKMVTVKLISHRECOQPHYGVSEVTTMCLCAADPWMTDSQQDGGPL 380
QY	353	VCSLOQRMTLTGIWSGRGCALKDKPGVYTRVSHFLPWIRSHTKENGIAL 403
DB	381	VCSLOQRMTLTGIWSGRGCALKDKPGVYTRVSHFLPWIRSHTKENGIAL 431
		RESULT 14
		AAR04253

RESULT 14
AAR04253

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RESULT 15
AAR63141
ID   AAR63141 standard; protein; 431 AA.
XX
XX   AAR63141;
XX
XX   25-MAR-2003 (revised)
XX   09-JUN-1995 (first entry)
XX
XX   Full length human urokinase protein.
DE
XX   Human urokinase glycoproteins; cardiovascular diseases;
XX   pulmonary embolism.
XX
XX   Homo sapiens.
XX
XX   Key      Location/Qualifiers
FH   Sig_peptide      1..20
FT   Disulfide-bond   70..151
FT   Disulfide-bond   91..133
FT   Disulfide-bond   122..146
FT   Disulfide-bond   168..299
FT   Cleavage-site    179..180
FT   /note="Cleavage of this site produces a bioactive two
FT   chain form of urokinase"
FT   Disulfide-bond   203..225
FT   Disulfide-bond   217..288
FT   Disulfide-bond   313..382
FT   Disulfide-bond   345..361
FT   Disulfide-bond   372..400
XX
XX   EP620279-A1.
XX
XX   19-OCT-1994.
XX
XX   14-APR-1983; 94EP-00104777.
XX
XX   15-APR-1982; 82US-00368773.
XX   14-MAR-1983; 83US-00474930.
XX   14-APR-1983; 83EP-00103629.
XX
XX   (GETH ) GENENTECH INC.
XX
XX   Heyneker HL, Holmes WE, Vohar GA;
XX
XX   WPI; 1994-318362/40.
XX   N-PSDB; AAR73483.
XX
XX   Prodn. of human urokinase glycoproteins - using a recombinant expression
XX   system used for the treatment of vascular diseases or conditions.
XX
XX   Claim 1; Fig 4; 4lpp; English.
XX
XX   AAR73483 is the cDNA sequence which encodes AAR63141 the full length
XX   54000 dalton human urokinase (UK) protein. This cDNA was used in the
XX   construction of a plasmid capable of transforming either yeast or
XX   vertebrate cells, enabling them to produce the 54000 dalton human UK
XX   protein. The UK glycoprotein produced could then be used in the treatment
XX   of cardiovascular diseases, including pulmonary embolism. The UK produced
XX   using this method had the advantage of a specific activity towards fibrin
XX   and extant thrombi, not demonstrated previously with UK isolated from
XX   natural sources. (Updated on 25-MAR-2003 to correct PN field.) (Updated
XX   on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
XX   PR field.)
XX
XX   Sequence 431 AA;
XX
XX   Query Match      99.4%; Score 2243; DB 2; Length 431;
XX   Best Local Similarity 98.1%; Pred. No. 1.2e-174;
XX   Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1
XX
XX   1 SNELEQVPSNCDLNGGTCVSNKYFSIHWCNCPKFGQFCIEDKSKTCYEGRHGYRG 60

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1 21 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNCPKFGGQHCEIDKSKTCYEGNGHYRG 80
 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRPNRRPWCYVQVGLK 120
 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRPNRRPWCYVQVGLK 140
 121 PLVQECMVHDCADGK-----LKFCGQOKTLRPRFKIIGBEFTTIENQPFPAALYRRH 172
 141 PLVQECMVHDCADGKPPSPPEELKFCGQOKTLRPRFKIIGBEFTTIENQPFPAALYRRH 200
 173 RGSVTVYVCGSLISPCWISATHCFIDYPKKEDIYVILGRSLNSNTQGMKFEVENLI 232
 201 RGSVTVYVCGSLISPCWISATHCFIDYPKKEDIYVILGRSLNSNTQGMKFEVENLI 260
 233 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQIICLPSMYNDPQFSGTSCITGFGK 292
 261 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQIICLPSMYNDPQFSGTSCITGFGK 320
 293 ENSTDYLYPEQLKMTVVVKLISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDSDGGPL 352
 321 ENSTDYLYPEQLKMTVVVKLISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDSDGGPL 380
 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 431

RESULT 16
 AAY50869
 ID AAY50869 standard; protein; 431 AA.
 XX
 AC AAY50869;
 XX
 DT 13-JUL-1994 (first entry)
 XX
 DE Pro-urokinase derivative.
 XX
 KW Pro-urokinase; half-life; thrombolytic; thrombosis; fibrinolytic; factor.
 XX
 OS Homo sapiens.
 XX
 PN JP05336965-A.
 XX
 PD 21-DEC-1993.
 XX
 PF 17-OCT-1991; 91JP-00269615.
 XX
 PR 17-OCT-1991; 91JP-00269615.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PI WPI; 1994-030907/04.
 XX
 DR N-PSDB; AAQ55772.

Novel human pro-urokinase derivs. having long half-life - with high
 thrombolytic activity, useful for treatment of thrombosis.
 XX
 PS Disclosure; Page 15-17; 29pp; Japanese.
 XX

Sequences (AAQ55771-72) are pro-urokinase derivatives. The products have
 an inserted sugar moiety having an amino acid substituted, depleted or
 inserted variant around the thrombin cleavage site. They also have a long
 half-life allowing them to be used in the treatment of thrombosis
 XX
 Sequence 431 AA;
 XX

Query Match 99.4%; Score 2243; DB 2; Length 431;
 Best Local Similarity 98.1%; Pred. No. 1.2e-174;
 Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 XX

1 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNCPKFGGQHCEIDKSKTCYEGNGHYRG 60
 21 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNCPKFGGQHCEIDKSKTCYEGNGHYRG 80

QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRPNRRPWCYVQVGLK 120
 DB 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRPNRRPWCYVQVGLK 140
 QY 121 PLVQECMVHDCADGK-----LKFCGQOKTLRPRFKIIGBEFTTIENQPFPAALYRRH 172
 DB 141 PLVQECMVHDCADGKPPSPPEELKFCGQOKTLRPRFKIIGBEFTTIENQPFPAALYRRH 200
 QY 173 RGSVTVYVCGSLISPCWISATHCFIDYPKKEDIYVILGRSLNSNTQGMKFEVENLI 232
 DB 201 RGSVTVYVCGSLISPCWISATHCFIDYPKKEDIYVILGRSLNSNTQGMKFEVENLI 260
 QY 233 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQIICLPSMYNDPQFSGTSCITGFGK 292
 DB 261 LHKDYSADTLAHHNDIALLKIRSKEGRCAPSRITQIICLPSMYNDPQFSGTSCITGFGK 320
 QY 293 ENSTDYLYPEQLKMTVVVKLISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDSDGGPL 352
 DB 321 ENSTDYLYPEQLKMTVVVKLISHRECQOPHYGSEVTTKMLCAADPQWKTDSCQDSDGGPL 380
 QY 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
 DB 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 431

RESULT 17
 AAY50869
 ID AAY50869 standard; protein; 431 AA.
 XX
 AC AAY50869;
 XX
 DT 24-FEB-2000 (first entry)
 XX
 DE Human urokinase protein fragment.
 XX
 KW Urokinase; human; thrombolytic agent; streptokinase; antigenic;
 XX
 OS Homo sapiens.
 XX
 PN WO9957251-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 06-MAY-1999; 99WO-US010086.
 XX
 PR 06-MAY-1998; 98US-0084392P.
 XX
 PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 XX
 PI Zhang XC, Lin X, Tang JYN;
 XX
 DR WPI; 2000-052966/04.

New thrombolytic agents derived from modified humanized streptokinase,
 useful for treating blood clot disorders.
 XX

Disclosure; Page 46-48; 55pp; English.
 XX

This invention describes a novel thrombolytic agent comprising
 streptokinase where at least one nonessential portion has been modified.
 The invention also describes a method of forming a thrombolytic agent
 comprising determining a nonessential portion of streptokinase and
 modifying the nonessential portion to render the resulting protein less
 antigenic. The modified streptokinase is used to treat blood clot
 disorders, such as heart attacks. The modified streptokinase has less
 antigenicity than streptokinase but is still able to complex plasminogen
 and lead to plasminogen activation. Modified streptokinase with the
 nonessential portions removed or truncated simplify the molecule. Such
 smaller proteins are cheaper and easier to produce. This sequence
 represents a fragment of the human urokinase protein which is used in the
 description of the method of the invention
 CC

Sequence 431 AA;
Query Match 99.4%; Score 2243; DB 3; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
1 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 60
21 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 80
61 KASTDTMGPCPLPWSNATVLOQTYHAHRSALQGLGKHNYCRNPNRRRRCVYVQGLK 120
81 KASTDTMGPCPLPWSNATVLOQTYHAHRSALQGLGKHNYCRNPNRRRRCVYVQGLK 140
121 PLVQECWVHDCADGK-----LKFCQCKTLRPFKIIIGGEFTTIENQWFAAIYRRH 172
141 PLVQECWVHDCADGKPPSPPELAFQCGQKTLRPFKIIIGGEFTTIENQWFAAIYRRH 200
173 RGSVTVYVCGGSLISPCWISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
201 RGSVTVYVCGGSLISPCWISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
233 LHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPOFGTSCITGFGK 292
261 LHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPOFGTSCITGFGK 320
293 ENSTDYLYPEQLKMTVVKLIHSHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSSGGL 352
321 ENSTDYLYPEQLKMTVVKLIHSHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSSGGL 380
353 VCSLQGRMTLTGIVSWGRCALKDHPGVYTRVSHFLPWIRSHTKENGIAL 403
381 VCSLQGRMTLTGIVSWGRCALKDHPGVYTRVSHFLPWIRSHTKENGIAL 431
RE LT 18
AF 9591
ID AAY99591 standard; protein; 431 AA.
AC AAY99591;
XX
DT 13-SEP-2000 (first entry)
XX
DE Human plasminogen activator urokinase, u-PA.
XX
XX Human; serine protease; plasminogen activator; cardiant; thrombolytic;
XX heart attack; stroke; blood clotting disorder.
XX
XX Homo sapiens.
XX
XX WO200032759-A1.
XX
XX 08-JUN-2000.
XX
XX 06-MAY-1999; 99WO-US009991.
XX
XX 02-DEC-1998; 98US-0110588P.
XX
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
XX Lin X, Zhang XC, Tang JUN;
XX
XX WPI; 2000-422975/36.
XX
XX Polypeptide with plasminogen activator activity useful as thrombolytic
XX agent for treating blood clot disorders e.g. heart attack, comprises 10
XX amino acid peptide fragment for recognition or activation of plasminogen.
XX
XX Disclosure; Page 26-28; 41pp; English.
XX
XX The present sequence is human plasminogen activator urokinase (u-PA), a
XX serine protease which hydrolyses a peptide bond in human plasminogen to

convert it to its active form, plasmin. plasminogen is the principal
serine protease zymogen in the extracellular fluids of vertebrates.
plasmin is implicated in pericellular proteolysis associated with a wide
range of physiological and pathological processes. Plasminogen activators
regulate plasminogen expression either by hydrolysing a peptide bond, as
in the case of u-PA, or by forming tight binding complexes with
plasminogen to spontaneously convert it to plasmin. Review of sequence
homologies of several plasminogen activators and chymotrypsin has
identified a six amino acid peptide involved in plasminogen activation.
This peptide is particularly useful when inserted between amino acid
residues 64 and 84 of full length human plasminogen. Novel plasminogen
activators have been made based upon the plasminogen
activation/recognition site of plasminogen binding proteins. The
polypeptides are useful in preparing thrombolytic agents for treating
blood clotting disorders such as heart attack
Sequence 431 AA;
Query Match 99.4%; Score 2243; DB 3; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
1 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 60
21 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 80
61 KASTDTMGPCPLPWSNATVLOQTYHAHRSALQGLGKHNYCRNPNRRRRCVYVQGLK 120
81 KASTDTMGPCPLPWSNATVLOQTYHAHRSALQGLGKHNYCRNPNRRRRCVYVQGLK 140
121 PLVQECWVHDCADGK-----LKFCQCKTLRPFKIIIGGEFTTIENQWFAAIYRRH 172
141 PLVQECWVHDCADGKPPSPPELAFQCGQKTLRPFKIIIGGEFTTIENQWFAAIYRRH 200
173 RGSVTVYVCGGSLISPCWISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
201 RGSVTVYVCGGSLISPCWISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
233 LHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPOFGTSCITGFGK 292
261 LHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPOFGTSCITGFGK 320
293 ENSTDYLYPEQLKMTVVKLIHSHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSSGGL 352
321 ENSTDYLYPEQLKMTVVKLIHSHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSSGGL 380
353 VCSLQGRMTLTGIVSWGRCALKDHPGVYTRVSHFLPWIRSHTKENGIAL 403
381 VCSLQGRMTLTGIVSWGRCALKDHPGVYTRVSHFLPWIRSHTKENGIAL 431
RESULT 19
AAB84605
ID AAB84605 standard; protein; 431 AA.
XX
AC AAB84605;
XX
DT 05-SEP-2001 (first entry)
XX
DE Amino acid sequence of urokinase plasminogen activator.
XX
XX Growth factor; protein inhibitor; protease; damaged tissue;
XX platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
XX connective tissue derived growth factor; CTGF; chrysalin; VEGF;
XX keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
XX transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
XX granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
XX vascular endothelial growth factor; urokinase plasminogen activator;
XX dermal ulcer; wound.
XX
XX Homo sapiens.
XX
XX WO200149309-A2.
PN

```

X F 12-JUL-2001.
X F 21-DEC-2000; 2000WO-IB001935.
X F 29-DEC-1999; 99GS-00030768.
X F (PFI) PFIZER LTD.
X F (PFI) PFIZER INC.
X F Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
X F WPI; 2001-418351/44.
X F N-PSDB; AAH28220.
X F Composition for the treatment of damaged tissue i.e. chronic wounds and
X F dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
X F factor.
X F Disclosure; Page 550; 572pp; English.
X F The specification describes a pharmaceutical composition, comprising a
X F growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
X F inhibits the action of at least one specific adverse protein, i.e. a
X F protease, that is upregulated in a damaged tissue such as a wound
X F environment. Growth factors which are included in the composition of the
X F invention are platelet-derived growth factor (PDGF), fibroblast growth
X F factor (FGF), connective tissue derived growth factor (CTGF),
X F keratinocyte-derived growth factor (KGF), transforming growth factor-beta
X F (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
X F epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
X F and chrysalin. Inhibitors which are included in the composition of the
X F invention include inhibitors of urokinase-type plasminogen activator
X F (uPA) and matrix metalloproteinase (MMP). The composition is useful for
X F the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
X F The present sequence represents a human uPA, and is used to produce the
X F composition of the invention
X F
X F Sequence 431 AA;
X F
X F Query Match 99.4%; Score 2243; DB 4; Length 431;
X F Best Local Similarity 98.1%; Pred. No. 1.2e-174;
X F Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
X F
X F 1 SNELHQPNSCDLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
X F 21 SNELHQPNSCDLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 80
X F 61 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQLGLGKHCNCRPNRRPWCYVQVGLK 120
X F 81 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQLGLGKHCNCRPNRRPWCYVQVGLK 140
X F 121 PLVQECMWHDCADGK-----LKFCGQKTLRPRFKIIGGFTTIENQWPAAIYRRH 172
X F 141 PLVQECMWHDCADGKSPPEELKFCGQKTLRPRFKIIGGFTTIENQWPAAIYRRH 200
X F 173 RGSVTVVCGSLISPCWVISAHCIFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 232
X F 201 RGSVTVVCGSLISPCWVISAHCIFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 260
X F 233 LHKDYSADTLAHNDIALKIRSKGRCAQFSRTIQTICLPSMYNDPQFGTSCFITGFGK 292
X F 261 LHKDYSADTLAHNDIALKIRSKGRCAQFSRTIQTICLPSMYNDPQFGTSCFITGFGK 320
X F 293 ENSTDYLYPQLKMTVVKLISHRECOQPHYVGVSTTLMCAADPQWKTDSGCGDSGGL 352
X F 321 ENSTDYLYPQLKMTVVKLISHRECOQPHYVGVSTTLMCAADPQWKTDSGCGDSGGL 380
X F 353 VCSLQGRMTLTGIVSWRGCGCALDKPGVYTRVSHFLPWIRSHTKENGLAL 403
X F 381 VCSLQGRMTLTGIVSWRGCGCALDKPGVYTRVSHFLPWIRSHTKENGLAL 431

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RESULT 20
 ID AAEL7128 standard; protein; 431 AA.
 AC AAEL7128;
 DT 18-APR-2002 (first entry)
 DE Human uPA protein.
 KW Human; cancer; urokinase-type plasminogen activator; uPA; inflammation;
 KW Ets-1 transcription factor; N-acetylglucosaminyltransferase V; Gnt-V;
 KW matrix-type metalloproteinase; MMP-1; MMP-3; gene therapy.
 OS Homo sapiens.
 XX WO200196606-A2.
 XX 20-DEC-2001.
 XX 14-JUN-2001; 2001WO-US019248.
 XX 14-JUN-2000; 2000US-00593488.
 PA (NYXI-) NYXIS NEURO THERAPIES INC.
 PI Yamamoto H, Kroes R, Moskal JR;
 XX WPI; 2002-130746/17.
 DR N-PSDB; AAD27855.
 CC Identifying a compound for treating cancer, comprises detecting
 CC transcription factor Ets-1, N-acetylglucosaminyltransferase V, urokinase-
 CC type plasminogen activator, matrix-type metalloproteinase-1 and -3 gene
 CC expression.
 CC Example 1; Page 62-63; 63pp; English.
 CC The invention relates to a method of identifying a compound for treating
 CC cancer. The method involves detecting the expression of a panel of
 CC sequences selected from transcription factor Ets-1, urokinase-type
 CC plasminogen activator (uPA), N-acetylglucosaminyltransferase V (Gnt-V),
 CC matrix-type metalloproteinase (MMP)-1 and MMP-3 in the cell. The method
 CC is useful for identifying a compound that affects a cell, particularly a
 CC cancer cell or glioma cell, or a cell that is involved in inflammation.
 CC It is used for diagnosing and/or treating cancer or other conditions that
 CC are affected by one or more members of a panel of genes or their protein
 CC product. The method is also useful for drug discovery, drug safety
 CC evaluations and in gene therapy. The present sequence is human uPA
 CC protein
 CC
 CC Sequence 431 AA;
 CC
 CC Query Match 99.4%; Score 2243; DB 5; Length 431;
 CC Best Local Similarity 98.1%; Pred. No. 1.2e-174;
 CC Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 CC
 CC 1 SNELHQPNSCDLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
 CC 21 SNELHQPNSCDLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 80
 CC 61 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQLGLGKHCNCRPNRRPWCYVQVGLK 120
 CC 81 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQLGLGKHCNCRPNRRPWCYVQVGLK 140
 CC 121 PLVQECMWHDCADGK-----LKFCGQKTLRPRFKIIGGFTTIENQWPAAIYRRH 172
 CC 141 PLVQECMWHDCADGKSPPEELKFCGQKTLRPRFKIIGGFTTIENQWPAAIYRRH 200
 CC 173 RGSVTVVCGSLISPCWVISAHCIFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 232
 CC 201 RGSVTVVCGSLISPCWVISAHCIFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 260
 CC 233 LHKDYSADTLAHNDIALKIRSKGRCAQFSRTIQTICLPSMYNDPQFGTSCFITGFGK 292
 CC 261 LHKDYSADTLAHNDIALKIRSKGRCAQFSRTIQTICLPSMYNDPQFGTSCFITGFGK 320
 CC 293 ENSTDYLYPQLKMTVVKLISHRECOQPHYVGVSTTLMCAADPQWKTDSGCGDSGGL 352
 CC 321 ENSTDYLYPQLKMTVVKLISHRECOQPHYVGVSTTLMCAADPQWKTDSGCGDSGGL 380
 CC 353 VCSLQGRMTLTGIVSWRGCGCALDKPGVYTRVSHFLPWIRSHTKENGLAL 403
 CC 381 VCSLQGRMTLTGIVSWRGCGCALDKPGVYTRVSHFLPWIRSHTKENGLAL 431

Q; 233 LHKDYSADTLAHNDIALLLKIRSEKGRCAOPSRITQITCLPSMYNDPOFCTSCEITGFGK 292
 DE 261 LHKDYSADTLAHNDIALLLKIRSEKGRCAOPSRITQITCLPSMYNDPOFCTSCEITGFGK 320
 Q; 293 ENSTDYLYPEQLKVTIVVKLLISHRECCQPHYVGGSEVTTKMLCAADPQWKTDSCQSGGGPL 352
 DE 321 ENSTDYLYPEQLKVTIVVKLLISHRECCQPHYVGGSEVTTKMLCAADPQWKTDSCQSGGGPL 380
 Q; 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHYKEENGLAL 403
 DE 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHYKEENGLAL 431
 RE 21
 AF 2228
 II AAU99228 standard; protein; 431 AA.
 X; AAU99228;
 AC
 D; 24-SEP-2002 (first entry)
 X; Human plasminogen activator, urokinase (PLAU).
 DE Human; Plasminogen activator; urokinase; PLAU; cancer; enzyme;
 X; cytosolic; serine protease; thrombolytic disorder; isogene;
 K; pulmonary embolism; chromosome 10q24-qter; haplotype; genotype; SNP;
 W; single nucleotide polymorphism; thrombolytic; gene therapy.
 O; Homo sapiens.
 X; WO200240503-A2.
 P; 23-MAY-2002.
 X; 14-NOV-2001; 2001WO-US044001.
 X; 17-NOV-2000; 2000US-0249703P.
 X; (GENA-) GENAISSANCE PHARM INC.
 X; Anastasio AE, Bertivegna SC, Koshiy B;
 X; WPI: 2002-519370/55.
 DE N-PSDB; ABK86597, ABK86598.
 X; Genetic variants of Plasminogen activator, Urokinase (PLAU) isogenes,
 P; useful for improving efficiency and reliability in drug development for
 P; treating thrombolytic disorders and cancer.
 X; Claim 27; Fig 3; 92pp; English.
 X; The invention relates to a polynucleotide comprising a first nucleotide
 C; sequence (NS1) comprising a PLAU (plasminogen activator, urokinase, a
 C; serine protease) isogene selected from isogenes 1-9 and 11-20 given in
 C; the specification, where each isogene comprises the regions of the PLAU
 C; gene or cDNA and is further defined by the corresponding sequence of
 C; polymorphisms (defining single nucleotide polymorphisms, SNP). Also
 C; included are methods of haplotyping/genotyping (and predicting the
 C; haplotype/genotype of the PLAU gene of an individual, identifying an
 C; association between a trait and at least one haplotype or haplotype pair
 C; of the PLAU gene, an isolated oligonucleotide for detecting a
 C; polymorphism in the PLAU gene, a recombinant non-human organism
 C; transformed or transfected with the gene or cDNA, fragments of the
 C; polynucleotides of at least 10 base pairs encompassing a polymorphic
 C; site, an isolated polymorphic variant PLAU protein or fragment, an
 C; isolated monoclonal antibody specific for PLAU, a computer system for
 C; storing and analyzing polymorphism data for the PLAU gene and a genome
 C; anthology for the PLAU gene. PLAU is useful in screening for drugs
 C; targeting PLAU that are useful for treating thrombolytic disorders and
 C; cancers. The methods are useful for improving the efficiency and
 C; reliability of the discovery and development of drugs for treating
 C; diseases associated with PLAU activity, in validating PLAU as a drug
 C; target and in the design of clinical trials for treating a specific

CC condition of disease associated with PLAU activity. The antibody is
 CC useful in diagnostic, prognostic and therapeutic methods. PLAU
 CC polynucleotides are useful in studying the expression and function of
 CC PLAU, and in expressing PLAU protein for use in screening for candidate
 CC drugs to treat diseases related to PLAU activity. The gene for PLAU is
 CC located on chromosome 10q24-qter. The present sequence represents the
 CC PLAU protein
 XX
 SQ Sequence 431 AA;
 Query Match 99.4%; Score 2243; DB 5; Length 431;
 Best Local Similarity 98.1%; Pred. No. 1.2e-174;
 Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 QY 1 SNELHQPVSNCDCNLNGGTCVSNKYFSNIHWNCPCPKFGGQHCHEIDKSKTCYEGNGHFYRG 60
 DB 21 SNELHQPVSNCDCNLNGGTCVSNKYFSNIHWNCPCPKFGGQHCHEIDKSKTCYEGNGHFYRG 80
 QY 61 KASTDTMGRPCLPMSATVLOQTYHAHRS DALQLGLGHNYCRNPDPNRRRRCVYVQGLK 120
 DB 81 KASTDTMGRPCLPMSATVLOQTYHAHRS DALQLGLGHNYCRNPDPNRRRRCVYVQGLK 140
 QY 121 PLVQSCWVHDCADGK-----LKFCGCGQTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
 DB 141 PLVQSCWVHDCADGKPKSPPEELKFCGCGQTLRPRFKIIGGEFTTIENQWFAAIYRRH 200
 QY 173 RGSVTVYVCGGSLISPCWVISATHCFIDYPKKEDYVYLGSRSLNSNTQGENMKFEVENLI 232
 DB 201 RGSVTVYVCGGSLISPCWVISATHCFIDYPKKEDYVYLGSRSLNSNTQGENMKFEVENLI 260
 QY 233 LHKDYSADTLAHNDIALLLKIRSEKGRCAOPSRITQITCLPSMYNDPOFCTSCEITGFGK 292
 DB 261 LHKDYSADTLAHNDIALLLKIRSEKGRCAOPSRITQITCLPSMYNDPOFCTSCEITGFGK 320
 QY 293 ENSTDYLYPEQLKMTVVKLLISHRECCQPHYVGGSEVTTKMLCAADPQWKTDSCQSGGGPL 352
 DB 321 ENSTDYLYPEQLKMTVVKLLISHRECCQPHYVGGSEVTTKMLCAADPQWKTDSCQSGGGPL 380
 QY 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHYKEENGLAL 403
 DB 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHYKEENGLAL 431
 RESULT 22
 AAG79460
 ID AAG79460 standard; protein; 431 AA.
 XX AAG79460;
 AC
 XX 15-NOV-2002 (first entry)
 DT
 DE sc-uPA.
 DE
 XX Single chain prepro-urokinase; sc-uPA; pro-urokinase; HIV;
 XX high molecular weight urokinase-type plasminogen activator; HMW-uPA;
 XX long A; long B; EGF-like domain; kringle domain; urokinase receptor;
 XX low molecular weight urokinase-type plasminogen activator; LMW-uPA; CD87;
 XX binding domain.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..20
 FT /note= "Signal peptide"
 FT Protein 21..431
 FT /label= "Pro-urokinase/HMW-uPA"
 FT /note= "With a cleavage between amino acids 178-179"
 FT Protein 158..431
 FT /label= "LMW-uPA"
 FT /note= "With a cleavage between amino acids 178-179"
 XX
 PN EPI232755-A2.
 XX

1 21-AUG-2002.
2 15-FEB-2002; 2002EP-00003555.
3 20-FEB-2001; 2001JP-00042655.
4 19-JUN-2001; 2001JP-00184284.
5 (JCRP-) JCR PHARM CO LTD.
6 Wada M, Wada N;
7 WPI; 2002-610512/66.
8 N-PSDB; ABA00207.
9 Anti-HIV agents, comprises ligand molecule that binds to CD87, e.g. high
10 molecular weight urokinase-type plasminogen activator, amino-terminal
11 fragment or an anti-CD87 antibody.
12 Disclosure; Page 20-23; 38pp; English.
13 This sequence represents single chain prepro-urokinase (sc-UPA). Pro-
14 urokinase (amino acids 21-431) with a cleavage between amino acids 178
15 and 179 gives high molecular weight urokinase-type plasminogen activator
16 (HMW-UPA). HMW-UPA is a protein consisting of two peptide chains linked
17 by a di-sulphide bond. The chains, long A and B, are formed by enzymatic
18 cleavage between amino acids 178 and 179 of pro-urokinase. HMW-UPA
19 includes an EGF-like domain, a kringle domain and a urokinase receptor
20 (CD87) binding domain. HMW-UPA is then cleaved between amino acids 155
21 and 156 to give low molecular weight urokinase-type plasminogen activator
22 (LMW-UPA) (amino acids 156-178 and 179-431), that has no plasminogen
23 activator activity. sc-UPA, or fragments of it, may be used in the anti-
24 HIV agents of the invention which comprise a ligand molecule that binds
25 to CD87. The agents are useful for treating HIV-infected humans for
26 suppression of reproduction of HIV. The anti-HIV agents act by a
27 mechanism of action different from those of conventional drugs, widening
28 the choice of therapeutics agents and avoiding problems of resistant HIV
29 agents.
30 Sequence 431 AA;
31 Query Match 99.4%; Score 2243; DB 6; Length 431;
32 Best Local Similarity 98.1%; Pred. No. 1.2e-174;
33 Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
34
35 1 SNELHVPSCDCLNGTCVSNKFSNIHWCNPKFGGQHCIDSKTCYEGNGHYRG 60
36 21 SNELHVPSCDCLNGTCVSNKFSNIHWCNPKFGGQHCIDSKTCYEGNGHYRG 80
37 61 KASDTMGRPCLPWSATVLOQTYAHRS DALQLGLGKHNYCRPNDRRFPWCYVQGLK 120
38 81 KASDTMGRPCLPWSATVLOQTYAHRS DALQLGLGKHNYCRPNDRRFPWCYVQGLK 140
39 121 PLVQECMVHDCADGK-----LKFOGQKTLPRFKIIGBFTTIENQWFAALYRRH 172
40 141 PLVQECMVHDCADGKFSSEPEELKFOGQKTLPRFKIIGBFTTIENQWFAALYRRH 200
41 173 RGSVTVYCGSLSPCWVISATHCFDYPKKEDIYVILGRSLNSNTQEMKFEVENLI 232
42 201 RGSVTVYCGSLSPCWVISATHCFDYPKKEDIYVILGRSLNSNTQEMKFEVENLI 260
43 233 LHKDYSADTLAHNDIALKIRSEGCAPSRITQICLPSMNDPQFTSCIEITGFGK 292
44 261 LHKDYSADTLAHNDIALKIRSEGCAPSRITQICLPSMNDPQFTSCIEITGFGK 320
45 293 ENSTDYLYPEOLKMTVVKLISHRECCQPHYVYGSVTTKMLCAADPQWKTDCOGDSGGL 352
46 321 ENSTDYLYPEOLKMTVVKLISHRECCQPHYVYGSVTTKMLCAADPQWKTDCOGDSGGL 380
47 353 VCSLQGRMTLTGIVSWRGCGALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
48 381 VCSLQGRMTLTGIVSWRGCGALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 431
49
50 1 UT 23

ABR55855
ID ABR55855 standard; protein; 431 AA.
XX
AC ABR55855;
XX
DT 02-SEP-2003 (first entry)
XX
DE Human urokinase.
XX
KW Peptide remodeling; glycoconjugation; glycosyltransferase; glycan;
XX urokinase; human.
XX
OS Homo sapiens.
XX
PN WO2003031464-A2.
XX
PD 17-APR-2003.
XX
PF 09-OCT-2002; 2002WO-US032263.
XX
PR 10-OCT-2001; 2001US-0328523P.
PR 19-OCT-2001; 2001US-0344692P.
PR 28-NOV-2001; 2001US-0344233P.
PR 28-NOV-2001; 2001US-034301P.
PR 07-JUN-2002; 2002US-0387292P.
PR 25-JUN-2002; 2002US-0391777P.
PR 17-JUL-2002; 2002US-0396594P.
PR 16-AUG-2002; 2002US-0404249P.
PR 28-AUG-2002; 2002US-0407527P.
XX
PA (NEOS-) NEOSE TECHNOLOGIES INC.
XX
PI De Fries S, Zopf D, Bayer R, Bowe C, Hakes D, Chen X;
XX WPI; 2003-449162/42.
DR N-PSDB; ACC78885.
XX
PT Remodeling a peptide, by removing a saccharyl subunit from the peptide to
PT form truncated glycan, and adding or deleting glycosyl groups to a
PT peptide and/or adding modifying group of a peptide to remodel the
XX peptide.
XX Example; Fig 65B; 900pp; English.
XX
CC The invention relates to a cell-free, in vitro method of remodeling a
CC peptide. The method involves removing a saccharyl subunit from the
CC peptide, thus forming a truncated glycan, and contacting the truncated
CC glycan with at least one glycosyltransferase and at least one glycosyl
CC donor under conditions suitable to transfer at least one glycosyl donor
CC to the truncated glycan, thus remodeling the peptide. Conjugates can be
CC formed between a granulocyte colony stimulating factor (G-CSF) peptide,
CC interferon alpha peptide, interferon beta peptide, Factor VIIa peptide,
CC Factor IX peptide, follicle stimulating hormone peptide, erythropoietin
CC (EPO) peptide, granulocyte macrophage colony stimulating factor (GM-CSF)
CC peptide, interferon-gamma peptide, alpha-1-protease inhibitor (A-1-PI)
CC peptide, beta-glucosidase peptide, tissue plasminogen activator (TPA)
CC peptide, interleukin-2 (IL-2) peptide, Factor VIII peptide, TNFalpha
CC receptor/immunoglobulin (Ig) G fusion peptide, urokinase peptide, anti-
CC glycoprotein IIB/IIa monoclonal antibody peptide, chimeric anti HER2
CC antibody peptide, anti-respiratory syncytial virus (RSV) F peptide, anti-
CC CD20 antibody peptide, recombinant Dnase peptide, anti-TNF alpha peptide,
CC insulin peptide, hepatitis B surface antigen (HbsAg), human growth
CC hormone (HGH) peptide, and a modifying group, where the modifying group
CC is covalently attached to the peptide through an intact glycosyl linking
CC group. The method is useful for a cell-free, in vitro method of
CC remodeling the above mentioned peptides. The present sequence represents
CC a human urokinase
XX
SQ Sequence 431 AA;
Query Match 99.4%; Score 2243; DB 6; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

Qy 1 SNELHVPNSDCDCLNGGTCVSNKYPFNSIHWNCNPKKFGQHCIEDKSKTCYEGNGHFFYRG 60
 Df 21 SNELHVPNSDCDCLNGGTCVSNKYPFNSIHWNCNPKKFGQHCIEDKSKTCYEGNGHFFYRG 80
 Qy 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 120
 Df 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 140
 Qy 121 FLVQSCVHDCADGK-----LKFQCGQKTLRPRFKIIGGFTTIIENQWFAAIYRRH 172
 Df 141 FLVQSCVHDCADGKFKPSPPEELKFCQGQKTLRPRFKIIGGFTTIIENQWFAAIYRRH 200
 Qy 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRNSNTQGMKFEVENLI 232
 Df 201 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRNSNTQGMKFEVENLI 260
 Qy 233 LHKDYSADTLAHHNDIALKIRSKGRCAPQSRRTIOTICLPSMYNDPQFGTSCITGFGK 292
 Df 261 LHKDYSADTLAHHNDIALKIRSKGRCAPQSRRTIOTICLPSMYNDPQFGTSCITGFGK 320
 Qy 293 ENSTDYLYPEQLKMTVVKLIISHRECQPHYGYSEVTTKMLCAADPQWKTDSCQDSSGGPL 352
 Df 321 ENSTDYLYPEQLKMTVVKLIISHRECQPHYGYSEVTTKMLCAADPQWKTDSCQDSSGGPL 380
 Qy 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 403
 Df 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 431

RE 12T 24
 AF 6547
 II ABUS6547 standard; protein; 431 AA.
 XY ABUS6547;
 AC
 Xy 02-APR-2003 (first entry)
 Df Lung cancer-associated polypeptide #140.
 Xy Lung cancer-associated polypeptide; cytostatic; emphysema;
 Xy antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 Xy small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 Xy chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 Xy interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 Xy Unidentified.
 OS
 Xy WO200286443-A2.
 Pf 31-OCT-2002.
 Xy 18-APR-2002; 2002WO-US012476.
 Xy 18-APR-2001; 2001US-0284770P.
 Pf 10-MAY-2001; 2001US-0290492P.
 Pf 09-NOV-2001; 2001US-0339245P.
 Pf 13-NOV-2001; 2001US-0350666P.
 Pf 29-NOV-2001; 2001US-0334370P.
 Pf 12-APR-2002; 2002US-0372246P.
 Xy (EOSB-) EOS BIOTECHNOLOGY INC.
 Xy Aziz N, Murray R;
 Pf WPI; 2003-093161/08.
 Df N-PSDB; ABX76275.
 Xy Detecting a lung cancer-associated transcript in a cell from a patient
 Pf for treating lung cancer, by contacting a biological sample from the
 Pf patient with a polynucleotide that exhibits increased or decreased
 Pf expression in lung cancer.
 Xy

PS Claim 27; Page 296; 453pp; English.
 XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridizes
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX
 SQ Sequence 431 AA;
 Query Match 99.4%; Score 2243; DB 6; Length 431;
 Best Local Similarity 98.1%; Pred. No. 1.2e-174;
 Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 Qy 1 SNELHVPNSDCDCLNGGTCVSNKYPFNSIHWNCNPKKFGQHCIEDKSKTCYEGNGHFFYRG 60
 Df 21 SNELHVPNSDCDCLNGGTCVSNKYPFNSIHWNCNPKKFGQHCIEDKSKTCYEGNGHFFYRG 80
 Qy 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 120
 Df 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 140
 Qy 121 FLVQSCVHDCADGK-----LKFQCGQKTLRPRFKIIGGFTTIIENQWFAAIYRRH 172
 Df 141 FLVQSCVHDCADGKFKPSPPEELKFCQGQKTLRPRFKIIGGFTTIIENQWFAAIYRRH 200
 Qy 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRNSNTQGMKFEVENLI 232
 Df 201 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRNSNTQGMKFEVENLI 260
 Qy 233 LHKDYSADTLAHHNDIALKIRSKGRCAPQSRRTIOTICLPSMYNDPQFGTSCITGFGK 292
 Df 261 LHKDYSADTLAHHNDIALKIRSKGRCAPQSRRTIOTICLPSMYNDPQFGTSCITGFGK 320
 Qy 293 ENSTDYLYPEQLKMTVVKLIISHRECQPHYGYSEVTTKMLCAADPQWKTDSCQDSSGGPL 352
 Df 321 ENSTDYLYPEQLKMTVVKLIISHRECQPHYGYSEVTTKMLCAADPQWKTDSCQDSSGGPL 380
 Qy 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 403
 Df 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 431
 RESULT 25
 ABUS6708
 ID ABUS6708 standard; protein; 431 AA.
 XX
 AC ABUS6708;
 Xy 02-APR-2003 (first entry)
 Df Lung cancer-associated polypeptide #301.
 Xy Lung cancer-associated polypeptide; cytostatic; emphysema;
 Xy antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 Xy small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 Xy chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 Xy interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 Xy

Unidentified.
 WO200286443-A2.
 31-OCT-2002.
 18-APR-2002; 2002WO-US012476.
 18-APR-2001; 2001US-0284770P.
 10-MAY-2001; 2001US-0290492P.
 09-NOV-2001; 2001US-0339245P.
 13-NOV-2001; 2001US-0350866P.
 29-NOV-2001; 2001US-0334370P.
 12-APR-2002; 2002US-0372246P.
 (BOSB-) BOS BIOTECHNOLOGY INC.
 Aziz N, Murray R;
 WPI; 2003-093161/08.
 N-PSDB; ABX76437.
 Detecting a lung cancer-associated transcript in a cell from a patient for treating lung cancer, by contacting a biological sample from the patient with a polynucleotide that exhibits increased or decreased expression in lung cancer.
 Claim 27; Page 424; 453pp; English.
 The invention relates to a method for detecting a lung cancer-associated transcript in a cell from a patient, comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridises to a sequence that is at least 80 % identical to a gene that exhibits increased or decreased expression in lung cancer samples. Lung cancer-associated polynucleotides and polypeptides are used for identifying a compound that modulates a lung cancer-associated polypeptide, for inhibiting proliferation of a lung cancer-associated cell to treat lung cancer in a patient and for treating a mammal having lung cancer by administering a modulatory compound identified. The methods are useful for treating lung cancer, such as small cell lung cancer, non-small cell lung cancer or other benign or precancerous lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides and polypeptides are useful for diagnostic purposes and as targets for screening for therapeutic compounds that modulate lung cancer, such as antibodies. Sequences ABU56408-ABU56745 represent lung cancer-associated polypeptides of the invention.
 Sequence 431 AA;
 Query Match 99.4%; Score 2243; DB 6; Length 431;
 Best Local Similarity 98.1%; Pred. No. 1.2e-174;
 Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 1 SNELHQPVSNCCLNGGTCVSNKYFNSIHWNCNPKKFGQHCIDKSKTCYEGNGHFFYRG 60
 21 SNELHQPVSNCCLNGGTCVSNKYFNSIHWNCNPKKFGQHCIDKSKTCYEGNGHFFYRG 80
 61 KASTDTMGRPCLPWNSATVLOQTHAHRSDALQLGLGKHNYCRNPDNRPRPCVVOGLK 120
 81 KASTDTMGRPCLPWNSATVLOQTHAHRSDALQLGLGKHNYCRNPDNRPRPCVVOGLK 140
 121 PLVQECMVHDCADGK-----LKFCQGKTLRPRFKIIGGFTTIENQFWFAAIRRH 172
 141 PLVQECMVHDCADGKXSSPEELKFCQGKTLRPRFKIIGGFTTIENQFWFAAIRRH 200
 173 RGSVTVYCGSLSPCWVLSATCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 232
 201 RGSVTVYCGSLSPCWVLSATCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 260
 233 LHKDYSADTLAHHNDIALLKIRSEKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 292

261 LHKDYSADTLAHHNDIALLKIRSEKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 320
 293 ENSTDYLYPEQLKMTVVVKLISHRECQOPHYVGSVTTKMLCAADPQWKTDSCQDSSGGL 352
 321 ENSTDYLYPEQLKMTVVVKLISHRECQOPHYVGSVTTKMLCAADPQWKTDSCQDSSGGL 380
 353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHYKEENGLAL 403
 381 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHYKEENGLAL 431
 RESULT 26
 ABU11076
 ID ABU11076 standard; protein; 431 AA.
 XX
 AC ABU11076;
 XX
 DT 05-FEB-2003 (first entry)
 XX
 DE Human urokinase plasminogen activator.
 XX
 KW Urokinase plasminogen activator; gene therapy; cancer;
 KW hyperproliferative disorder; cancer; breast cancer; colon cancer;
 KW bone cancer; brain cancer; ovary cancer; cervix cancer;
 KW endometrium cancer; stomach cancer; kidney cancer; tumour metastasis.
 XX
 OS Homo sapiens.
 XX
 PN WO200279515-A1.
 XX
 PD 10-OCT-2002.
 XX
 PF 18-MAR-2002; 2002WO-US008112.
 XX
 PR 30-MAR-2001; 2001US-00821972.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Baker BP, Freier SM, Watt AT;
 XX
 WPI; 2003-058441/05.
 DR N-PSDB; ABX17681.
 XX
 PT New antisense compound, useful for preparing a composition for treating hyperproliferative disorders, cancer e.g., breast, colon, bone, brain, ovary, cervix, endometrium, stomach or kidney cancer, or tumor metastasis.
 PT
 XX
 PS Disclosure; Page 101-102; 153pp; English.
 XX
 CC A new compound, which is 8-50 nucleobases in length targeted to a nucleic acid molecule encoding urokinase plasminogen activator, specifically hybridises with and inhibits the expression of urokinase plasminogen activator. The compound is useful for preparing a composition for treating (e.g. by gene therapy) hyperproliferative disorder, cancer e.g., breast, colon, bone, brain, ovary, cervix, endometrium, stomach or kidney cancer, or tumour metastasis. This is the amino acid sequence of a urokinase plasminogen activator
 XX
 SQ Sequence 431 AA;
 Query Match 99.4%; Score 2243; DB 6; Length 431;
 Best Local Similarity 98.1%; Pred. No. 1.2e-174;
 Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
 1 SNELHQPVSNCCLNGGTCVSNKYFNSIHWNCNPKKFGQHCIDKSKTCYEGNGHFFYRG 60
 21 SNELHQPVSNCCLNGGTCVSNKYFNSIHWNCNPKKFGQHCIDKSKTCYEGNGHFFYRG 80
 61 KASTDTMGRPCLPWNSATVLOQTHAHRSDALQLGLGKHNYCRNPDNRPRPCVVOGLK 120
 81 KASTDTMGRPCLPWNSATVLOQTHAHRSDALQLGLGKHNYCRNPDNRPRPCVVOGLK 140

QY 121 PLVQECMWHDCADGK-----LKFOGQKTLRPRFKIIGBFTTNIENQFWFAAIYRRH 172
D: 141 PLVQECMWHDCADGKPPSPPEELKFOGQKTLRPRFKIIGBFTTNIENQFWFAAIYRRH 200
QY 173 RGGSVTVYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
D: 201 RGGSVTVYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHHNDIALKIRSEKGRCAQPSRTIOTICLPSMNDPQFSTCEITGFGK 292
D: 261 LHKDYSADTLAHHNDIALKIRSEKGRCAQPSRTIOTICLPSMNDPQFSTCEITGFGK 320
QY 293 ENSTDYLYPEQLKMTVVKVLIHRECCQPHYVYGVSEVTTKMLCAADPOWKTDSCQDGGPL 352
D: 321 ENSTDYLYPEQLKMTVVKVLIHRECCQPHYVYGVSEVTTKMLCAADPOWKTDSCQDGGPL 380
QY 353 VCSLQGRMTLTGIVSWGRCALDKPKGYVTVRSHFLPWIRSHYKEENGLAL 403
D: 381 VCSLQGRMTLTGIVSWGRCALDKPKGYVTVRSHFLPWIRSHYKEENGLAL 431

RE 27
AE 2137
IL ABR92137 standard; protein; 431 AA.
XX ABR92137;
XX 10-SEP-2003 (first entry)
XX Human cervical cancer cell marker protein SEQ ID NO:184.
XX Human; cervical cancer; cervical cancer marker; cancer therapy;
XX detection; gene therapy; vaccine.
XX Homo sapiens.
XX WO2002101075-A2.
XX 19-DEC-2002.
XX 12-JUN-2002; 2002WO-US018638.
XX 13-JUN-2001; 2001US-0298155P.
XX 13-JUN-2001; 2001US-0298159P.
XX 14-NOV-2001; 2001US-033938P.
XX (MILL-) MILLENNIUM PHARM INC.
XX Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
P1 Gannavarapu M, Glatt K, Hoersch S;
XX N-PSDB; ACF12920.
D: New isolated nucleic acid molecule useful for detecting, characterizing,
D: preventing and treating human cervical cancers, in various prognostic and
D: diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
PE Claim 4; Page 345-346; 386pp; English.
XX ACF12828 to ACF12947 encode the human cervical cancer marker proteins (I)
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC normal indicates the presence of cervical cancer. Also described: (1) a
CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (I) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (I) is useful in detecting, characterizing,
CC preventing and treating human cervical cancers. (I) may also be used in

CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials
XX Sequence 431 AA;
Query Match 99.4%; Score 2243; DB 6; Length 431;
Best Local Similarity 98.1%; Pred. No. 1.2e-174;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHFYRG 60
D: 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRPNDRRRPWCYVQVGLK 120
D: 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRPNDRRRPWCYVQVGLK 140
QY 121 PLVQECMWHDCADGK-----LKFOGQKTLRPRFKIIGBFTTNIENQFWFAAIYRRH 172
D: 141 PLVQECMWHDCADGKPPSPPEELKFOGQKTLRPRFKIIGBFTTNIENQFWFAAIYRRH 200
QY 173 RGGSVTVYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
D: 201 RGGSVTVYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHHNDIALKIRSEKGRCAQPSRTIOTICLPSMNDPQFSTCEITGFGK 292
D: 261 LHKDYSADTLAHHNDIALKIRSEKGRCAQPSRTIOTICLPSMNDPQFSTCEITGFGK 320
QY 293 ENSTDYLYPEQLKMTVVKVLIHRECCQPHYVYGVSEVTTKMLCAADPOWKTDSCQDGGPL 352
D: 321 ENSTDYLYPEQLKMTVVKVLIHRECCQPHYVYGVSEVTTKMLCAADPOWKTDSCQDGGPL 380
QY 353 VCSLQGRMTLTGIVSWGRCALDKPKGYVTVRSHFLPWIRSHYKEENGLAL 403
D: 381 VCSLQGRMTLTGIVSWGRCALDKPKGYVTVRSHFLPWIRSHYKEENGLAL 431

RESULT 28
AAR20537
ID AAR20537 standard; protein; 434 AA.
XX AAR20537;
XX 25-MAR-2003 (revised)
XX 21-MAY-1992 (first entry)
XX Amidated deriv. of pro-urokinase (2).
XX Pro-urokinase; plasminogen activator; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Protein 1..431
FT /label= pro-UK
XX DE4122688-A.
XX 16-JAN-1992.
XX 09-JUL-1991; 91DE-04122688.
XX 12-JUL-1990; 90GB-00015369.
XX 10-JUL-1991; 91GB-00014846.
XX (FARM) FARMITALIA ERBA SRL CARLO.
XX Gozzini L, Visco C, Perego R, Roncucci R, Sarmientos P;
PI WPI; 1992-025815/04.
XX New amidated derivs. of human pro-urokinase - are fibrinolytic and can be

used to treat acute myocardial infarction, pulmonary embolism or deep venous thrombosis.

Claim 4,8; Page 8; 18pp; German.

The protein has fibrinolytic activity and can be used in the same way as PUK, e.g. for treating acute myocardial infarction, lung embolism and deep venous thrombosis. It has greater affinity for plasminogen bound to fibrin than for circulating plasminogen, so have high selectivity for thrombi with reduced chance of bleeding. Compared with the COOH-terminated cpds., it has a better stability against most carboxypeptidases and prolonged half life. See also AAQ20754-58 and AAR20536-38. (Updated on 25-MAR-2003 to correct PA field.)

Sequence 434 AA;

Query Match 99.4%; Score 2243; DB 2; Length 434;
 Best Local Similarity 98.1%; Pred. No. 1.2e-174; Indels 8; Gaps 1;
 Matches 403; Conservative 0; Mismatches 0;

1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 80
 61 KASDTMTGRPCLPNSATVLQOQTYHAHRS DALQLGLGKHNCRPNDRRRPWCYVQVGLK 120
 81 KASDTMTGRPCLPNSATVLQOQTYHAHRS DALQLGLGKHNCRPNDRRRPWCYVQVGLK 140
 121 PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGSEFTTIENQPFAAIYRRH 172
 141 PLVQECMVHDCADGKPPSELPKFCQGXQLRPRFKIIGSEFTTIENQPFAAIYRRH 200
 173 RGSVTVVCGSLSPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 232
 201 RGSVTVVCGSLSPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 260
 233 LHKDYSADTLAHNDIALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 292
 261 LHKDYSADTLAHNDIALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 320
 293 ENSTDYLYPEQLKMTVVKLI SHRECQOPHYVGSVTTKMLCAADPQWKTDSCQDSDGGPL 352
 321 ENSTDYLYPEQLKMTVVKLI SHRECQOPHYVGSVTTKMLCAADPQWKTDSCQDSDGGPL 380
 353 VCSLQGRMTLTGIVSWGRCALKKPGVYTRVSHFLPWIRSHTKENGLAL 403
 381 VCSLQGRMTLTGIVSWGRCALKKPGVYTRVSHFLPWIRSHTKENGLAL 431

ULT 29
 20538
 AAR20538 standard; protein; 434 AA.

AAR20538;
 25-MAR-2003 (revised)
 21-MAY-1992 (first entry)

Amidated deriv. of pro-urokinase (3).

Pro-urokinase; plasminogen activator; ss.

Homo sapiens.

Key Location/Qualifiers
 Protein 1.431
 /label= pro-UK

DE4122688-A.
 16-JAN-1992.
 09-JUL-1991; 91DE-04122688.

12-JUL-1990; 90GB-00015369.
 10-JUL-1991; 91GB-00014846.
 (FARM) FARMITALIA ERBA SRL CARLO.

Gozzini L, Visco C, Perrego R, Roncucci R, Sarmientos P;
 WPI; 1992-035815/04.

New amidated derivs. of human pro-urokinase - are fibrinolytic and can be used to treat acute myocardial infarction, pulmonary embolism or deep venous thrombosis.

Claim 4,9; Page 8; 18pp; German.

The protein has fibrinolytic activity and can be used in the same way as PUK, e.g. for treating acute myocardial infarction, lung embolism and deep venous thrombosis. It has greater affinity for plasminogen bound to fibrin than for circulating plasminogen, so have high selectivity for thrombi with reduced chance of bleeding. Compared with the COOH-terminated cpds., it has a better stability against most carboxypeptidases and prolonged half life. See also AAQ20360, AAQ20754-58 and AAR20536-38. (Updated on 25-MAR-2003 to correct PA field.)

Sequence 434 AA;

Query Match 99.4%; Score 2243; DB 2; Length 434;
 Best Local Similarity 98.1%; Pred. No. 1.2e-174; Indels 8; Gaps 1;
 Matches 403; Conservative 0; Mismatches 0;

1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 80
 61 KASDTMTGRPCLPNSATVLQOQTYHAHRS DALQLGLGKHNCRPNDRRRPWCYVQVGLK 120
 81 KASDTMTGRPCLPNSATVLQOQTYHAHRS DALQLGLGKHNCRPNDRRRPWCYVQVGLK 140
 121 PLVQECMVHDCADGK-----LKFQCGQKTLRPRFKIIGSEFTTIENQPFAAIYRRH 172
 141 PLVQECMVHDCADGKPPSELPKFCQGXQLRPRFKIIGSEFTTIENQPFAAIYRRH 200
 173 RGSVTVVCGSLSPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 232
 201 RGSVTVVCGSLSPCWVISATHCFIDYPKEDYIVLGRSLNSNTQGMKFEVENLI 260
 233 LHKDYSADTLAHNDIALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 292
 261 LHKDYSADTLAHNDIALLKIRSKGRCQAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 320
 293 ENSTDYLYPEQLKMTVVKLI SHRECQOPHYVGSVTTKMLCAADPQWKTDSCQDSDGGPL 352
 321 ENSTDYLYPEQLKMTVVKLI SHRECQOPHYVGSVTTKMLCAADPQWKTDSCQDSDGGPL 380
 353 VCSLQGRMTLTGIVSWGRCALKKPGVYTRVSHFLPWIRSHTKENGLAL 403
 381 VCSLQGRMTLTGIVSWGRCALKKPGVYTRVSHFLPWIRSHTKENGLAL 431

RESULT 30
 AAR20536
 ID AAR20536 standard; protein; 436 AA.

AC AAR20536;
 25-MAR-2003 (revised)
 21-MAY-1992 (first entry)

Amidated deriv. of pro-urokinase (1).

Pro-urokinase; plasminogen activator; ss.

O6 XX Homo sapiens. Location/Qualifiers
PF 1 431
FT Protein
F1 /label= pro-UK
F1 /note= "the amidated form of pro-UK is claimed in claim 1"
F7 Misc-difference 433...436
F7 /note= "may be any amino acid, pref. Lys or Arg, or 0-4 amino acids may be omitted"
XX
XX DE4122688-A.
XX 16-JAN-1992.
XX 09-JUL-1991; 91DE-04122688.
XX 12-JUL-1990; 90GB-00015369.
XX 10-JUL-1991; 91GB-00014846.
XX (FARM) FARMITALIA ERBA SRL CARLO.
XX Gozzini L, Visco C, Perego R, Roncucci R, Sarmientos P;
XX WPI; 1992-025815/04.
XX New amidated derivs. of human pro-urokinase - are fibrinolytic and can be used to treat acute myocardial infarction, pulmonary embolism or deep venous thrombosis.
XX Claim 1,4,7; Page 8; 18pp; German.
XX The protein has fibrinolytic activity and can be used in the same way as PUK, e.g. for treating acute myocardial infarction, lung embolism and deep venous thrombosis. It has greater affinity for plasminogen bound to fibrin than for circulating plasminogen, so have high selectivity for thrombi with reduced chance of bleeding. Compared with the COOH-terminated cpds., it has a better stability against most carboxypeptidases and prolonged half life. See also AAQ20360, AAQ20754-58 and AA2036-38. (Updated on 25-MAR-2003 to correct PA field.)
XX Sequence 436 AA;
XX ery Match 99.4%; Score 2243; DB 2; Length 436;
XX st Local Similarity 98.1%; Pred. No. 1.2e-174;
XX tches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
Q3 1 SNELHVPNSCDLNGGTCVSNKYFSNTHWCNCPKFGGHCETDKSKTCYEGNGHFPYRG 60
D1 21 SNELHVPNSCDLNGGTCVSNKYFSNTHWCNCPKFGGHCETDKSKTCYEGNGHFPYRG 80
Q3 61 KASDTMGRPCLPWNATVLAQTYHAHRSALQGLGKHNYCRNPDNRPRWCYVQVGLK 120
D1 81 KASDTMGRPCLPWNATVLAQTYHAHRSALQGLGKHNYCRNPDNRPRWCYVQVGLK 140
Q3 121 PLVQECMVDGADGK-----LKFGCGKTLPRPKITGGETTIENTOPWFAAIVRRH 172
D1 141 PLVQECMVDGADGKPPSPPEELKFGCGKTLPRPKITGGETTIENTOPWFAAIVRRH 200
Q3 173 RGGSVYVCGSLISPCWVISAHCDFIDYPKKEDYIVYVGLSRSLNSNTQCEMFEVENLI 232
D1 201 RGGSVYVCGSLISPCWVISAHCDFIDYPKKEDYIVYVGLSRSLNSNTQCEMFEVENLI 260
Q3 233 LHKYSADTLAHHNDIALKLRSEKRCQAQPSRTIQICLPSMYNDPQFTSCBITGFGK 292
D1 261 LHKYSADTLAHHNDIALKLRSEKRCQAQPSRTIQICLPSMYNDPQFTSCBITGFGK 320
Q3 293 ENSTDYLYPEQLKMTVVKLI SHRECCQPHYYGSEVTTKQCAADPQWKTDSCQDSDGGPL 352
D1 321 ENSTDYLYPEQLKMTVVKLI SHRECCQPHYYGSEVTTKQCAADPQWKTDSCQDSDGGPL 380
Q3 353 VCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
|||||

DB 381 VCSLQGRWTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431
RESULT 31
ADE25745
ID ADE25745 standard; protein; 431 AA.
XX AC ADE25745;
XX DT 29-JAN-2004 (first entry)
XX DE Human protein differentially expressed in foam cells #22.
XX KW Human; differential expression; foam cell; LPS; lipopolysaccharide; cardiovascular disease; atherosclerosis.
XX OS Homo sapiens.
XX PN US2003194721-A1.
XX PD 16-OCT-2003.
XX PF 18-SEP-2002; 2002US-00247671.
XX PR 19-SEP-2001; 2001US-0323784P.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Mikita T, Shiffman D, Porter JG, Kaser MR;
XX WPI; 2003-875398/81.
XX N-PSDB; ADE25630.
XX Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
XX Disclosure; SEQ ID NO 149; 37pp; English.
XX The invention relates to a combination comprising several polynucleotides having any one of 127 sequences (S1) such as the sequence of human calmodulin gene, human mRNA for KIAA0930 protein, leukotriene A4 hydrolase, human CGI-142 protein mRNA, human K+ channel beat 2 subunit mRNA, etc., and their complements. The cDNAs are differentially expressed in LPS (lipopolysaccharide)-treated foam cells. Also included are obtaining an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the nucleic acids, a host cell containing the vector, a purified polypeptide appearing as ADE25750 and ADE25751, producing a protein by culturing the host cell, and a composition comprising a purified antibody that specifically binds to the proteins. The foam cell-expressed nucleic acids are useful for a high throughput detection of differential expression of one or more polynucleotides in a sample. The sample is from a subject with atherosclerosis and comparison with a standard defines early, mid or late stages of the disorder. The foam cell-expressed nucleic acids are useful for high throughput screening of a library of molecules or compounds to identify a ligand which binds a polynucleotide. The library is chosen from DNA molecules, peptides, proteins and RNA molecules. The protein is useful for a high throughput screening of library of molecules or compounds to identify at least one ligand which specifically binds a protein, for purifying a ligand from a sample for making an antibody. The foam cell-expressed nucleic acids are useful for diagnosing cardiovascular disorder. The foam cell-expressed nucleic acids are useful as elements on a microarray which can be used for detecting related polynucleotides in a sample, diagnosing cardiovascular disease, atherosclerosis. The present sequence represents a protein differentially expressed in LPS treated foam cells.
XX SQ Sequence 431 AA;
Query Match 99.3%; Score 2241; DB 7; Length 431;
Best Local Similarity 97.8%; Pred. No. 1.7e-174; Indels 8; Gaps 1;
Matches 402; Conservative 1; Mismatches 0;

1 SNELHQPVSNCDCCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIDKSKTCYEGNGHFYRG 60
21 SNELHQPVSNCDCCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIDKSKTCYEGNGHFYRG 80
61 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQGLGKKNYCRNPDRRPPWCYVQVGLK 120
81 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQGLGKKNYCRNPDRRPPWCYVQVGLK 140
121 PLVQECMVHDCADGK-----LKFCQGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
141 PLVQECMVHDCADGKSSPPEELKFCQGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 200
173 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
201 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
233 LHKDYSADTLAHNDIALKIRSKGRCAPSRITQICLPMSVNDPQFGTSCIEITGFGK 292
261 LHKDYSADTLAHNDIALKIRSKGRCAPSRITQICLPMSVNDPQFGTSCIEITGFGK 320
293 ENSTDYLYPEQLKMTVVVKLIASHRECQPPHYVGSVTTKMLCAADPQWKTDSCQDGGPL 352
321 ENSTDYLYPEQLKMTVVVKLIASHRECQPPHYVGSVTTKMLCAADPQWKTDSCQDGGPL 380
353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
381 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431

ULT 32
24578 AAW24578 standard; protein; 430 AA.
AAW24578;
25-MAR-2003 (revised)
11-NOV-1997 (first entry)
Inhibitor resistant urokinase.

Urokinase; inhibitor resistant; plasminogen; human; whey acid protein;
plasminogen activator inhibitor-1; plasminogen activator; protease; WAP;
plasmin; proteolytic enzyme; clot lysis; heart attack; heart muscle.
Homo sapiens.
Synthetic.
Key Location/Qualifiers
Peptide 1..19 /note= "whey acid protein signal peptide"
Protein 20..430 /note= "urokinase"
Domain 20..64 /note= "E-domain"
Domain 61..150 /note= "Kringler-1 domain"
Domain 179..430 /note= "P-domain"
Misc-difference 198..203 /note= "deleted in modified urokinase of the invention"

US5648253-A;
15-JUL-1997.
08-SEP-1992; 92US-00942157.
20-DEC-1990; 90US-00631673.
(TSIT-) TSI CORP.
Wei C;

XX WPI; 1997-372062/34.
DR N-PSDB; AAT80075.
XX Deletion-modified urokinase protein - with increased resistance to
PT inhibition by plasminogen activator inhibitor-1.
XX Disclosure; Col 15-18; 16pp; English.
XX This sequence represents the full length urokinase, including the whey
acid protein (WAP) signal peptide. This sequence has residues 179-184 of
the urokinase sequence deleted to create the modified urokinase of the
invention. The modified urokinase (see AAW4578) cleaves plasminogen, and
has a lower binding affinity for plasminogen activator inhibitor-1 than
the corresponding unmodified urokinase. Urokinase is one of two types of
mammalian plasminogen activators (PA), the other being tissue type PA.
PAs catalyze the conversion of the circulating zymogen plasminogen to the
broad spectrum protease plasmin by limited proteolysis. The modified
urokinase can be used for clot lysis, specifically to dissolve heart
attack-causing clots before they cause permanent damage to heart muscle.
The urokinase mutant is more resistant to inhibition by plasminogen
activator inhibitors than the unmodified urokinase. It can be selectively
expressed and secreted from the mammary glands of transgenic animals.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX

SQ Sequence 430 AA;
Query Match 99.2%; Score 2240; DB 2; Length 430;
Best Local Similarity 97.8%; Pred. No. 2.1e-174;
Matches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQPVSNCDCCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIDKSKTCYEGNGHFYRG 60
DB 20 SNELHQPVSNCDCCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIDKSKTCYEGNGHFYRG 79
QY 61 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQGLGKKNYCRNPDRRPPWCYVQVGLK 120
DB 80 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQGLGKKNYCRNPDRRPPWCYVQVGLK 139
QY 121 PLVQECMVHDCADGK-----LKFCQGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
DB 140 PLVQECMVHDCADGKSSPPEELKFCQGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 199
QY 173 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
DB 200 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKFEVENLI 259
QY 233 LHKDYSADTLAHNDIALKIRSKGRCAPSRITQICLPMSVNDPQFGTSCIEITGFGK 292
DB 260 LHKDYSADTLAHNDIALKIRSKGRCAPSRITQICLPMSVNDPQFGTSCIEITGFGK 319
QY 293 ENSTDYLYPEQLKMTVVVKLIASHRECQPPHYVGSVTTKMLCAADPQWKTDSCQDGGPL 352
DB 320 ENSTDYLYPEQLKMTVVVKLIASHRECQPPHYVGSVTTKMLCAADPQWKTDSCQDGGPL 379
QY 353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
DB 380 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 430

RESULT 33
AAP91886
ID AAP91886 standard; protein; 431 AA.
XX
AC AAP91886;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 16-APR-1990 (first entry)
XX
DE Sequence of prourokinase.
XX
KW Low mol. wt. plasminogen activator; prourokinase; dissolve blood clot.

XX Homo sapiens.
 O6 Key
 XX Location/Qualifiers
 FH 21..431
 P1 Protein
 FT /note= "Mature prourokinase."
 FT 170..179
 FT /note= "Preferred initiation region for the low mol. wt.
 FT plasminogen activators."
 XX
 XX EP316068-A.
 XX
 XX 17-MAY-1989.
 XX
 XX 07-OCT-1988; 88EP-00309417.
 XX
 XX 09-OCT-1987; 87US-00107370.
 XX 27-SEP-1988; 88US-00248727.
 XX
 XX (COLB) COLLABORATIVE RES INC.
 XX
 XX Mao JI;
 XX WPI; 1989-146601/20.
 XX N-PSDB; AAN91740.
 XX
 XX Modified low mol. wt. plasminogen activator - formed of amino acids
 XX comprising the amino acid portion of prourokinase from 150 to 411.
 XX
 XX Fig 1; Page -; 27pp; English.
 XX
 XX A low mol. wt. polypeptide plasminogen activator (PA) is claimed which is
 XX formed from amino acids 150-411 of prourokinase. The preferred initiation
 XX region for the low mol. wt. PA is indicated (see FT). A low mol. wt. PA
 XX can be injected into blood in the body in vivo to dissolve clots without
 XX harm. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-
 XX MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI
 XX field.)
 XX
 XX Sequence 431 AA;
 XX
 XX Query Match 99.2%; Score 2240; DB 1; Length 431;
 XX st Local Similarity 97.8%; Pred. No. 2.1e-174;
 XX tches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;
 QY 1 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCEDKSKTCYEGNGHFYRG 60
 DL 21 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCEDKSKTCYEGNGHFYRG 80
 QY 61 KASTDTMGRPCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
 DL 81 KASTDTMGRPCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 140
 QY 121 PLVQECWVHDCADGK-----LKFCQCGQKTLRPRFKIIGGEFTTIENQWPAIYRRH 172
 DL 141 PLVQECWVHDCADGKPKSPPEELKFCQCGQKTLRPRFKIIGGEFTTIENQWPAIYRRH 200
 QY 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVVILGRSRLNSNTQGEKMFVENLI 232
 DL 201 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVVILGRSRLNSNTQGEKMFVENLI 260
 QY 233 LHKDYSADTLAHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPFGTSCITGFGK 292
 DL 261 LHKDYSADTLAHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPFGTSCITGFGK 320
 QY 293 ENSTDYLYPEQLKMTVWKLISHRECCQPHYVGVSEVTTKMLCAADPQWKTDSCQDSSGGL 352
 DL 321 ENSTDYLYPEQLKMTVWKLISHRECCQPHYVGVSEVTTKMLCAADPQWKTDSCQDSSGGL 380
 QY 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHPLPWIRSHKTEENGLAL 403
 DL 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHPLPWIRSHKTEENGLAL 431

RESULT 34
 AAP94764
 ID AAP94764 standard; protein; 431 AA.
 XX
 AC AAP94764;
 XX
 DT 25-MAR-2003 (revised)
 DT 27-JUN-1990 (first entry)
 XX
 DE Non-glycosylated prourokinase.
 XX
 KW Prourokinase; CGE 195; plasminogen activator; blood clot lysis.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region
 FT /label= signal sequence
 XX
 PN EP299706-A.
 XX
 XX 18-JAN-1989.
 XX
 XX 12-JUL-1988; 88EP-00306334.
 XX
 PR 13-JUL-1987; 87US-00072426.
 PR 29-JUN-1988; 88US-00211279.
 XX
 XX (COLB) COLLABORATIVE RES INC.
 XX
 XX Baltimore D, Moir DT, Broeze RJ;
 XX WPI; 1989-017204/03.
 XX N-PSDB; AAN93079.
 XX
 XX New non glycosylated, secreted plasminogen activator - pref. with
 XX asparagine replaced or deleted, useful for treating blood clots,
 XX expressed in non mammalian cells.
 XX
 PS Disclosure; Page; 26pp; English.
 XX
 CC myocardial infarction. DNA encoding the protein was sequenced from
 CC plasmid pCE195, a subclone of two inserts isolated by screening a cDNA
 CC library prep'd. from kidney cell RNA. One of the original inserts, clone
 CC CGF31 (tag c) started in the middle of the signal sequence. Mutants of
 CC the sequence, pref. in which gcc (Ala) replaces aat (Asn) at nucleotides
 CC 1002-1004 (residue 302) are used to transform hosts for the prodn. of non
 CC -glycosylated prourokinase. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 431 AA;
 XX
 XX Query Match 99.2%; Score 2240; DB 1; Length 431;
 XX Best Local Similarity 97.8%; Pred. No. 2.1e-174;
 XX Matches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;
 QY 1 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCEDKSKTCYEGNGHFYRG 60
 DL 21 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCEDKSKTCYEGNGHFYRG 80
 QY 61 KASTDTMGRPCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
 DL 81 KASTDTMGRPCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 140
 QY 121 PLVQECWVHDCADGK-----LKFCQCGQKTLRPRFKIIGGEFTTIENQWPAIYRRH 172
 DL 141 PLVQECWVHDCADGKPKSPPEELKFCQCGQKTLRPRFKIIGGEFTTIENQWPAIYRRH 200
 QY 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVVILGRSRLNSNTQGEKMFVENLI 232
 DL 201 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVVILGRSRLNSNTQGEKMFVENLI 260
 QY 233 LHKDYSADTLAHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPFGTSCITGFGK 292

261 LKDYADTLAHND:ALLKIRSKGRCAQPSRTIQTICLPMSYNDPQGTSCETGFGK 320
 293 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 352
 321 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 380
 353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
 381 LCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431
 ULT 35
 37128 AAE37128 standard; protein; 431 AA.
 AAE37128;
 07-AUG-2003 (first entry)
 Human urokinase-type plasminogen activator (uPA) protein.
 Osteoarthritis; rheumatoid arthritis; plasmin; plasminogen; human;
 urokinase-type plasminogen activator; uPA; degenerative joint disease;
 spondyloarthritis; antisense-therapy; antibody therapy; osteopathic;
 urokinase-type plasminogen activator receptor; psoriatic arthritis;
 plasminogen-activator inhibitor type 1; PAI-1; uPAR.
 Homo sapiens.
 WO2003033009-A2.
 24-APR-2003.
 10-JUL-2002; 2002WO-IB005797.
 10-JUL-2001; 2001US-0304461P.
 10-JUL-2001; 2001US-0304490P.
 13-JUL-2001; 2001US-0305182P.
 (OMNI-) OMNIO AB.
 Ny T, Holmdahl R, Li J;
 WPI; 2003-393477/37.
 N-PSDB; AAD56133.
 Treating or preventing arthritis e.g. osteoarthritis, rheumatoid
 arthritis in mammals, by administering inhibitors of plasmin.
 plasminogen, urokinase-type plasminogen activator or plasminogen-
 activator inhibitor type 1.
 Disclosure; Page 71-73; 85pp; English.
 The invention relates to a method for treating or preventing arthritis
 e.g. osteoarthritis, rheumatoid arthritis in mammals, by administering
 inhibitors of plasmin, plasminogen, urokinase-type plasminogen
 (uPA), plasminogen-activator inhibitor type 1 (PAI-1) and urokinase-type
 plasminogen activator receptor (uPAR). The method is useful for treating
 or preventing arthritis caused by degenerative joint disease, preferably
 rheumatoid arthritis, psoriatic arthritis, infectious arthritis, juvenile
 rheumatoid arthritis, osteoarthritis and spondyloarthritis in a
 mammal, especially a human. It is also useful for identifying agents for
 treating or preventing arthritis in a mammal and it is also useful in
 antisense-therapy and antibody therapy. The present sequence is human uPA
 protein. Note: This sequence is said to be encoded by SEQ ID NO:3
 (AAD56133), but this does not appear to be the case
 Sequence 431 AA;
 very March 99, 24; Score 2240; DB 6; Length 431;
 st Local Similarity 97.8%; Pred. No. 2.1e-174;
 arches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQPNSDCCLNGCTCVSNKYFSNIHWCNPKPKFGGQHCEIDKSKTCYEGNGHYRG 60
 DB 21 SNELHQPNSDCCLNGCTCVSNKYFSNIHWCNPKPKFGGQHCEIDKSKTCYEGNGHYRG 80
 QY 61 KASDTWTGRPCLPNSATVLQOTVHAHRSALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
 DB 81 KASDTWTGRPCLPNSATVLQOTVHAHRSALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 140
 QY 121 PLVQECMVHDCADGK-----LKFGCGKTLRPRFKIIGGEFTTTIENOPWFAAIYRRH 172
 DB 141 PLVQECMVHDCADGKPPPEELKFGCGKTLRPRFKIIGGEFTTTIENOPWFAAIYRRH 200
 QY 173 RGGSVTVVCGSLSPCWVISATHCFIDYPKEDYIVVLGSRSLNSNTQGMKFEVENLI 232
 DB 201 RGGSVTVVCGSLSPCWVISATHCFIDYPKEDYIVVLGSRSLNSNTQGMKFEVENLI 260
 QY 233 LHKDYSADTLAHNDIALALKIRSKGRCAQPSRTIQTICLPMSYNDPQGTSCETGFGK 292
 DB 261 LHKDYSADTLAHNDIALALKIRSKGRCAQPSRTIQTICLPMSYNDPQGTSCETGFGK 320
 QY 293 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 352
 DB 321 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 380
 QY 353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
 DB 381 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKENGLAL 431
 RESULT 36
 ADD46429
 ID ADD46429 standard; protein; 431 AA.
 XX
 AC ADD46429;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P00749, SEQ ID NO 12109.
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 PD
 XX 27-FEB-2003.
 PP 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX (GHEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; P00749.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell

comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

Sequence 431 AA;
Query Match 99.2%; Score 2240; DB 7; Length 431;
Best Local Similarity 97.8%; Pred. No. 2.1e-174; Indels 8; Gaps 1;
Matches 402; Conservative 1; Mismatches 0;
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 80
61 KASTDTMGRPCLPNWSATVLOOTVHAHRS DALQLGLKHNYCRPNDRRPPWCYVQVGLK 120
81 KASTDTMGRPCLPNWSATVLOOTVHAHRS DALQLGLKHNYCRPNDRRPPWCYVQVGLK 140
121 PLVQECMVHDCADGK-----LKFCQGQKTLRPFKIIIGGEFTTIENQPFWFAAIYRRH 172
141 PLVQECMVHDCADGKPPSSPPEELKFCQGQKTLRPFKIIIGGEFTTIENQPFWFAAIYRRH 200
173 RGGSTVYVCGSLSPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
201 RGGSTVYVCGSLSPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
233 LHKDYSADTLAHNDIALLKIRSKRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGK 292
261 LHKDYSADTLAHNDIALLKIRSKRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGK 320
293 ENSTDYLYPEQLKMTVVKLI SHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPL 352
321 ENSTDYLYPEQLKMTVVKLI SHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPL 380
353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVSVHFLPWIRSHTKKEENGLAL 403
381 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVSVHFLPWIRSHTKKEENGLAL 431

RE IT 37
AF 4584
II AAR34584 standard; protein; 411 AA.
XZ AAR34584;
XZ
DZ 25-MAR-2003 (revised)
DZ 14-SEP-1993 (first entry)
XZ
XZ Mutant human prourokinase.
XZ PUK; increased half life; improved fibrin affinity.
XZ Homo sapiens.

XX EP541952-A1.
PN 19-MAY-1993.
XX 06-OCT-1992; 92EP-00117000.
XX 07-OCT-1991; 91JP-00289257.
XX (GREC) GREEN CROSS CORP.
XX Tanabe T, Morita M, Hirose M, Amatsuji Y;
XX WPI; 1993-160551/20.
XX N-PSDB; AAQ41450.
XX New human pro-urokinase mutants with thrombolytic activity - have a neutral aminoacid in the epidermal growth factor region replaced with a basic aminoacid, or an acid residue replaced with a non-acidic residue.
XX Claim 1; Page 17-20; 38pp; English.
XX The sequence is that of a mutant human prourokinase, in which a neutral amino acid in the epidermal growth region has been replaced with a basic amino acid, or an acidic amino acid has been replaced by a non-acidic amino acid. Preferred replacements are 16Gly->Lys, 38Gly->Lys and 45Asp->Asn. The mutant has an increased half-life in blood as compared to the prior art mutant with a deleted EGF region. It has improved affinity for fibrin, and has other features the same as human prourokinase. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 411 AA;
Query Match 99.2%; Score 2239; DB 2; Length 411;
Best Local Similarity 97.8%; Pred. No. 2.4e-174; Indels 8; Gaps 1;
Matches 402; Conservative 1; Mismatches 0;
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
61 KASTDTMGRPCLPNWSATVLOOTVHAHRS DALQLGLKHNYCRPNDRRPPWCYVQVGLK 120
61 KASTDTMGRPCLPNWSATVLOOTVHAHRS DALQLGLKHNYCRPNDRRPPWCYVQVGLK 120
121 PLVQECMVHDCADGK-----LKFCQGQKTLRPFKIIIGGEFTTIENQPFWFAAIYRRH 172
121 PLVQECMVHDCADGKPPSSPPEELKFCQGQKTLRPFKIIIGGEFTTIENQPFWFAAIYRRH 180
173 RGGSTVYVCGSLSPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
181 RGGSTVYVCGSLSPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 240
233 LHKDYSADTLAHNDIALLKIRSKRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGK 292
241 LHKDYSADTLAHNDIALLKIRSKRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGK 300
293 ENSTDYLYPEQLKMTVVKLI SHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPL 352
301 ENSTDYLYPEQLKMTVVKLI SHRECOQPHYGVSEVTTKMLCAADPOWKTDSCQDGGPL 360
353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVSVHFLPWIRSHTKKEENGLAL 403
361 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTVSVHFLPWIRSHTKKEENGLAL 411

RESULT 38
AAU99230
ID AAU99230 standard; protein; 431 AA.
XX AAU99230;
XX AC AAU99230;
XX 24-SEP-2002 (first entry)
DT

X I Human plasminogen activator, urokinase (PLAU) variant #2.
X F Human; Plasminogen activator; urokinase; PLAU; cancer; enzyme;
X F cytosolic; serine protease; thrombolytic disorder; isogene;
X F pulmonary embolism; chromosome 10q24-qter; haplotype; genotype; SNP;
X F single nucleotide polymorphism; thrombolytic; gene therapy.
X C Homo sapiens.
X C
X C
X C
X C
X C Key Location/Qualifiers
X F Misc-difference 231
X F /note= "Wild-type Lys substituted by Gln"
X F WQ2002040503-A2.
X F
X F 23-MAY-2002.
X F 14-NOV-2001; 2001WQ-US044001.
X F 17-NOV-2000; 2000US-0249703P.
X F (GENA-) GENA-1999-0249703P.
X F Anastasio AE, Bentivegna SC, Koshy B;
X F WPI; 2002-519370/55.
X F Genetic variants of Plasminogen activator. Urokinase (PLAU) isogenes,
X F useful for improving efficiency and reliability in drug development for
X F treating thrombolytic disorders and cancer.
X F Claim 27; Page; 92pp; English.
X C The invention relates to a polynucleotide comprising a first nucleotide
X C sequence (NSI) comprising a PLAU (plasminogen activator, urokinase, a
X C serine protease) isogene selected from isogenes 1-9 and 11-20 given in
X C the specification, where each isogene comprises the regions of the PLAU
X C gene or cDNA and is further defined by the corresponding sequence of
X C polymorphisms (defining single nucleotide polymorphisms, SNP). Also
X C included are methods of haplotyping/genotyping (and predicting the
X C haplotype/genotype of the PLAU gene of an individual, identifying an
X C association between a trait and at least one haplotype or haplotype pair
X C of the PLAU gene, an isolated oligonucleotide for detecting a
X C polymorphism in the PLAU gene, a recombinant non-human organism
X C transformed or transfected with the gene or cDNA, fragments of the
X C polynucleotides of at least 10 base pairs encompassing a polymorphic
X C site, an isolated polymorphic variant PLAU protein or fragment, an
X C isolated monoclonal antibody specific for PLAU, a computer system for
X C storing and analysing polymorphism data for the PLAU gene and a genome
X C anchoring for the PLAU gene. PLAU is useful in screening for drugs
X C targeting PLAU that are useful for treating thrombolytic disorders and
X C cancers. The methods are useful for improving the efficiency and
X C reliability of the discovery and development of drugs for treating
X C diseases associated with PLAU activity, in validating PLAU as a drug
X C target and in the design of clinical trials for treating a specific
X C condition of disease associated with PLAU activity. The antibody is
X C useful in diagnostic, prognostic and therapeutic methods. PLAU
X C polynucleotides are useful in studying the expression and function of
X C PLAU, and in expressing PLAU protein for use in screening for candidate
X C drugs to treat diseases related to PLAU activity. The gene for PLAU is
X C located on chromosome 10q24-qter. The present sequence represents a
X C polymorphic variant of the PLAU protein. Note: The present sequence is
X C not shown in the specification but was created by the indexer using the
X C wild-type PLAU protein appearing as AAU99228 and the information on page
X C 28
X C
X C Sequence 431 AA;
X C
X C Query Match 99.2%; Score 2239; DB 5; Length 431;
X C Best Local Similarity 97.8%; Pred. No. 2.5e-174;
X C Matches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;
X C

QY 1 SNELHQPSPNCDCCLNGGTCVSNKYFNSNIHWCNCPKFKGGQHCIDSKSKTCYEGNGHFYRG 60
DB 21 SNELHQPSPNCDCCLNGGTCVSNKYFNSNIHWCNCPKFKGGQHCIDSKSKTCYEGNGHFYRG 80
QY 61 KASDTMTGRPCLPWNSATVLCQTYHAHRSDALQIGLGHNYCRNPNRRRPPWCYVQVGLK 120
DB 81 KASDTMTGRPCLPWNSATVLCQTYHAHRSDALQIGLGHNYCRNPNRRRPPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFOGOGKTLRPRFKIIGGEBFTTIENOPWPAAIYRRH 172
DB 141 PLVQECMVHDCADGKFKSSPPEELKFOGOGKTLRPRFKIIGGEBFTTIENOPWPAAIYRRH 200
QY 173 RGSVTVVCGGSLSPCWISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
DB 201 RGSVTVVCGGSLSPCWISATHCFIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHNDIALKIRSKEGCAOPSRITQICLPMSYNDPQFGTSCBITGFGK 292
DB 261 LHKDYSADTLAHNDIALKIRSKEGCAOPSRITQICLPMSYNDPQFGTSCBITGFGK 320
QY 293 ENSTDYLYPEQLKMTVVVKLISHRECCQPHYVYGVSEVTTMLCAADPQWKTSCQDGGPL 352
DB 321 ENSTDYLYPEQLKMTVVVKLISHRECCQPHYVYGVSEVTTMLCAADPQWKTSCQDGGPL 380
QY 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVSHFLPWIRSHTKENGLAL 403
DB 381 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVSHFLPWIRSHTKENGLAL 431

RESULT 39
AAP96146
ID AAP96146 standard; protein; 411 AA.
XX
AC AAP96146;
XX
DT 03-OCT-2002 (revised)
DT 21-JAN-1991 (first entry)
XX
XX Sequence encoded by entire prourokinase (PKU) gene from PKU-producing
DE tumour cell line ATCC CCL138 clone PUC20.
XX
XX Thrombosis; fibrinolytic agent; venous disease; arterial disease therapy.
XX Unidentified.
XX
XX EP312941-A.
XX
PD 26-APR-1989.
XX
PF 15-OCT-1988; 88EP-00117186.
XX
PR 23-OCT-1987; 87DE-03735917.
XX
XX (BADI) BASF AG.
XX
XX Koerwer W, Kurfurst M, Baldinger V, Doerper T, Schwarz M;
PI WPI; 1989-123847/17.
XX N-PSDB; AAN91617.
XX
XX New N-shortened pro-urokinase peptide cpds. with thrombolytic activity -
PT and longer in vivo half life, opt. with replacement of arginine-156.
XX
XX Example; Fig 2, p 705-8; Zipp; German.
XX
XX New N-shortened pro-urokinase peptide cpds. were prepd. from pUC20. The
CC new peptides are useful for treating venous and arterial occlusive
CC diseases. (Updated on 03-OCT-2002 to add missing OS field.)
XX
XX Sequence 411 AA;
XX
XX Query Match 99.2%; Score 2238; DB 1; Length 411;
XX Best Local Similarity 97.8%; Pred. No. 2.8e-174;

	atches	402;	Conservative	0;	Mismatches	1;	Indels	8;	Gaps	1;
Qy	1	SNELHQPNSCDCLNGTCTVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG	60							
Df	1	SNELHQPNSCDCLNGTCTVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG	60							
Qy	61	KASDTMTGRPCLPWNSATVLTQTYHAHRSDALQGLGKHNCRPNPNRRPWCYVQVGLK	120							
Df	61	KASDTMTGRPCLPWNSATVLTQTYHAHRSDALQGLGKHNCRPNPNRRPWCYVQVGLK	120							
Qy	121	PLVQECMWHDCADGK-----LKFCQCGKTLRPFKIIGGFTTIENQPFPAALYRRH	172							
Df	121	PLVQECMWHDCADGKPPPEELKFCQCGKTLRPFKIIGGFTTIENQPFPAALYRRH	180							
Qy	173	RGGSVTYVCGSLISPCWVISAHCDFIDYPKKEDIYVILGRSLNSNTQCEMKFEVENLI	232							
Df	181	RGGSVTYVCGSLISPCWVISAHCDFIDYPKKEDIYVILGRSLNSNTQCEMKFEVENLI	240							
Qy	233	LHKDYSADTLAHNDIALLKIRSEKGRCAQPSRTIOTICLPSMYNDPQGTSCETITGFGK	292							
Df	241	LHKDYSADTLAHNDIALLKIRSEKGRCAQPSRTIOTICLPSMYNDPQGTSCETITGFGK	300							
Qy	293	ENSTDYLYPEQLKMTVVKLIHSHRECQPHYVYGSVTTKMLCAADPQWKTDSCQDSSGGL	352							
Df	301	ENSTDYLYPEQLKMTVVKLIHSHRECQPHYVYGSVTTKMLCAADPQWKTDSCQDSSGGL	360							
Qy	353	VCSLQGRMTLGTIVSGRGKALKDKPGVYTVSHFLPWIRSHTKXENGLAL	403							
Df	361	VCSLQGRMTLGTIVSGRGKALKDKPGVYTVSHFLPWIRSHTKXENGLAL	411							
RE	40									
AA	2926									
II	AAAR92926	standard; protein; 411 AA.								
XX	AAAR92926;									
XX	03-AUG-1996	(first entry)								
XX	Pro-urokinase.									
XX	Pro-urokinase; plasminogen activator; fusion drug; drug delivery;									
Kx	platelet; cardiovascular disease; thrombolytic.									
XX	Homo sapiens.									
XX	Key	Location/Qualifiers								
Ft	Region	1..132	/label= A-chain							
Ft	Domain	1..45	/label= Growth_factor_domain							
Ft	Disulfide-bond	11	/note= "disulfide between Cys11 and Cys19"							
Ft	Disulfide-bond	13	/note= "disulfide bond between Cys13 and Cys31"							
Ft	Disulfide-bond	33	/note= "disulfide bond between Cys33 and Cys42"							
Ft	Domain	46..132	/label= Kringle_domain							
Ft	Disulfide-bond	50	/note= "disulfide bond between Cys50 and Cys131"							
Ft	Disulfide-bond	71	/note= "disulfide bond between Cys71 and Cys113"							
Ft	Disulfide-bond	102	/note= "disulfide bond between Cys102 and Cys126"							
Ft	Region	133..158	/label= Linker_region							
Ft	Disulfide-bond	148	/note= "disulfide bond between Cys148 and Cys279"							
Ft	Cleavage-site	156..157	/note= "thrombin cleavage site"							
Ft	Cleavage-site	159..159	/note= "plasmin cleavage site"							

FT	Region	159..411	/label= B-chain							
FT	Disulfide-bond	189	/note= "disulfide bond between Cys189 and Cys205"							
FT	Disulfide-bond	197	/note= "disulfide bond between Cys197 and Cys268"							
FT	Disulfide-bond	293	/note= "disulfide bond between Cys293 and Cys362"							
FT	Disulfide-bond	325	/note= "disulfide bond between Cys325 and Cys341"							
FT	Disulfide-bond	352	/note= "disulfide bond between Cys352 and Cys380"							
XX	WO9604004-A1.									
XX	15-FEB-1996.									
XX	03-AUG-1995;	95WO-US009848.								
XX	05-AUG-1994;	94US-00286748.								
XX	(NEW-) NEW ENGLAND DEACONESS HOSPITAL.									
XX	Gurewich V;									
XX	WPI; 1996-129123/13.									
XX	N-PSDB; AAT18237.									
XX	Fusion product of plasminogen activator A chain and drug - targeted to platelets, useful for treatment of cardiovascular disease.									
XX	Claim 3; Page 39-40; 61pp; English.									
XX	A portion of the A-chain (pref. amino acids 1-132) of pro-urokinase (AAR92926) can be linked to a drug, e.g. hirudin, somatostatin or their analogues (see also AAR92925 and AAR92927-33) and used in the prodn. of new fusion drugs. The constructs can be obtcd. by expression of the CC appropriate nucleotide sequences in transformed host cells. When CC administered to a patient, the A-chain binds the fusion drug to the CC platelet outer membrane, i.e. to the site of thrombosis or vascular CC injury. Cleavage sites for thrombin and/or plasmin with the fusion drug CC allow the release of the drug at the target site									
XX	Sequence 411 AA;									
Qy	Query Match	99.2%;	Score 2238;	DB 2;	Length 411;					
Df	Best Local Similarity	97.8%;	Pred. No. 2.8e-174;							
Qy	Matches	402;	Conservative	0;	Mismatches	1;	Indels	8;	Gaps	1;
Df	1	SNELHQPNSCDCLNGTCTVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG	60							
Qy	61	KASDTMTGRPCLPWNSATVLTQTYHAHRSDALQGLGKHNCRPNPNRRPWCYVQVGLK	120							
Df	61	KASDTMTGRPCLPWNSATVLTQTYHAHRSDALQGLGKHNCRPNPNRRPWCYVQVGLK	120							
Qy	121	PLVQECMWHDCADGK-----LKFCQCGKTLRPFKIIGGFTTIENQPFPAALYRRH	172							
Df	121	PLVQECMWHDCADGKPPPEELKFCQCGKTLRPFKIIGGFTTIENQPFPAALYRRH	180							
Qy	173	RGGSVTYVCGSLISPCWVISAHCDFIDYPKKEDIYVILGRSLNSNTQCEMKFEVENLI	232							
Df	181	RGGSVTYVCGSLISPCWVISAHCDFIDYPKKEDIYVILGRSLNSNTQCEMKFEVENLI	240							
Qy	233	LHKDYSADTLAHNDIALLKIRSEKGRCAQPSRTIOTICLPSMYNDPQGTSCETITGFGK	292							
Df	241	LHKDYSADTLAHNDIALLKIRSEKGRCAQPSRTIOTICLPSMYNDPQGTSCETITGFGK	300							
Qy	293	ENSTDYLYPEQLKMTVVKLIHSHRECQPHYVYGSVTTKMLCAADPQWKTDSCQDSSGGL	352							
Df	301	ENSTDYLYPEQLKMTVVKLIHSHRECQPHYVYGSVTTKMLCAADPQWKTDSCQDSSGGL	360							

353 VCSLQGRMTLTGIVSWGRGALKDKDGGVYTRVSHFLPWIRSHRSTKBEINGIAL 403
 361 VCSLQGRMTLTGIVSWGRGALKDKDGGVYTRVSHFLPWIRSHRSTKBEINGIAL 411

E JLT 41
 A 74797
 A AAB74797 standard; protein; 411 AA.
 A AAB74797;
 X 12-JUN-2001 (first entry)
 X Prourokinase protein sequence.
 X Prourokinase; Pro-309; mutagenic; urokinase; zymogen; mutant;
 F lowered fibrinogen dissolving activity; fibrin; E segment; D segment;
 K lowered non-specific fibrin dissolving zymogen activation.
 K Unidentified.
 X
 X Key Location/Qualifiers
 F Disulfide-bond 11..19
 F Disulfide-bond 13..31
 F Disulfide-bond 33..42
 F Disulfide-bond 50..131
 F Disulfide-bond 71..113
 F Disulfide-bond 102..126
 F Disulfide-bond 148..279
 F Disulfide-bond 189..205
 F Disulfide-bond 197..268
 F Disulfide-bond 293..362
 F Disulfide-bond 325..341
 F Disulfide-bond 352..380
 X CN1277262-A.
 X 20-DEC-2000.
 X 10-JUL-2000; 2000CN-00109829.
 X 10-JUL-2000; 2000CN-00109829.
 F (LIU/) LIU J.
 F Sun Z, Liu J;
 F WPI; 2001-266614/28.
 L Urokinase zymogen mutant.
 F Example; Fig.1; 11pp; Chinese.
 X The present invention describes a prourokinase mutant comprising the
 C amino acid sequence point mutation at proline 309. The mutation makes the
 C mutant have an intrinsic activity 2.5-20 times lower than that of natural
 C prourokinase, including lowered fibrinogen dissolving activity and
 C lowered non-specific fibrin dissolving zymogen activation. Compared with
 C the natural prourokinase, the fibrin dissolving zymogen activation of the
 C mutant may be promoted by not only the E segment of degraded fibrin but
 C also the D segment. The present sequence represents a wild type
 C prourokinase-protein sequence which is used in an example from the
 C present invention. N.B. The sequence in the specification is of poor
 C quality so the sequence given here is of the indexers best interpretation
 X Sequence 411 AA;
 S
 ery Match 99.2%; Score 2238; DB 4; Length 411;
 est Local Similarity 97.8%; Pred. No. 2.8e-174; Gaps 1;
 atches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1
 1 SNEHQVPSNCDLNGGTCVSNKTPSNTHWCNCPKFGGHCEDSKTCYEGNGHFYRG 60

polymorphisms (defining single nucleotide polymorphisms, SNP). Also included are methods of haplotyping/genotyping (and predicting the haplotype/genotype of the PLAU gene of an individual, identifying an association between a trait and at least one haplotype or haplotype pair of the PLAU gene, an isolated oligonucleotide for detecting a polymorphism in the PLAU gene, a recombinant non-human organism transformed or transfected with the gene or cDNA, fragments of the polynucleotides of at least 10 base pairs encompassing a polymorphic site, an isolated polymorphic variant PLAU protein or fragment, an isolated monoclonal antibody specific for PLAU, a computer system for storing and analysing polymorphism data for the PLAU gene and a genome anchoring for the PLAU gene. PLAU is useful in screening for drugs and targeting PLAU that are useful for treating thrombolytic disorders and cancers. The methods are useful for improving the efficiency and reliability of the discovery and development of drugs for treating diseases associated with PLAU activity, in validating PLAU as a drug target and in the design of clinical trials for treating a specific condition of disease associated with PLAU activity. The antibody is useful in diagnostic, prognostic and therapeutic methods. PLAU polynucleotides are useful in studying the expression and function of PLAU, and in expressing PLAU protein for use in screening for candidate drugs to treat diseases related to PLAU activity. The gene for PLAU is located on chromosome 10q24-qter. The present sequence represents a polymorphic variant of the PLAU protein. Note: The present sequence is not shown in the specification but was created by the indexer using the wild-type PLAU protein appearing as AAU92228 and the information on page 28

Sequence 431 AA;

Query Match 99.2%; Score 2238; DB 5; Length 431;
Best Local Similarity 97.8%; Pred. No. 3e-174;
Matches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 60
21 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 80
61 KASTDTMGRPCLPWNASATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPWCYVQVGLK 120
81 KASTDTMGRPCLPWNASATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPWCYVQVGLK 140
121 PLVQECWVHDCADGK-----LKFCQCGQKTLPRFKIIGGETTIENQPFPAALYRRH 172
141 PLVQECWVHDCADGKPKSPPEELKFQCGQKTLPRFKIIGGETTIENQPFPAALYRRH 200
173 RGSVTVYVCGGSLISPCWISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 232
201 RGSVTVYVCGGSLISPCWISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 260
233 LHKDYSADTLAHHNDIALLKIRSGRCAQPSRTIQTICLPSMYNDPOFGTSCBITGFGK 292
261 LHKDYSADTLAHHNDIALLKIRSGRCAQPSRTIQTICLPSMYNDPOFGTSCBITGFGK 320
293 ENSTDYLYPEQLKMTVVKLISHRECQPHYVGSVTTKMLCAADPOWKTDSCQDSSGGL 352
321 ENSTDYLYPEQLKMTVVKLISHRECQPHYVGSVTTKMLCAADPOWKTDSCQDSSGGL 380
353 VCSLQGRMTLTGIVSGRGKALCKDPGVYTRVSHFPLWIRSHTEKENGIAL 403
381 VCSLQGRMTLTGIVSGRGKALCKDPGVYTRVSHFPLWIRSHTEKENGIAL 431

UT 43
AJ 3999
II AAR62999 standard; protein; 411 AA.
XX AAR62999;
XX
XX
D1 25-MAR-2003 (revised)
D1 21-SEP-1995 (first entry)
XX Pro-urokinase mutant His313.

XX Pro-urokinase; thrombolysis; fibrin clot lysis; mutant His313;
KW reduced fibrinogenolysis; non-specific plasminogen activation;
XX systemic bleeding.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Disulfide-bond 11..19
FT Disulfide-bond 13..31
FT Disulfide-bond 33..42
FT Disulfide-bond 50..131
FT Disulfide-bond 71..113
FT Disulfide-bond 102..126
FT Disulfide-bond 148..279
FT Disulfide-bond 189..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
FT Domain 297..313 /note="flexible loop"
FT Disulfide-bond 325..341
FT Disulfide-bond 352..380
XX W09501427-A1.
XX
PD 12-JAN-1995.
XX
XX 28-JUN-1994; 94WO-US007278.
XX
XX 02-JUL-1993; 93US-00087163.
XX
PA (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
XX
XX Liu J, Gurewich V;
XX
XX WPI; 1995-060991/08.
XX
XX Pro-urokinase mutants - have thrombolytic activity but reduced
PT fibrinogenolysis activity and non-specific plasminogen activation.
XX
XX Claim 11; Fig 1; 46pp; English.
XX
XX AAR62991 is the wild type pro-urokinase, from which the new mutants
CC described in AAR62992-R3008 were derived. These mutants retain the
CC thrombolytic activity of the wild type protein, useful for the treatment
CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
CC specific plasminogen activation. The mutants can therefore be used for
CC the lysis of fibrin clots without inducing systemic bleeding, as can be
CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
XX Sequence 411 AA;
SQ
Query Match 99.1%; Score 2237; DB 2; Length 411;
Best Local Similarity 97.8%; Pred. No. 3.4e-174;
Matches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 60
DB 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYRG 60
QY 61 KASTDTMGRPCLPWNASATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPWCYVQVGLK 120
DB 61 KASTDTMGRPCLPWNASATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPWCYVQVGLK 120
QY 121 PLVQECWVHDCADGK-----LKFCQCGQKTLPRFKIIGGETTIENQPFPAALYRRH 172
DB 121 PLVQECWVHDCADGKPKSPPEELKFQCGQKTLPRFKIIGGETTIENQPFPAALYRRH 180
QY 173 RGSVTVYVCGGSLISPCWISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 232
DB 181 RGSVTVYVCGGSLISPCWISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 240

233 LHKDYSADTLAHHNDIALKIRSKGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 292
241 LHKDYSADTLAHHNDIALKIRSKGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 300
293 ENSTDYLYPEQLKMTVVVKLI SHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDGGGGL 352
301 ENSTDYLYPEQLKMTVVVKLI SHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDGGGGL 360
353 VCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKBEENGLAL 403
361 VCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKBEENGLAL 411

JUL 44
62992
AAR62992 standard; protein; 411 AA.
AAR62992;
25-MAR-2003 (revised)
21-SEP-1995 (first entry)
Pro-urokinase mutant Ala300.
Pro-urokinase; thrombolysis; fibrin clot lysis; mutant Ala300;
reduced fibrinogenolysis; non-specific plasminogen activation;
systemic bleeding.
Homo sapiens.
Key Location/Qualifiers
Disulfide-bond 11..19
Disulfide-bond 13..31
Disulfide-bond 33..42
Disulfide-bond 50..131
Disulfide-bond 71..113
Disulfide-bond 102..126
Disulfide-bond 148..279
Disulfide-bond 189..205
Disulfide-bond 197..268
Disulfide-bond 293..362
Domain 297..313
Disulfide-bond 325..341
Disulfide-bond 352..380
WO9501427-A1.
12-JAN-1995.
28-JUN-1994; 94WO-US007278.
02-JUL-1993; 93US-00087163.
(NEW)- NEW ENGLAND DEACONESS HOSPITAL.
Liu J, Gurewich V;
WPI; 1995-060991/08.
Pro-urokinase mutants - have thrombolytic activity but reduced
fibrinogenolysis activity and non-specific plasminogen activation.
Claim 5; Fig 1; 46pp; English.
AAR62991 is the wild type pro-urokinase, from which the new mutants
described in AAR62992-R63008 were derived. These mutants retain the
thrombolytic activity of the wild type protein, useful for the treatment
of thromboembolism, but have a reduced fibrinogenolysis activity and non-
specific plasminogen activation. The mutants can therefore be used for
the lysis of fibrin clots without inducing systemic bleeding, as can be
the case with the wild type protein. (Updated on 25-MAR-2003 to correct
PN field.)

XX Sequence 411 AA;
SQ
Query Match 99.1%; Score 2237; DB 2; Length 411;
Best Local Similarity 97.8%; Pred. No. 3.4e-174;
Matches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;
QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKGQHQCEIDKSKTCYEGKHGFYRG 60
DB 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKGQHQCEIDKSKTCYEGKHGFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDRRRRWCYVQGLK 120
DB 61 KASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDRRRRWCYVQGLK 120
QY 121 PLVQECMVHDCADGK-----LKFCQCGQKTLPRPKLIIGGEFTTIENQWFAAIYRRH 172
DB 121 PLVQECMVHDCADGKPPSEELKFCQCGQKTLPRPKLIIGGEFTTIENQWFAAIYRRH 180
QY 173 RGSVTVYVCGGSLISPCWVISATHCIFIDYPKKEDYIVVLGRSRLNSNTQGEKKEVENLI 232
DB 181 RGSVTVYVCGGSLISPCWVISATHCIFIDYPKKEDYIVVLGRSRLNSNTQGEKKEVENLI 240
QY 233 LHKDYSADTLAHHNDIALKIRSKGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 292
DB 241 LHKDYSADTLAHHNDIALKIRSKGRCAPSRITQITICLPSMYNDPQFGTSCIEITGFGK 300
QY 293 ENSTDYLYPEQLKMTVVVKLI SHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDGGGGL 352
DB 301 ENSTDYLYPEQLKMTVVVKLI SHRECCQPHYGVSEVTTKMLCAADPQWKTDSCQDGGGGL 360
QY 353 VCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKBEENGLAL 403
DB 361 VCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKBEENGLAL 411

RESULT 45
AAR62998
ID AAR62998 standard; protein; 411 AA.
AC AAR62998;
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
DE Pro-urokinase mutant Ala313.
XX
KW Pro-urokinase; thrombolysis; fibrin clot lysis; mutant Ala313;
KW reduced fibrinogenolysis; non-specific plasminogen activation;
systemic bleeding.
XX Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 11..19
FT Disulfide-bond 13..31
FT Disulfide-bond 33..42
FT Disulfide-bond 50..131
FT Disulfide-bond 71..113
FT Disulfide-bond 102..126
FT Disulfide-bond 148..279
FT Disulfide-bond 189..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
FT Domain 297..313
FT Disulfide-bond 325..341
FT Disulfide-bond 352..380
XX WO9501427-A1.
XX 12-JAN-1995.
XX

C 293 ENSTDYLYPEQLKMTVVVKLIHRECOQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 352
D 301 ENSTDYLYPEQLKMTVVVKLIHRECOQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 360
C 353 VCSLQGRWTLTGIVSWGRCALKDXPGVTVRVSHFLPWIRSHTKENGLAL 403
E 361 VCSLQGRWTLTGIVSWGRCALKDXPGVTVRVSHFLPWIRSHTKENGLAL 411

ULT 47
A 53000
I AAR63000 standard; protein; 411 AA.
X AAR63000;
X
X
X 25-MAR-2003 (revised)
D 21-SEP-1995 (first entry)
X
X
X Pro-urokinase mutant Ser175 His187.
D
K Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
K non-specific plasminogen activation; systemic bleeding;
K mutant Ser175 His187.
X
X Homo sapiens.
X
X
X Key Location/Qualifiers
E Disulfide-bond 11..19
E Disulfide-bond 13..31
E Disulfide-bond 33..42
E Disulfide-bond 50..131
E Disulfide-bond 71..113
E Disulfide-bond 102..126
E Disulfide-bond 148..279
E Disulfide-bond 189..205
E Disulfide-bond 197..268
E Disulfide-bond 293..362
E Domain 297..313
F /note= "flexible loop"
F Disulfide-bond 325..341
F Disulfide-bond 352..380
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X WO9501427-A1
X
X 12-JAN-1995.
X
X 28-JUN-1994; 94WO-US007278.
X
X 02-JUL-1993; 93US-00087163.
X (NEWB-) NEW ENGLAND DEACONESS HOSPITAL.
X
X Liu J, Gurewich V;
X WPI; 1995-060991/08.
X
X Pro-urokinase mutants - have thrombolytic activity but reduced
E fibrinogenolysis activity and non-specific plasminogen activation.
X
X Claim 15; Fig 1; 46pp; English.
X
X AAR62991 is the wild type pro-urokinase, from which the new mutants
C described in AAR62992-R63008 were derived. These mutants retain the
C thrombolytic activity of the wild type protein, useful for the treatment
C of thromboembolism, but have a reduced fibrinogenolysis activity and non-
C specific plasminogen activation. The mutants can therefore be used for
C the lysis of fibrin clots without inducing systemic bleeding, as can be
C the case with the wild type protein. (Updated on 25-MAR-2003 to correct
C PN field.)
X
X Sequence 411 AA;
X
X very Match 99.0%; Score 2235; DB 2; Length 411;

Best Local Similarity 97.6%; Pred. No. 5e-174;
Matches 401; Conservative 2; Mismatches 0; Indels 8; Gaps 1;
QY 1 SNELHQVPSNCDCLNGGTCVSNKYFNSIHWNCNPKKFGGQHCIDKSKTCYEGNGHFYRG 60
DB 1 SNELHQVPSNCDCLNGGTCVSNKYFNSIHWNCNPKKFGGQHCIDKSKTCYEGNGHFYRG 60
QY 61 KASDTMTGRPCLPNWSATVLQOTYHAHRSALQGLGKHNYCRNPNRRRPWCYVQVGLK 120
DB 61 KASDTMTGRPCLPNWSATVLQOTYHAHRSALQGLGKHNYCRNPNRRRPWCYVQVGLK 120
QY 121 PLVOECMVHDCADGK-----LKFCGGKTLRPRFKIIGGBFTTIENOPWFAAIYRRH 172
DB 121 PLVOECMVHDCADGKESPPEELKFCGGKTLRPRFKIIGGBFTTIENOPWFAAIYRRH 180
QY 173 RGSVTVVCGSLISPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQEMKFEVENLI 232
DB 181 RGSVTVVCGSLISPCWVISATHCFIDYPKEDYIVYLGSRSLNSNTQEMKFEVENLI 240
QY 233 LHKDYSADTLAHNDIALALKIRSKGRCAPSRITQICLPSPMYNDPQFGTSCIEITGFGK 292
DB 241 LHKDYSADTLAHNDIALALKIRSKGRCAPSRITQICLPSPMYNDPQFGTSCIEITGFGK 300
QY 293 ENSTDYLYPEQLKMTVVVKLIHRECOQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 352
DB 301 ENSTDYLYPEQLKMTVVVKLIHRECOQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 360
QY 353 VCSLQGRWTLTGIVSWGRCALKDXPGVTVRVSHFLPWIRSHTKENGLAL 403
DB 361 VCSLQGRWTLTGIVSWGRCALKDXPGVTVRVSHFLPWIRSHTKENGLAL 411

RESULT 48
AAY39343
ID AAY39343 standard; protein; 411 AA.
XX
AC AAY39343;
XX
DT 01-DEC-1999 (first entry)
DE Human pro-urokinase.
XX
KW Serine protease; plasminogen; plasmin; activation; matrix; cancer;
KW tumour; metastasis; X-ray crystallography; inhibitor.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Protein 1..158
FT /label= Mature_urokinase_A_chain
FT Protein 1..135
FT /label= Low_molecular_weight_urokinase
FT Disulfide-bond 11..19
FT Disulfide-bond 13..31
FT Disulfide-bond 33..42
FT Disulfide-bond 50..131
FT Disulfide-bond 71..113
FT Disulfide-bond 102..126
FT Disulfide-bond 135..136
FT Cleavage-site /note= "Additional cleavage at this site generates low
FT molecular weight (LMW) urokinase"
FT Disulfide-bond 148..279
FT /note= "Links mature urokinase A- and B-chains"
FT Cleavage-site 158..159
FT /note= "Cleavage at this site generates mature urokinase
FT A- and B-chains"
FT Protein 159..411
FT /label= Mature_urokinase_B_chain
FT Disulfide-bond 189..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
FT Modified-site 302
FT /note= "N-glycosylated"
FT

Disulfide-bond 325. .341
Disulfide-bond 352. .380
Cleavage-site 405. .406
WO9945379-A2.
10-SEP-1999.
05-MAR-1999; 99WO-US004967.
06-MAR-1998; 98US-00036184.
(ABBO) ABBOTT LAB.
Nienaber VL, Greer J, Abad-Zapatero C, Norbeck DW;
WPI; 1999-571607/48.
Identifying ligands for target biomolecules using X-ray crystallography.
Example 1; Fig 5; 57pp; English.
This sequence represents human pro-urokinase. The mature urokinase consists of an A- and B-chain, linked by a single disulphide bond, and is generated by proteolytic cleavage of the peptide bond between Lys 158 and Ile 159. Additional cleavage of the peptide bond between Lys 135 and Lys 136 generates a low molecular weight urokinase. The urokinase A-chain contains an EGF-like domain and a kringle domain, while the B-chain contains the catalytic domain. Urokinase is a serine protease and is strongly associated with tumour cells. Urokinase activates plasminogen which, in turn, activates the matrix metalloproteinases. Plasmin and the metalloproteinases degrade the extracellular matrix and promote tumour growth and metastasis. Inhibitors that specifically target urokinase may serve as effective anticancer agents. A novel method for identifying such ligands used X-ray crystallography to determine if a complex is formed between a ligand and a target biomolecule. However, crystals of a native urokinase/inhibitor complex had poor diffraction quality. Human urokinase was therefore engineered so that it would produce crystals with the desired qualities. This engineered urokinase was designated mu-UK (AA939344).

Sequence 411 AA;
ery Match 99.0%; Score 2235; DB 2; Length 411;
st Local Similarity 97.8%; Pred. No. 5e-174;
tches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;
1 SNEHQVPSNCDCLNGTGVSNKYFSNIHWCNPKFGQHCIDKSKTCYEGNGHYRG 60
1 SNEHQVPSNCDCLNGTGVSNKYFSNIHWCNPKFGQHCIDKSKTCYEGNGHYRG 60
61 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPNRRPWCYVQGLK 120
61 KASDTMTGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPNRRPWCYVQGLK 120
121 PLVQECMVHDCADGK-----LKFCGQKTLAPRKLIIGGFTTINQFWFAAIYRRH 172
121 PLVQECMVHDCADGKSPPEELKFCGQKTLAPRKLIIGGFTTINQFWFAAIYRRH 180
173 RGGSVTYVCGGSLSPCWVISAHCFTIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
181 RGGSVTYVCGGSLSPCWVISAHCFTIDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 240
233 LHKDYSADTLAHHNDIALKTRSKRGCAQPSRTIQCILPSMYNDPQFGTSCEITGFGK 292
241 LHKDYSADTLAHHNDIALKTRSKRGCAQPSRTIQCILPSMYNDPQFGTSCEITGFGK 300
293 ENSDTLYPEQLKMTVVKLISHRECCQPHYVGSSEVTTMCLCAADPQWKTSQCQDSGGPL 352
301 ENSDTLYPEQLKMTVVKLISHRECCQPHYVGSSEVTTMCLCAADPQWKTSQCQDSGGPL 360
353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGLAL 403

Db 361 VCSLQGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGLAL 411
RESULT 49
RAY42284
ID RAY42284 standard; protein; 411 AA.
XX AAY42284;
AC AAY42284;
DT 01-DEC-1999 (first entry)
XX Human pro-urokinase.
KW Serine protease; plasminogen; plasmin; activation; matrix; cancer;
KW tumour; metastasis; X-ray crystallography; inhibitor.
OS Homo sapiens.
XX Key Location/Qualifiers
FH Protein 1. .158
FT /label= Mature_urokinase_A_chain
FT Protein 1. .135
FT /label= Low_molecular_weight_urokinase
FT Disulfide-bond 11. .19
FT Disulfide-bond 13. .31
FT Disulfide-bond 33. .42
FT Disulfide-bond 50. .131
FT Disulfide-bond 71. .113
FT Disulfide-bond 102. .126
FT Cleavage-site 135. .136
FT /note= "Additional cleavage at this site generates low molecular weight (LMW) urokinase"
FT Disulfide-bond 148. .279
FT Cleavage-site 158. .159
FT /note= "Links mature urokinase A- and B-chains"
FT /note= "Cleavage at this site generates mature urokinase A- and B-chains"
FT Protein 159. .411
FT /label= Mature_urokinase_B_chain
FT Disulfide-bond 189. .205
FT Disulfide-bond 197. .268
FT Disulfide-bond 293. .362
FT Modified-site 302
FT /note= "N-glycosylated"
FT Disulfide-bond 325. .341
FT Disulfide-bond 352. .380
FT Cleavage-site 405. .406
XX WO9945389-A2.
XX 10-SEP-1999.
XX 01-MAR-1999; 99WO-US004518.
XX 06-MAR-1998; 98US-00036184.
XX (ABBO) ABBOTT LAB.
XX Nienaber VL, Greer J, Abad-Zapatero C, Norbeck DW;
XX WPI; 1999-551079/46.
DR Identifying ligands for target biomolecules using X-ray crystallography,
XX used for designing ligands with improved biological activity for target receptor.
XX Example 1; Fig 5; 57pp; English.
XX This sequence represents human pro-urokinase. The mature urokinase consists of an A- and B-chain, linked by a single disulphide bond, and is generated by proteolytic cleavage of the peptide bond between Lys 158 and Ile 159. Additional cleavage of the peptide bond between Lys 135 and Lys 136 generates a low molecular weight urokinase. The urokinase A-chain

contains an EGF-like domain and a kringle domain, while the B-chain contains the catalytic domain. Urokinase is a serine protease and is strongly associated with tumour cells. Urokinase activates plasminogen which, in turn, activates the matrix metalloproteinases. Plasmin and the metalloproteinases degrade the extracellular matrix and promote tumour growth and metastasis. Inhibitors that specifically target urokinase may serve as effective anticancer agents. A novel method for identifying such ligands used X-ray crystallography to determine if a complex is formed between a ligand and a target biomolecule. However, crystals of a native urokinase/inhibitor complex had poor diffraction quality. Human urokinase was therefore engineered so that it would produce crystals with the desired qualities. This engineered urokinase was designated mu-UK (AAV42285)

Sequence 411 AA;

Query Match 99.0%; Score 2235; DB 2; Length 411;
 Best Local Similarity 97.8%; Pred. No. 5e-174;
 Matches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

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 61 KASTDTMGPRCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPNRRPWCYVQGLK 120
 61 KASTDTMGPRCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPNRRPWCYVQGLK 120
 121 PLVQECWHDCA DKGK-----LKFQCGQKTLRPFKLI GFEFTIENQWFAAIVERH 172
 121 PLVQECWHDCA DKGKPPPELFPQCGQKTLRPFKLI GFEFTIENQWFAAIAIRH 180
 173 RGSVTVYVCGSLIGSPCWISATHCFIDYPKKEDYIVLGRSLNSNTQGEKPFVENLI 232
 181 RGSVTVYVCGSLIGSPCWISATHCFIDYPKKEDYIVLGRSLNSNTQGEKPFVENLI 240
 233 LHKDYSADTLAHNDIALKIRSKGRCAQPERTTQICLPNMDPQEGSCITGTGK 292
 241 LHKDYSADTLAHNDIALKIRSKGRCAQPERTTQICLPNMDPQEGSCITGTGK 300
 293 ENSTDVLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPQWKDSCQGS GGPL 352
 301 ENSTDVLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPQWKDSCQGS GGPL 360
 353 VCSLQGRMTLTGVSWGRGCA LKDPGVTVRVSHFLPWTIRSHTKENGIAL 403
 361 VCSLQGRMTLTGVSWGRGCA LKDPGVTVRVSHFLPWTIRSHTKENGIAL 411

ULT 50
 A 20489
 X 1
 X 20489 standard; protein; 411 AA.
 A AAB20489;
 X 21-JUN-2001 (first entry)
 X Human pro-urokinase plasminogen activator.
 X Urokinase plasminogen activator; uPA; human; tumour; cell migration;
 K cell invasion; cell proliferation; angiogenesis; apoptosis; antitumour;
 K diagnosis; therapy.
 K Homo sapiens.
 X Key Location/Qualifiers
 F 1. .135
 F Domain /label= ATF
 F /note= "the ATF domain alternatively comprises residues 1-43"
 F Domain 4
 F /label= Growth_factor_domain
 F Disulfide-bond 11. .19

Disulfide-bond 13. .31
 Disulfide-bond 33. .42
 Disulfide-bond 50. .131
 Disulfide-bond 71. .113
 Disulfide-bond 102. .126
 Disulfide-bond 148. .279
 Disulfide-bond 158. .159
 Cleavage-site /note= "cleavage at this site results in the formation of the two-chain active uPA (tcuPA)"
 Disulfide-bond 189. .205
 Disulfide-bond 197. .268
 Disulfide-bond 293. .362
 Disulfide-bond 325. .341
 Disulfide-bond 352. .380

WO200125410-A2.

12-APR-2001.

27-SEP-2000; 2000WO-US026502.

01-OCT-1999; 99US-0157012P.

(ANGS-) ANGSTROM PHARM INC.

Mazar AP, Jones TR;

WPI; 2001-290611/30.

Novel urokinase plasminogen activator cell surface receptor-targeting protein or peptide, useful for inhibiting angiogenesis or cell migration, invasion or proliferation, is diagnostically or therapeutically labeled. Disclosure; Fig 1; 35pp; English.

The present sequence is that of human pro-urokinase plasminogen activator (pro-uPA). The invention provides a uPA receptor (uPAR) targeting protein or peptide that is labelled and used in methods of diagnosis and therapy. The labelled protein or peptide preferably has the following properties: It comprises at least 38 amino acid residues, including residues 13-30 of the uPAR binding site of uPA; competes with labelled BFP-uPA for binding to a cell or molecule that has a binding site for uPA; has an IC50 value of about 10 nM or less; and is not a fusion protein. Preferred molecules are uPA, (residues 1-411), single chain uPA, tcuPA (inactivated with the suicide inhibitor diisopropyl fluorophosphate), the N-terminal ATF fragment (amino acids 1-135 or 1-143) of uPA, or the growth factor domain (residues 4-43). Suitable labels include a radionuclide, a PET-imageable agent, an MRI-imageable agent, a fluorophore, a fluorochrome, a chromophore, a chromogen, a phosphorescent, a chemiluminescent or a bioluminescent. The methods are used to inhibit cell migration, cell invasion (preferably invasiveness of tumour cells), cell proliferation or angiogenesis, or to induce apoptosis, preferably in the treatment of a subject having a disease or condition associated with undesired cell migration, invasion, proliferation or angiogenesis (claimed). The protein or peptide is also useful for treating diseases or conditions including primary growth of a solid tumour, leukaemia or lymphoma, tumour invasion, metastasis, atherosclerosis, myocardial angiosclerosis, telangiectasia, corneal disease, rubeosis, neovascular glaucoma, diabetic and other retinopathy, macular degeneration, arthritis, fibrosis, wound healing with scarring and fibrosis, peptic ulcers, bone fracture, keloids, or a disorder of vasculogenesis, haematopoiesis, ovulation, menstruation, pregnancy or placental invasion associated with pathogenic cell invasion or with angiogenesis. The protein or peptide probe is internalised by the cells to which it binds, e.g. tumour cells, and is useful for imaging techniques in which it reduces the background signal relative to specifically bound probes. This uptake permits clearance of circulating probe so that the ratio of labelled probe inside tumour cells to the probe elsewhere in the body increases

Sequence 411 AA;

Query Match 99.0%; Score 2235; DB 4; Length 411;
 Best Local Similarity 97.8%; Pred. No. 5e-174;

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: ches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;
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Db |||
Qy 1 SNELHQVPSNCDCLNGTCTVSNKYFSNIHWCNCPKFKGQCHCEIDKSKTCYEQNGHGYRG 60
Db |||
Qy 61 KASTDTMGRCPLPNSATVLOQTYHAHRSDALQLGLGKHNVCNPDNRRRPWCYVQVGLK 120
Db |||
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Db |||
Qy 121 PLVQECMVHDCADGK-----LKFQCGOKTLRPRFKIIGGEFTTIENQPFFAAIYRRH 172
Db |||
Qy 121 PLVQECMVHDCADGKPPPEELKFCGOKTLRPRFKIIGGEFTTIENQPFFAAIYRRH 180
Db |||
Qy 173 RGGSVTVCGGSLISPCWVISATHCFIDYPKKEDIYVYLGSRSLNSNTQGMKFVENLI 232
Db |||
Qy 181 RGGSVTVCGGSLISPCWVISATHCFIDYPKKEDIYVYLGSRSLNSNTQGMKFVENLI 240
Db |||
Qy 233 LHKDYSADTLAHNDIALKLRSGRCAQPSRTIQTICLPSMYNDPQFGTSCFITGFGK 292
Db |||
Qy 241 LHKDYSADTLAHNDIALKLRSGRCAQPSRTIQTICLPSMYNDPQFGTSCFITGFGK 300
Db |||
Qy 293 ENSTDYLYPEQLKMTVVVKLI SHRECQOPHYGSEVTTKMLCAADPOWKTDSCQDSGGPL 352
Db |||
Qy 301 ENSTDYLYPEQLKMTVVVKLI SHRECQOPHYGSEVTTKMLCAADPOWKTDSCQDSGGPL 360
Db |||
Qy 353 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
Db |||
Qy 361 VCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411
Db |||
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Jc time : 101.543 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

C protein - protein search, using sw model
P on: May 25, 2004, 14:53:05 ; Search time 73.4654 Seconds
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T le: US-09-880-503-6
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S ring table:
Gapex 10.0 , Gapext 0.5

S rched: 1149313 seqs, 278921704 residues
T al number of hits satisfying chosen parameters: 1149313
M inum DB seq length: 0
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F t-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

F ult      Query      Score      Match      Length      DB      ID      Description
No.         #
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1 2257 100.0 403 9 US-09-880-503-6 Sequence 5, Appli
2 2243 99.4 411 9 US-09-880-503-3 Sequence 3, Appli
3 2243 99.4 431 12 US-10-411-037-34 Sequence 34, Appl
4 2243 99.4 431 12 US-10-411-026-34 Sequence 34, Appl
5 2243 99.4 431 13 US-10-076-421-2 Sequence 2, Appli
6 2243 99.4 431 14 US-10-171-311-184 Sequence 184, App
7 2243 99.4 431 14 US-10-301-822-161 Sequence 161, App
8 2243 99.4 431 15 US-10-131-985-21 Sequence 21, Appl
9 2243 99.4 431 15 US-10-395-027-414 Sequence 414, App
10 2243 99.4 431 15 US-10-395-027-1275 Sequence 1275, Ap
11 2243 99.4 431 16 US-10-410-962-34 Sequence 34, Appl
12 2243 99.4 431 16 US-10-411-049-34 Sequence 34, Appl
13 2243 99.4 437 12 US-10-087-192-594 Sequence 594, App
14 2241 99.3 431 14 US-10-247-671-149 Sequence 149, App
15 2240 99.2 431 14 US-10-193-656-4 Sequence 4, Appli

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16 2233 98.9 411 15 US-10-407-821-2 Sequence 2, Appli
17 2225 98.6 431 9 US-09-264-458B-1 Sequence 1, Appli
18 2203 97.6 431 12 US-10-382-174-562 Sequence 562, App
19 2176 96.4 445 15 US-10-360-101-266 Sequence 266, App
20 1703 75.5 323 9 US-09-880-503-7 Sequence 7, Appli
21 1626.5 72.1 433 12 US-10-087-192-591 Sequence 591, App
22 1477 65.4 337 14 US-10-106-698-6266 Sequence 6266, Ap
23 1477 65.4 337 15 US-10-264-049-2927 Sequence 2927, Ap
24 1465 64.9 276 9 US-09-880-503-5 Sequence 5, Appli
25 1464 64.9 268 15 US-10-407-821-3 Sequence 3, Appli
26 1333 59.1 246 9 US-09-264-458B-2 Sequence 2, Appli
27 1318 58.4 241 10 US-09-898-837A-27 Sequence 47, Appl
28 1081.5 47.9 650 15 US-10-401-077-1 Sequence 1, Appli
29 858.5 38.0 527 10 US-09-987-457-18 Sequence 18, Appl
30 858.5 38.0 527 10 US-09-987-455-19 Sequence 19, Appl
31 858.5 38.0 527 12 US-10-432-842-1 Sequence 1, Appli
32 858.5 38.0 527 15 US-10-360-101-203 Sequence 203, App
33 858.5 38.0 562 9 US-09-969-271-7 Sequence 7, Appli
34 858.5 38.0 562 9 US-09-974-298-145 Sequence 145, App
35 858.5 38.0 562 12 US-10-411-037-26 Sequence 26, Appl
36 858.5 38.0 562 12 US-10-411-026-26 Sequence 26, Appl
37 858.5 38.0 562 14 US-10-193-656-8 Sequence 8, Appli
38 858.5 38.0 562 14 US-10-443-701-4 Sequence 4, Appli
39 858.5 38.0 562 16 US-10-410-962-26 Sequence 26, Appl
40 858.5 38.0 562 16 US-10-411-049-26 Sequence 26, Appl
41 793 35.1 135 9 US-09-880-503-4 Sequence 4, Appli
42 793 35.1 138 9 US-09-984-186-12 Sequence 12, Appl
43 793 35.1 138 14 US-10-237-667-12 Sequence 12, Appl
44 793 35.1 138 14 US-10-237-708-12 Sequence 12, Appl
45 793 35.1 138 14 US-10-237-866-12 Sequence 12, Appl
46 793 35.1 138 14 US-10-237-871-12 Sequence 12, Appl
47 793 35.1 138 14 US-10-237-824-12 Sequence 12, Appl
48 793 35.1 138 16 US-10-702-536-12 Sequence 12, Appl
49 793 35.1 138 16 US-10-702-636-12 Sequence 12, Appl
50 793 35.1 143 9 US-09-880-503-8 Sequence 8, Appli
51 789.5 35.0 372 9 US-09-084-491A-3 Sequence 3, Appli
52 789.5 35.0 372 13 US-10-102-704-3 Sequence 3, Appli
53 784 34.7 354 10 US-09-987-457-10 Sequence 10, Appli
54 784 34.7 354 10 US-09-987-455-11 Sequence 11, Appli
55 784 34.7 377 10 US-09-987-455-8 Sequence 8, Appli
56 745 33.0 343 10 US-09-987-457-14 Sequence 14, Appli
57 745 33.0 343 10 US-09-987-455-15 Sequence 15, Appli
58 744 33.0 339 10 US-09-987-457-12 Sequence 12, Appli
59 744 33.0 339 10 US-09-987-455-13 Sequence 13, Appli
60 741 32.8 331 10 US-09-987-457-11 Sequence 11, Appli
61 741 32.8 331 10 US-09-987-455-12 Sequence 12, Appli
62 735 32.6 343 10 US-09-987-457-15 Sequence 15, Appli
63 735 32.6 343 10 US-09-987-455-16 Sequence 16, Appli
64 731 32.4 335 10 US-09-987-457-13 Sequence 13, Appli
65 731 32.4 335 10 US-09-987-455-14 Sequence 14, Appli
66 726.5 32.2 655 14 US-10-172-712-28 Sequence 28, Appli
67 688 30.5 308 10 US-09-987-457-16 Sequence 16, Appli
68 688 30.5 308 10 US-09-987-455-17 Sequence 17, Appli
69 681 30.2 615 10 US-09-858-909-2 Sequence 2, Appli
70 681 30.2 615 14 US-10-172-712-30 Sequence 30, Appli
71 681 30.2 615 16 US-10-449-132-2 Sequence 2, Appli
72 652.5 28.9 560 15 US-10-391-215-6 Sequence 6, Appli
73 651.5 28.9 560 14 US-09-912-559-3 Sequence 3, Appli
74 651.5 28.9 560 14 US-10-172-712-32 Sequence 32, Appli
75 651.5 28.9 560 15 US-10-391-215-5 Sequence 5, Appli

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ALIGNMENTS

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RESULT 1
US-09-880-503-6
; Sequence 6, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Root
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

```

;; TITLE OF INVENTION: TISSUE CONTRACTABILITY
;; FILE REFERENCE: 9596-331
;; CURRENT APPLICATION NUMBER: US/09/880,503
;; CURRENT FILING DATE: 2001-06-13
;; PRIOR APPLICATION NUMBER: US 60/212,847
;; PRIOR FILING DATE: 2000-06-20
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: Patent In Ver. 2.1
;; Q ID NO 6
;; LENGTH: 403
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US 9-880-503-6

Query Match 99.4%; Score 2243; DB 9; Length 411;
Best Local Similarity 98.1%; Pred. No. 2.6e-189;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
DB 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
QY 61 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDNRREPWCYVQVGLK 120
DB 61 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDNRREPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK-----LKFCGQKTLRPFKIIIGGEFTTIENQWFAAIYRRH 172
DB 121 PLVQECMVHDCADGKPPSPPEELKFCGQKTLRPFKIIIGGEFTTIENQWFAAIYRRH 180
QY 173 RGSVTVYVCGSLISPCWISATHCFIDYPKKEDYIVLGRSRLNSNTQGMKFEVENLI 232
DB 181 RGSVTVYVCGSLISPCWISATHCFIDYPKKEDYIVLGRSRLNSNTQGMKFEVENLI 240
QY 233 LHKDYSADTLAHDNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPOFGTSCITGFGK 292
DB 241 LHKDYSADTLAHDNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPOFGTSCITGFGK 300
QY 293 ENSTDYLYPEQLKMTVVKLISHRECOQPHYYGSEVTTKMLCAADPQWKTDCQGDSSGGL 352
DB 301 ENSTDYLYPEQLKMTVVKLISHRECOQPHYYGSEVTTKMLCAADPQWKTDCQGDSSGGL 360
QY 353 VCSLQGRMTLTGIYSWGRGCALCKDPGVYTRVSHFLPWIRSHTKENGLAL 403
DB 361 VCSLQGRMTLTGIYSWGRGCALCKDPGVYTRVSHFLPWIRSHTKENGLAL 411

RESULT 3
US-10-411-037-34
; Sequence 34, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zcpi, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-34

Query Match 99.4%; Score 2243; DB 12; Length 431;
Best Local Similarity 98.1%; Pred. No. 2.8e-189;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60

;; TITLE OF INVENTION: TISSUE CONTRACTABILITY
;; FILE REFERENCE: 9596-331
;; CURRENT APPLICATION NUMBER: US/09/880,503
;; CURRENT FILING DATE: 2001-06-13
;; PRIOR APPLICATION NUMBER: US 60/212,847
;; PRIOR FILING DATE: 2000-06-20
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: Patent In Ver. 2.1
;; Q ID NO 6
;; LENGTH: 403
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US 9-880-503-6

Query Match 99.4%; Score 2243; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 1.5e-190;
Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
DB 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
QY 61 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDNRREPWCYVQVGLK 120
DB 61 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDNRREPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGKLPKPCQCKTLRPFKIIIGGEFTTIENQWFAAIYRRHGGSVTVV 180
DB 121 PLVQECMVHDCADGKLPKPCQCKTLRPFKIIIGGEFTTIENQWFAAIYRRHGGSVTVV 180
QY 181 CGGSLISPCWISATHCFIDYPKKEDYIVLGRSRLNSNTQGMKFEVENLILHKDYSAD 240
DB 181 CGGSLISPCWISATHCFIDYPKKEDYIVLGRSRLNSNTQGMKFEVENLILHKDYSAD 240
QY 241 TLAHNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPOFGTSCITGFGKENSTDYLY 300
DB 241 TLAHNDIALKIRSKGRCQAQPSRTIOTICLPMSYNDPOFGTSCITGFGKENSTDYLY 300
QY 301 PEQLKMTVVKLISHRECOQPHYYGSEVTTKMLCAADPQWKTDCQGDSSGGLVCSLQGRM 360
DB 301 PEQLKMTVVKLISHRECOQPHYYGSEVTTKMLCAADPQWKTDCQGDSSGGLVCSLQGRM 360
QY 361 TLTGIVSWGRGCALCKDPGVYTRVSHFLPWIRSHTKENGLAL 403
DB 361 TLTGIVSWGRGCALCKDPGVYTRVSHFLPWIRSHTKENGLAL 403

UT 2
US 9-880-503-3
; Sequence 3, Application US/09880503
; Publication No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; FILE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.1
; Q ID NO 3
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US 9-880-503-3

Query Match 99.4%; Score 2243; DB 9; Length 411;
Best Local Similarity 98.1%; Pred. No. 2.6e-189;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 293 ENSTDYLYPEQLKMTVVKLISHRECOQPHYVGGSEVTTKMLCAADPQWKTDSCQDSGGPL 352
DB 321 ENSTDYLYPEQLKMTVVKLISHRECOQPHYVGGSEVTTKMLCAADPQWKTDSCQDSGGPL 380
QY 353 VCSLOGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 403
DB 381 VCSLOGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 431

UT 6
US 0-171-311-184
; Tuence 184, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US 0-171-311-184

Query Match 99.4%; Score 2243; DB 14; Length 431;
Best Local Similarity 98.1%; Pred. No. 2.8e-189;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNPKKFGQHCEDKSKTCYEGNGHFYRG 60
DB 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNPKKFGQHCEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNASATVLOQTYHAHRSALQGLGKHNYCRNPDNRPRPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNASATVLOQTYHAHRSALQGLGKHNYCRNPDNRPRPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFCQCGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
DB 141 PLVQECMVHDCADGKPKSPPEELKFCQCGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 200
QY 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGEKKEVENLI 232
DB 201 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGEKKEVENLI 260
QY 233 LHKDYSADTLAHHNDIALKIRSKGRCACQPSRTIQTICLPSMYNDPOFGTSCETIGFGK 292
DB 261 LHKDYSADTLAHHNDIALKIRSKGRCACQPSRTIQTICLPSMYNDPOFGTSCETIGFGK 320
QY 293 ENSTDYLYPEQLKMTVVKLISHRECOQPHYVGGSEVTTKMLCAADPQWKTDSCQDSGGPL 352
DB 321 ENSTDYLYPEQLKMTVVKLISHRECOQPHYVGGSEVTTKMLCAADPQWKTDSCQDSGGPL 380
QY 353 VCSLOGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 403
DB 381 VCSLOGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 431

RESULT 7

US-10-822-161
; Sequence 161, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-161

Query Match 99.4%; Score 2243; DB 14; Length 431;
Best Local Similarity 98.1%; Pred. No. 2.8e-189;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNPKKFGQHCEDKSKTCYEGNGHFYRG 60
DB 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNPKKFGQHCEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNASATVLOQTYHAHRSALQGLGKHNYCRNPDNRPRPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNASATVLOQTYHAHRSALQGLGKHNYCRNPDNRPRPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFCQCGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
DB 141 PLVQECMVHDCADGKPKSPPEELKFCQCGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 200
QY 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGEKKEVENLI 232
DB 201 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGEKKEVENLI 260
QY 233 LHKDYSADTLAHHNDIALKIRSKGRCACQPSRTIQTICLPSMYNDPOFGTSCETIGFGK 292
DB 261 LHKDYSADTLAHHNDIALKIRSKGRCACQPSRTIQTICLPSMYNDPOFGTSCETIGFGK 320
QY 293 ENSTDYLYPEQLKMTVVKLISHRECOQPHYVGGSEVTTKMLCAADPQWKTDSCQDSGGPL 352
DB 321 ENSTDYLYPEQLKMTVVKLISHRECOQPHYVGGSEVTTKMLCAADPQWKTDSCQDSGGPL 380
QY 353 VCSLOGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 403
DB 381 VCSLOGRMTLTGIVSWGRCALKDKPGVYTVRSHFLPWIRSHTKENGIAL 431

RESULT 8

US-10-131-985-21
; Sequence 21, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:

APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleston, Nicholas L
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131.985
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/726.295
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: GB 9930768.8
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 21
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-985-21

Query Match 99.4%; Score 2243; DB 14; Length 431;
Best Local Similarity 98.1%; Pred. No. 2.8e-189;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 80
61 KASTDTMGRPCLPNSATVLOQTYHAHRSALQGLGKHNYCRNPNRRPWCYVQVGLK 120
81 KASTDTMGRPCLPNSATVLOQTYHAHRSALQGLGKHNYCRNPNRRPWCYVQVGLK 140
121 PLVQECMVHDCADGK-----LKFCGQKTLAPRKIIIGSEFTTIENQWFAAIYRRH 172
141 PLVQECMVHDCADGKSPPEELKFQCGQKTLAPRKIIIGSEFTTIENQWFAAIYRRH 200
173 RGGSVTVVCGSLISPCWVISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 232
201 RGGSVTVVCGSLISPCWVISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 260
233 LHKDYSADTLAHDNDIALLKIRSKGRCAPSRITQICLPSMYNDPQFGTSCITGFGK 292
261 LHKDYSADTLAHDNDIALLKIRSKGRCAPSRITQICLPSMYNDPQFGTSCITGFGK 320
293 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPWKTDSCQDSDGGPL 352
321 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPWKTDSCQDSDGGPL 380
353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
381 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 431

APPLICANT: Dack, Kevin N
APPLICANT: Davies, Michael J
APPLICANT: Fish, Paul V
APPLICANT: Huggins, Jonathan P
APPLICANT: McIntosh, Fraser S
APPLICANT: Occleston, Nicholas L
TITLE OF INVENTION: Composition
FILE REFERENCE: PCS 10391A
CURRENT APPLICATION NUMBER: US/10/131.985
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: US/09/726.295
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: GB 9930768.8
PRIOR FILING DATE: 1999-12-29
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 21
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-131-985-21

Query Match 99.4%; Score 2243; DB 15; Length 431;
Best Local Similarity 98.1%; Pred. No. 2.8e-189;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 80
61 KASTDTMGRPCLPNSATVLOQTYHAHRSALQGLGKHNYCRNPNRRPWCYVQVGLK 120
81 KASTDTMGRPCLPNSATVLOQTYHAHRSALQGLGKHNYCRNPNRRPWCYVQVGLK 140
121 PLVQECMVHDCADGK-----LKFCGQKTLAPRKIIIGSEFTTIENQWFAAIYRRH 172
141 PLVQECMVHDCADGKSPPEELKFQCGQKTLAPRKIIIGSEFTTIENQWFAAIYRRH 200
173 RGGSVTVVCGSLISPCWVISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 232
201 RGGSVTVVCGSLISPCWVISATHCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 260
233 LHKDYSADTLAHDNDIALLKIRSKGRCAPSRITQICLPSMYNDPQFGTSCITGFGK 292
261 LHKDYSADTLAHDNDIALLKIRSKGRCAPSRITQICLPSMYNDPQFGTSCITGFGK 320
293 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPWKTDSCQDSDGGPL 352
321 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPWKTDSCQDSDGGPL 380
353 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
381 VCSLQGRMTLTGIVSWGRGKALKDKPGVYTRVSHFLPWIRSHTKKEENGLAL 431

RESULT 10
US-10-295-027-1275
Sequence 1275, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.

APPLICANT: Glynn, Richard
 APPLICANT: Hevezi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Eos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 RIOR APPLICATION NUMBER: US 09/663,733
 RIOR FILING DATE: 2000-09-15
 RIOR APPLICATION NUMBER: US 60/350,666
 RIOR FILING DATE: 2001-11-13
 RIOR APPLICATION NUMBER: US 60/335,394
 RIOR FILING DATE: 2001-11-15
 RIOR APPLICATION NUMBER: US 60/332,464
 RIOR FILING DATE: 2001-11-21
 RIOR APPLICATION NUMBER: US 60/334,393
 RIOR FILING DATE: 2001-11-29
 RIOR APPLICATION NUMBER: US 60/340,376
 RIOR FILING DATE: 2001-12-14
 RIOR APPLICATION NUMBER: US 60/347,211
 RIOR FILING DATE: 2002-01-08
 RIOR APPLICATION NUMBER: US 60/347,349
 RIOR FILING DATE: 2002-01-10
 RIOR APPLICATION NUMBER: US 60/355,250
 RIOR FILING DATE: 2002-02-08
 RIOR APPLICATION NUMBER: US 60/356,714
 RIOR FILING DATE: 2002-02-13
 Summary Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 1275
 LENGTH: 431
 TYPE: PRT
 ORGANISM: Homo sapiens
 9-295-027-1275

37	Match	99.4%	Score	2243	DB	15	Length	431
38	Local Similarity	98.1%	Pred. No.	2.8e-189				
39	Matches	403	Conservative	0	Mismatches	0	Indels	8
40	Gaps	1						
Qy	1	SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNPKKFGGQHCIEDKSKTCYEGNGHFYRG	60					
Dd	21	SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNPKKFGGQHCIEDKSKTCYEGNGHFYRG	80					
Qy	61	KASTDTMRGCPCLPWN SATVLOOTYHAHRS DAL OLGIGKKNYCRNPDRRPPWCYVQVGLK	120					
Dd	81	KASTDTMRGCPCLPWN SATVLOOTYHAHRS DAL OLGIGKKNYCRNPDRRPPWCYVQVGLK	140					
Qy	121	PLVQECMVHDCADGK-----LKPCOGKTLRPRFKIGGEBFTTIENQPFAAIYRRH	172					
Dd	141	PLVQECMVHDCADGKPPSEELKFCOGKTLRPRFKIGGEBFTTIENQPFAAIYRRH	200					
Qy	173	RGGSVTVCGGSLSPCWVISA THCFIDYPKKSDYIVYLGSRSLNSNTOGEMKPFVENLI	232					
Dd	201	RGGSVTVCGGSLSPCWVISA THCFIDYPKKSDYIVYLGSRSLNSNTOGEMKPFVENLI	260					
Qy	233	LHKQYSADTLAHNDIALLLKRSKEGRCAOPSRITOTICLPMSYNDPQFGTSCITGFGK	292					
Dd	261	LHKQYSADTLAHNDIALLLKRSKEGRCAOPSRITOTICLPMSYNDPQFGTSCITGFGK	320					
Qy	293	ENSTDYLVPEQLKMTVVKLI SHRCQOPHYVGSSEVTTKMLCAADPOWKTDSCQGS GGPL	352					
Dd	321	ENSTDYLVPEQLKMTVVKLI SHRCQOPHYVGSSEVTTKMLCAADPOWKTDSCQGS GGPL	380					
Qy	353	VCSLQGRMTLTGIVSWGRCALKDKPGYVTVRSHFIPWIRSHTKENGLAL	403					
Dd	381	VCSLQGRMTLTGIVSWGRCALKDKPGYVTVRSHFIPWIRSHTKENGLAL	431					

RESULT 11
US-10-410-962-34
Sequence 34, Application US/10410962
Publication No. US20040077836A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bove, Carolyn
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
FILE REFERENCE: 040853-01-5054
CURRENT APPLICATION NUMBER: US/10/410,962
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 34
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens
US-10-410-962-34

Query Match	99.4%	Score	2243	DB	16	Length	431
Best Local Similarity	98.1%	Pred. No.	2.8e-189				
Matches	403	Conservative	0	Mismatches	0	Indels	8
						Gaps	1
Qy	1	SNELHQVPSNCDCLNGGTCVSNKYFSNIHNCNCPKFKGGQHCDEIDKSKTCYEGNGHFRG	60				
Db	21	SNELHQVPSNCDCLNGGTCVSNKYFSNIHNCNCPKFKGGQHCDEIDKSKTCYEGNGHFRG	80				
Qy	61	KASTDTMGRPCLPWN SATVLQOTTHAURSDALOLGIGKINYCHNPNNRRPWCYVQVGLK	120				
Db	81	KASTDTMGRPCLPWN SATVLQOTTHAURSDALOLGIGKINYCHNPNNRRPWCYVQVGLK	140				
Qy	121	PLVQBCWVHDCADGK-----LKFCGGOKTLPFRPKIIGGFTTIEQNQFAAIYRSH	172				
Db	141	PLVQBCWVHDCADGKPKSSPPEELKFCGGOKTLPFRPKIIGGFTTIEQNQFAAIYRSH	200				
Qy	173	RGGSVTVYCGSLSLSPCWVISATHCFIDYPKKEDIYVILGRSLNNTGEMKFEVENLI	232				
Db	201	RGGSVTVYCGSLSLSPCWVISATHCFIDYPKKEDIYVILGRSLNNTGEMKFEVENLI	260				
Qy	233	LHKQYSADTLAHHNDIALLKTRSEKGRCAQPSRTIQITICLPMSYNDPOFGTSCETIGFGK	292				
Db	261	LHKQYSADTLAHHNDIALLKTRSEKGRCAQPSRTIQITICLPMSYNDPOFGTSCETIGFGK	320				
Qy	293	ENSTDYLYPEQLKMTVVKLI SHRECCQPHYVYGSEVITTKMLCAADPOWKTDSCQDSDGGPL	352				
Db	321	ENSTDYLYPEQLKMTVVKLI SHRECCQPHYVYGSEVITTKMLCAADPOWKTDSCQDSDGGPL	380				
Qy	353	VCSLQGRWTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKENGIAL	403				
Db	381	VCSLQGRWTLTGIVSWGRCALKDKPGVYTRVSHFLPWIRSHTKENGIAL	431				

RESULT 12


```

; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
US 0-247-671-149

ary Match 99.3%; Score 2241; DB 14; Length 431;
st Local Similarity 97.8%; Pred. No. 4.2e-189;
ches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFNSIHWNCNCPKFGQHCIEDKSKTCYEGNGHFYRG 60
DB 21 SNELHQVPSNCDCLNGGTCVSNKYFNSIHWNCNCPKFGQHCIEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGGEFTTIENQFWFAAIYRRH 172
DB 141 PLVQECMVHDCADGKPPPEELKFCGQKTLRPRFKIIGGEFTTIENQFWFAAIYRRH 200
QY 173 RGGSVTYVCGGSLISPCWVISAHCDFIDYPKKEDYIVVLGRSRLNSNTQGEKFEVENLI 232
DB 201 RGGSVTYVCGGSLISPCWVISAHCDFIDYPKKEDYIVVLGRSRLNSNTQGEKFEVENLI 260
QY 233 LHKDYSADTLAHHNDIALLLKIRSKRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGK 292
DB 261 LHKDYSADTLAHHNDIALLLKIRSKRCAQPSRTIQTICLPSMYNDPQFGTSCBITGFGK 320
QY 293 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPOWKTDCQDSSGGL 352
DB 321 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPOWKTDCQDSSGGL 380
QY 353 VCSLQGRMTLTCIVSWGRCALCKDKPGYVTRVSHFLPWIRSHTEENGLAL 403
DB 381 VCSLQGRMTLTCIVSWGRCALCKDKPGYVTRVSHFLPWIRSHTEENGLAL 431

RESULT 16
US-10-407-821-2
; Sequence 2, Application US/10407821
; Publication No. US20030219386A1
; GENERAL INFORMATION:
; APPLICANT: IDELL, STEVEN
; TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
; TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
; TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURITIS IN RABBITS
; FILE REFERENCE: UTEN:022US
; CURRENT APPLICATION NUMBER: US/10/407,821
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/414,202
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/370,466
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 411
; ORGANISM: Homo sapiens
US-10-407-821-2

Query Match 98.9%; Score 2233; DB 15; Length 411;
Best Local Similarity 97.8%; Pred. No. 2e-188;
Matches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFNSIHWNCNCPKFGQHCIEDKSKTCYEGNGHFYRG 60
DB 1 SNELHQVPSNCDCLNGGTCVSNKYFNSIHWNCNCPKFGQHCIEDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 120
DB 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDNRPRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGGEFTTIENQFWFAAIYRRH 172
DB 121 PLVQECMVHDCADGKPPPEELKFCGQKTLRPRFKIIGGEFTTIENQFWFAAIYRRH 180
QY 173 RGGSVTYVCGGSLISPCWVISAHCDFIDYPKKEDYIVVLGRSRLNSNTQGEKFEVENLI 232

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181 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGRLNSNTGEMKFEVENLI 240
233 LHKDYSADTLAHNDIALLKIRSKGRCACQPSRTIQTICLPSMYNDPQGTSCITGFGK 292
241 LHKDYSADTLAHNDIALLKIRSKGRCACQPSRTIQTICLPSMYNDPQGTSCITGFGK 300
293 ENSTDYLYPBQLKWTWVKLIHRECOQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 352
301 ENSTDYLYPBQLKWTWVKLIHRECOQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 360
353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
361 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

ULT 17
US-10-282-174-562
; Sequence 562, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gornul
; APPLICANT: Eliios, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lynne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/369,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 562
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 15, 58, 141, 214, 231, 274, 366
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-282-174-562

Query Match 97.6%; Score 2203; DB 12; Length 431;
Best Local Similarity 96.6%; Pred. No. 9.4e-186;
Matches 397; Conservative 0; Mismatches 6; Indels 8; Gaps 1;

QY 1 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
DB 21 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 80
QY 61 KASDTMTGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNCRPNDRRRCWYVQVGLK 120
DB 81 KASDTMTGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNCRPNDRRRCWYVQVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
DB 141 XLVQECMVHDCADGKPPPEELKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 200

181 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGRLNSNTGEMKFEVENLI 240
233 LHKDYSADTLAHNDIALLKIRSKGRCACQPSRTIQTICLPSMYNDPQGTSCITGFGK 292
241 LHKDYSADTLAHNDIALLKIRSKGRCACQPSRTIQTICLPSMYNDPQGTSCITGFGK 300
293 ENSTDYLYPBQLKWTWVKLIHRECOQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 352
301 ENSTDYLYPBQLKWTWVKLIHRECOQPHYGSEVTTKMLCAADPOWKTDSCQDSSGGL 360
353 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
361 VCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

ULT 17
US-264-468B-1
; Sequence 1, Application US/09264468B
; Patent No. US20020106775A1
; GENERAL INFORMATION:
; APPLICANT: Nienaber, Vicki L.
; APPLICANT: Henkin, Jack
; APPLICANT: Smith, Richard A.
; APPLICANT: Walter, Karl A.
; APPLICANT: Severin, Jean M.
; APPLICANT: Edalji, Rohinton
; APPLICANT: Johnson Jr., Robert W.
; APPLICANT: Holzman, Thomas F.
; TITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
; FILE REFERENCE: 6310.US.P1
; CURRENT APPLICATION NUMBER: US/09/264,468B
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 09/036,361
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Leader sequence
; NAME/KEY: VARIANT
; LOCATION: (279)...(279)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: VARIANT
; LOCATION: (302)...(302)
; OTHER INFORMATION: Xaa = any amino acid
US-264-468B-1

Query Match 98.6%; Score 2225; DB 9; Length 431;
Best Local Similarity 97.6%; Pred. No. 1.1e-187;
Matches 403; Conservative 0; Mismatches 2; Indels 8; Gaps 1;

Q 1 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 60
D 21 SNELHQPNSCCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFYRG 80
Q 61 KASDTMTGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNCRPNDRRRCWYVQVGLK 120
D 81 KASDTMTGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNCRPNDRRRCWYVQVGLK 140
Q 121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
D 141 PLVQECMVHDCADGKPPPEELKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 200
Q 173 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGRLNSNTGEMKFEVENLI 232
D 201 RGSVTVVCGSLSPCWISATHCFIDYPKKEDYIVYLGRLNSNTGEMKFEVENLI 260

QY 173 RGGSVTVCGSLSPCWISATHCFTDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 232
 DE 201 RGGSVTVCGSLSPCWISATHCFTDYPKEDYIVYLGSRSLNSNTQGMKFEVENLI 260
 QY 233 LHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIQICLPSMYNDPQFQTSCEITGFGK 292
 DE 261 LHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIQICLPSMYNDPQFQTSCEITGFGK 320
 QY 293 ENSTDYLYPEQLKMTVVKLISHRECOQPHYGSEVTTMCAADPQWKTDSCQDGGPL 352
 DE 321 ENSTDYLYPEQLKMTVVKLISHRECOQPHYGSEVTTMCAADPQWKTDSCQDGGPL 380
 QY 353 VCSLQGRMTLGTIVSWGRGCKADKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
 DE 381 VCSLQGRMTLGTIVSWGRGCKADKPGVYTRVSHFLPWIRSHTKKEENGLAL 431

RE 19
 US 0-360-101-266
 ; Sequence 266, Application US/10360101
 ; Publication No. US20040009550A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Moll, Gert N.
 ; PPLICANT: Leenhouts, Cornelis J.
 ; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
 ; FILE REFERENCE: 2183-5673
 ; CURRENT APPLICATION NUMBER: US/10/360.101
 ; PRIOR FILING DATE: 2003-02-07
 ; RIOR APPLICATION NUMBER: EP 02077060.8
 ; RIOR FILING DATE: 2002-05-24
 ; UMBER OF SEQ ID NOS: 309
 ; Q ID NO 266
 ; SOFTWARE: Patent in version 3.1
 ; LENGTH: 445
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: sequence of urokinase
 US 0-360-101-266

ary Match 96.4%; Score 2176; DB 15; Length 445;
 st Local Similarity 94.8%; Pred. No. 2.3e-183;
 tches 403; Conservative 0; Mismatches 0; Indels 22; Gaps 7;

QY 1 SNELHQPVSNCCLNGGTCVSNKYF--SNHWCNCPKFGQCHCEIDKSKTCYEGNGHFY 58
 DE 21 SNELHQPVSNCCLNGGTCVSNKYFFTSNIHWCNCPKFGQCHCEIDKSKTCYEGNGHFY 80
 QY 59 RGKASTDTMGPRCLPWN SATVLQTY--HAHRS DALQLGLGKHNYCRNPDRRRPWCYVQ 116
 DE 81 RGKASTDTMGPRCLPWN SATVLQTYFTHAHRSDALQLGLGKHNYCRNPDRRRPWCYVQ 140
 QY 117 VOLKPLVQECMWHDCADGK-----LKFQCGQKTLRPRFKIIGBEFTTIENQWFA 166
 DE 141 VOLKPLVQECMWHDCADGKSPSEPTLKFQCGQKTLRPRFKIIGBEFTTIENQWFA 200
 QY 167 AIYRHRGGSVTVYCGGSLISPCWISA--THCFIDYPKEDYIVYLGSRSLNSNTQGM 224
 DE 201 AIYRHRGGSVTVYCGGSLISPCWISAFTHCFIDYPKEDYIVYLGSRSLNSNTQGM 260
 QY 225 KFEVENLILHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIQICLPSMYNDPQFG 282
 DE 261 KFEVENLILHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIQICLPSMYNDPQFG 320
 QY 283 TSCEITGFGKENS TDYLYPEQLKMTVVKLI--SHRECOQPHYGSEVTTMCAADPQWK 340
 DE 321 TSCEITGFGKENS TDYLYPEQLKMTVVKLI FTSHRECOQPHYGSEVTTMCAADPQWK 380
 QY 341 TDSQCGDGGPLVCSLQGRMTLGTIVSWGRG--CALKDXPGVYTRVSHFLPWIRSHTKKEE 398
 DE 381 TDSQCGDGGPLVCSLQGRMTLGTIVSWGRGFTCALKDXPGVYTRVSHFLPWIRSHTKKEE 440

QY 399 NGLAL 403
 DE 441 NGLAL 445

RESULT 20
 US-09-880-503-7
 ; Sequence 7, Application US/09880503
 ; Patent No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHINES, Douglas B
 ; APPLICANT: HIGAZI, Adil Al-Rooof
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; TITLE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880.503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/212,847
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 323
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-503-7

Query Match 75.5%; Score 1703; DB 9; Length 323;
 Best Local Similarity 79.2%; Pred. No. 8.2e-142;
 Matches 319; Conservative 2; Mismatches 2; Indels 80; Gaps 3;

QY 1 SNELHQPVSNCCLNGGTCVSNKYF--SNHWCNCPKFGQCHCEIDKSKTCYEGNGHFYRG 60
 DE 1 SNELHQPVSNCCLNGGTCVSNKYF--SNHWCNCPKFGQCHCEIDKSK-----48
 QY 61 KASTDTMGPRCLPWN SATVLQTYHAHRS DALQLGLGKHNYCRNPDRRRPWCYVQVGLK 120
 DE 49 -----PSSP-----PE-----54
 QY 121 PLVQECMWHDCADGKLTQCGQKTLRPRFKIIGBEFTTIENQWFAAIYRHRGGSVTVY 180
 DE 55 -----ELKFPQCGQKTLRPRFKIIGBEFTTIENQWFAAIYRHRGGSVTVY 100
 QY 181 CGSLISPCWISATHCFTDYPKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSAD 240
 DE 101 CGSLISPCWISATHCFTDYPKEDYIVYLGSRSLNSNTQGMKFEVENLILHKDYSAD 160
 QY 241 TLAHNDIALKIRSKGRCQAQPSRTIQICLPSMYNDPQFQTSCEITGFGKENS TDYLY 300
 DE 161 TLAHNDIALKIRSKGRCQAQPSRTIQICLPSMYNDPQFQTSCEITGFGKENS TDYLY 220
 QY 301 PSOLKMTVVKLISHRECOQPHYGSEVTTMCAADPQWKTDSCQDGGPLVCSLQGRM 360
 DE 221 PSOLKMTVVKLISHRECOQPHYGSEVTTMCAADPQWKTDSCQDGGPLVCSLQGRM 280
 QY 361 TLTGIVSWGRGCKADKPGVYTRVSHFLPWIRSHTKKEENGLAL 403
 DE 281 TLTGIVSWGRGCKADKPGVYTRVSHFLPWIRSHTKKEENGLAL 323

RESULT 21
 US-10-087-192-591
 ; Sequence 591, Application US/10087192
 ; Publication No. US20020182586A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Morris, David W.
 ; APPLICANT: Engelhard, Eric K.
 ; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: CANCER
 ; FILE REFERENCE: 529452000122
 ; CURRENT APPLICATION NUMBER: US/10/087.192
 ; CURRENT FILING DATE: 2002-03-01
 ; PRIOR APPLICATION NUMBER: US 09/747,377

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PRIORITY FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US 09/798,586
PRIORITY FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 591
LENGTH: 433
TYPE: PRT
ORGANISM: Mus musculus
10-087-192-591.

Query Match
est Local Similarity 72.1%; Score 1626.5; DB 12; Length 433;
atches 283; Conservative 50; Mismatches 61; Indels 9; Gaps 2;

9 SNCDLNGGTCVSNKYFNSNIHWCNPKKFGGQHCIDKSKTCYEGNGHFYRGKASTDTWG 68
30 SNCCQNGGVCVSYKYSRIRRCSPKRFQEGHCEIDASKTCYHGNGDSYRGKANTDTKG 89
69 RPCLPWNASATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRNRRPWCYVQVGLKPLVQECMV 128
90 RPCLAWAPALQKPYNAHRPDAISLGLGKHNYCRNPDNQKRPWCYVQIGLRQFVQECMV 149
129 HDCADGKLGK-----PQCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRHGS-VTY 179
150 HDGSLSKKPSVDDQCGQKALRPRFKIIGGEFTTIENQWFAAIYRRHGS-VTY 209
180 VCGSLSPPCWVISATHCFIDYPKKEDIYVILGRSRLNSNTQGMKPEVENLILHKDYSA 239
210 KCGSLSPPCWVSAACFCIOLPKKENYVYVLSGKSSSYNPGEMKFEVQLILHYYRE 269
240 DTLAHDNDIALKIRSEKRCAPSRIOICILPSMYNDPQPTSCETITGFGKENTDYL 299
270 DSLAYHDNDIALKIRSEKRCAPSRIOICILPPRPTDAPFGSDCEITGFGKESDYL 329
300 YPEQLQKTVKVLISHRCQPHYYSBVTTKMLCAADPQWTKDSGCGDGLVCSLQGR 359
330 YPNLKMVSVKLVSHQCMQPHYYSBVTTKMLCAADPQWTKDSGCGDGLVCSLQGR 389
360 MTLTGIVSGRGKALDKPKGVYTRVSHFLPWIRSHTKENGLA 402
390 PTLGIVSGRGKALDKPKGVYTRVSHFLPWIRSHTKENGLA 432

ULT 22
10-106-698-6266
Sequence 6266, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
FILE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
CURRENT APPLICATION NUMBER: US/10/106,698
PRIORITY FILING DATE: 2002-03-27
PRIORITY APPLICATION NUMBER: PCT/US00/26524
PRIORITY FILING DATE: 2000-09-28
PRIORITY APPLICATION NUMBER: US 60/157,137
PRIORITY FILING DATE: 1999-09-29
PRIORITY APPLICATION NUMBER: US 60/163,280
PRIORITY FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 8564
SOFTWARE: Patent In Ver. 3.0
SEQ ID NO 6266
LENGTH: 337
TYPE: PRT
ORGANISM: Homo sapiens
10-106-698-6266

Query Match
est Local Similarity 65.4%; Score 1477; DB 14; Length 337;
atches 267; Conservative 3; Mismatches 5; Indels 14; Gaps 2;

1 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWCNPKKFGGQHCIDKSKTCYEGNGHFYRG 60
27 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWCNPKKFGGQHCIDKSKTCYEGNGHFYRG 86
61 KASDTMTGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRNRRPWCYVQVGLK 120
87 KASDTMTGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRNRRPWCYVQVGLK 146
121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
147 PLVQECMVHDCADGKCKSSPPEELKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 206
173 RGGSVTYVCGGSLSPPCWVISATHCFIDYPKKEDIYVILGRSRLNSNTQGMKPEVENLI 232
207 RGGSVTYVCGGSLSPPCWVISATHCFIDYPKKEDIYVILGRSRLNSNTQGMKPEVENLI 266
233 LHKDYSDATLAHDNDIALKIRSEKRCAPSRIOICILPSMYNDPQPTSCETITGFGKENTDYL 275
267 LHKDYSDATLAHDNDIALKIRSEKRCAPSRIOICILPSMYNDPQPTSCETITGFGKENTDYL 315

RESULT 23
US-10-264-049-2927
Sequence 2927, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
FILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
CURRENT APPLICATION NUMBER: US/10/264,049
PRIORITY FILING DATE: 2002-10-04
PRIORITY APPLICATION NUMBER: PCT/US01/18569
PRIORITY FILING DATE: 2001-06-07
PRIORITY APPLICATION NUMBER: US 60/209,467
PRIORITY FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patent In Ver. 3.1
SEQ ID NO 2927
LENGTH: 337
TYPE: PRT
ORGANISM: Homo sapiens
US-10-264-049-2927

Query Match
est Local Similarity 65.4%; Score 1477; DB 15; Length 337;
atches 267; Conservative 3; Mismatches 5; Indels 14; Gaps 2;

1 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWCNPKKFGGQHCIDKSKTCYEGNGHFYRG 60
27 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWCNPKKFGGQHCIDKSKTCYEGNGHFYRG 86
61 KASDTMTGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRNRRPWCYVQVGLK 120
87 KASDTMTGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRNRRPWCYVQVGLK 146
121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
147 PLVQECMVHDCADGKCKSSPPEELKFCGQKTLRPRFKIIGGEFTTIENQWFAAIYRRH 206
173 RGGSVTYVCGGSLSPPCWVISATHCFIDYPKKEDIYVILGRSRLNSNTQGMKPEVENLI 232
207 RGGSVTYVCGGSLSPPCWVISATHCFIDYPKKEDIYVILGRSRLNSNTQGMKPEVENLI 266
233 LHKDYSDATLAHDNDIALKIRSEKRCAPSRIOICILPSMYNDPQPTSCETITGFGKENTDYL 275
267 LHKDYSDATLAHDNDIALKIRSEKRCAPSRIOICILPSMYNDPQPTSCETITGFGKENTDYL 315

RESULT 24
US-09-880-503-5
Sequence 5, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
```


APPLICANT: HIGAZI, Abd Al-Boof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTABILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
RIOR APPLICATION NUMBER: US 60/212,847
RIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent in Ver. 2.1
Q ID NO 5
LENGTH: 276
TYPE: PRT
ORGANISM: Homo sapiens
US-880-503-5

ary Match 64.9%; Score 1465; DB 9; Length 276;
st Local Similarity 99.6%; Pred. No. 6.6e-121;
tches 268; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 135 KLKFCQGGKTLRPRFKIIGGFTTIENQWPAAIYRRHGGSVTVVCGSLISPCWISA 194
Db 8 ELKFCQGGKTLRPRFKIIGGFTTIENQWPAAIYRRHGGSVTVVCGSLISPCWISA 67

Qy 195 THCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIR 254
De 68 THCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIR 127

Qy 255 SKEGRCAQPSRTIOTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMTVVKLISH 314
De 128 SKEGRCAQPSRTIOTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMTVVKLISH 187

Qy 315 RECOQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRCAL 374
De 188 RECOQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRCAL 247

Qy 375 KDKPGVYTRVSHFLPWIRSHKTEENGLAL 403
De 248 KDKPGVYTRVSHFLPWIRSHKTEENGLAL 276

RE UT 25
US 0-407-821-3
Squence 3, Application US/10407821
Slication No. US20030219386A1
GENERAL INFORMATION:
APPLICANT: IDELL, STEVEN
TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
FILE REFERENCE: UTSN:022US
CURRENT APPLICATION NUMBER: US/10/407,821
CURRENT FILING DATE: 2003-04-04
RIOR APPLICATION NUMBER: 60/414,202
RIOR FILING DATE: 2002-09-27
RIOR APPLICATION NUMBER: 60/370,466
RIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patent in Ver. 2.1
Q ID NO 3
LENGTH: 268
TYPE: PRT
ORGANISM: Homo sapiens
US-407-821-3

ary Match 64.9%; Score 1464; DB 15; Length 268;
st Local Similarity 100.0%; Pred. No. 7.9e-121;
tches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 136 LKFCQGGKTLRPRFKIIGGFTTIENQWPAAIYRRHGGSVTVVCGSLISPCWISAT 195
De 1 LKFCQGGKTLRPRFKIIGGFTTIENQWPAAIYRRHGGSVTVVCGSLISPCWISAT 60

Qy 196 HCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRS 255
Db 61 HCFIDYPKKEDYIVLGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRS 120

Qy 256 KEGRCQAQPSRTIOTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMTVVKLISHR 315
Db 121 KEGRCQAQPSRTIOTICLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMTVVKLISHR 180

Qy 316 EQQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRCAL 375
Db 181 EQQPHYGVSEVTTKMLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRCAL 240

Qy 376 KDPGVYTRVSHFLPWIRSHKTEENGLAL 403
Db 241 KDPGVYTRVSHFLPWIRSHKTEENGLAL 268

RESULT 26
US-09-264-468B-2
Sequence 2, Application US/09264468B
Patent No. US20020106775A1
GENERAL INFORMATION:
APPLICANT: Wang, Jieyi
APPLICANT: Nienaber, Vicki L.
APPLICANT: Henkin, Jack
APPLICANT: Smith, Richard A.
APPLICANT: Walter, Karl A.
APPLICANT: Severin, Jean M.
APPLICANT: Edalji, Rohinton
APPLICANT: Johnson Jr., Robert W.
APPLICANT: Holzman, Thomas F.
TITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
FILE REFERENCE: 6310.US.P1
CURRENT APPLICATION NUMBER: US/09/264,468B
CURRENT FILING DATE: 1999-03-05
PRIOR FILING DATE: US 09/036,361
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Homo sapiens
US-09-264-468B-2

Query Match 59.1%; Score 1333; DB 9; Length 246;
Best Local Similarity 99.2%; Pred. No. 2.5e-109;
Matches 244; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 151 IIGGFTTIENQWPAAIYRRHGGSVTVVCGSLISPCWISATHCFIDYPKKEDYIVY 210
Db 1 IIGGFTTIENQWPAAIYRRHGGSVTVVCGSLISPCWISATHCFIDYPKKEDYIVY 60

Qy 211 LGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIOTI 270
Db 61 LGRSLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIOTI 120

Qy 271 CLPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMTVVKLISHRECOQPHYGVSEVTTK 330
Db 121 ALPSMYNDPQFGTSCBITGFGKENSTDYLYPEQLKMTVVKLISHRECOQPHYGVSEVTTK 180

Qy 331 MLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPW 390
Db 181 MLCAADPQWKTDSCQDGGPLVCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFLPW 240

Qy 391 IRSHTK 396
Db 241 IRSHTK 246

RESULT 27
US-09-898-837A-47
Sequence 47, Application US/09898837A

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Publication No. US20030077697A1
GENERAL INFORMATION:
APPLICANT: Quinn, Kerry E.
APPLICANT: Spyttek, Kimberly A.
APPLICANT: Majumder, Kumud
APPLICANT: Vernet, Corine
APPLICANT: Herrmann, John L.
APPLICANT: Burgess, Catherine
APPLICANT: Fernandes, Elma
APPLICANT: Taupier Jr., Raymond
APPLICANT: Rastelli, Luca
APPLICANT: Curagen Corporation
APPLICANT: Gerlach, Valerie L
APPLICANT: MacDougall, John R
TITLE OF INVENTION: NOVEL SERINE/THREONINE PROTEIN-KINASE LIKE PROTEINS AND
FILE REFERENCE: NUCLEIC ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/09/898,837A
CURRENT FILING DATE: 2001-07-03
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/165,986
PRIORITY FILING DATE: 1999-11-17
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/194,839
PRIORITY FILING DATE: 2000-04-05
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/195,637
PRIORITY FILING DATE: 2000-04-07
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/197,080
PRIORITY FILING DATE: 2000-04-13
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/232,677
PRIORITY FILING DATE: 2000-09-15
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/181,347
PRIORITY FILING DATE: 2000-02-09
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/194,195
PRIORITY FILING DATE: 2000-04-03
PRIORITY APPLICATION NUMBER: U.S.S.N. 60/215,906
PRIORITY FILING DATE: 2000-07-03
PRIORITY APPLICATION NUMBER: U.S.S.N. 09/715,427
PRIORITY FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 47
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens
US-898-837A-47

Query Match 58.4%; Score 1318; DB 10; Length 241;
Best Local Similarity 99.6%; Pred. No. 5.2e-108;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

C 151 IIGGETTTIENQWPFAAIYRRHGGSVTVVCGSLSPCWVISATHCFIDYPKKEDIYVY 210
D 1 IIGGETTTIENQWPFAAIYRRHGGSVTVVCGSLSPCWVISATHCFIDYPKKEDIYVY 60
Q 211 LGSRLNSNTQGMKFEVENLILHKDYSADTLAHHNDIALLKIRSGEGRCAQPSRTIQT 270
D 61 LGSRLNSNTQGMKFEVENLILHKDYSADTLAHHNDIALLKIRSGEGRCAQPSRTIQT 120
Q 271 CLPSMTNDPQFGTSCITGFKENSTDYLYPEQLKMTYVYLKSHRECQOPHYGSEVTTK 330
D 121 CLPSMTNDPQFGTSCITGFKENSTDYLYPEQLKMTYVYLKSHRECQOPHYGSEVTTK 180
Q 331 MLCADDPQWKTDSCQDGGPLVCSLQGRMTLTGIVSGRGKALDKPKGVYTRVSHFLPW 390
D 181 MLCADDPQWKTDSCQDGGPLVCSLQGRMTLTGIVSGRGKALDKPKGVYTRVSHFLPW 240
C 391 I 391
D 241 I 241

F JLT 28
U 10-401-077-1
Sequence 1, Application US/10401077
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Publication No. US20040002137A1
GENERAL INFORMATION:
APPLICANT: Hung, Paul Porwen
APPLICANT: Wu, Bryan T. H.
TITLE OF INVENTION: HUMAN TISSUE UROKINASE TYPE PLASMINOGEN
FILE REFERENCE: 12133-006001
CURRENT APPLICATION NUMBER: US/10/401,077
CURRENT FILING DATE: 2003-03-27
PRIORITY APPLICATION NUMBER: US 60/371,013
PRIORITY FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 650
TYPE: PRT
ORGANISM: Homo sapiens
US-10-401-077-1

Query Match 47.9%; Score 1081.5; DB 15; Length 650;
Best Local Similarity 39.2%; Pred. No. 1.3e-86;
Matches 226; Conservative 49; Mismatches 116; Indels 185; Gaps 10;

QY 3 ELHQVP-SNCD---CLNGGTCVSNKYPFSNIHWCNPKFGGQCEIDKSKTCYEGNGHFY 58
DB 77 QCHSVPVKSCSEPRCFNGGTCQQALYFSDP-VCCQPEGPAGKCEIDTRATCTYEGNGHFY 135
QY 59 RGKASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGHKHYCRNPDNRPRPCVYQVG 118
DB 136 RGKASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGHKHYCRNPDNRPRPCVYQVG 195
QY 119 LKPLVQECMWHDCADG----- 134
DB 196 LKPLVQECMWHDCSEGNSDCYEQGISYRGTSWTAESGAECTNWSALAKQPYSGRRPD 255
QY 135 ----- 134
DB 256 AIRLGLGNHYCRNPDNRD SKPWCYVFKAGKYSSEFCSTPACSEGNSDCYFNGSAYRGTH 315
QY 135 -----KLK 137
DB 316 SLTESGASCLPWNMILIGKYYTAQNPDAALGLGHKHYCRNPDGDAKPWCHVLKNRRLT 375
QY 138 FQ-----CG-QKTLRPRFKIIGGEFTTIENQWPFAAIYRRH-RGGSVTVVCGGSLI 186
DB 376 WEYCDVPSCSTCGLRQVSPQFRIKGLPADIASHPWQAALFAKHRESGPERFLCGGILI 435
QY 187 SPQWVLSATHCFIDYPKKEDIYVYLGSRLNSNTQGMKFEVENLILHKDYSADTLAHHN 246
DB 436 SSCWILSAAHCFQERFPFPHLTVLIGRTYRVVPEEESQKFEVEKYIVHKEFDDDT--YDN 493
QY 247 DIALLKIRSGEGRCAQPSRTIQTICLPSMTYNDPQFGTSCITGFKENSTDYLYPEQLKM 306
DB 494 DIALLQLKDSRSSCAQSSVVTVCLPPADLQLPDWTCELSGVGKHEALSPFYSERLKE 553
QY 307 TVVKLISHRCQOPHYGSEVTTMCLCAAD-----POWKT-DSQCGDGGPLVCSLQGRM 360
DB 554 AHVELYSSRCTSCHLLNRTVTDNMLCAGTRSGGPOANLHDACQDGGSGGPLVCLNDGRM 613
QY 361 TLTCIVSGRGKALDKPKGVYTRVSHFLPWIRSHTK 396
DB 614 TLVGIIISGLGCGQKQDVPGVYTKVTNYLDWIRDNMR 649

RESULT 29
US-09-987-457-18
Sequence 18, Application US/09987457
Publication No. US20030013150A1
GENERAL INFORMATION:
APPLICANT: Manosroi, Aranya
APPLICANT: Manosroi, Jiradej
APPLICANT: Tayapiwatana, Chatchai
APPLICANT: Goetz, Friedrich
```

APPLICANT: Werner, Rolf-Guenther
TITLE OF INVENTION: Methods for Large Scale Protein Production in Prokaryotes
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION NUMBER: US/09/987,457
CURRENT FILING DATE: 2001-11-14
RIOR APPLICATION NUMBER: 60/268,573
RIOR FILING DATE: 2001-02-15
RIOR APPLICATION NUMBER: GB 00 27 782.2
RIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent in Ver. 2.1
Q ID NO 18
LENGTH: 527
TYPE: PRT
ORGANISM: Homo sapiens (tpe)
US-987-457-18

Query Match 38.0%; Score 858.5; DB 10; Length 527;
Best Local Similarity 37.5%; Pred. NO. 4.5e-67; Indels 97; Gaps 10;
Matches 183; Conservative 56; Mismatches 152;

QY 3 ELHQP-SNCD---CLNGGTCVSNKYSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHGY 58
DB 42 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPGPGAGKCEIDTRATCYEDQGISY 100
QY 59 RGASTDTMGRPCLPWNASATVLOQTYHAHRSALQGLGKHNYCRNPDNRPRKCYVQVG 118
DB 101 RGTWSTAESGAECTNWNSSALAQKPYSGRRPDALRLGLGNHNYCRNPDNRDSKPCWYVFK 160
QY 119 LKPLVQECMVHDCADG----- 134
DB 161 KYSSEFCSTPACSEGNSDCYFGNGSAVRGTHSLTESGASCLPWNMILIGKYVTAQNP 220
QY 135 -----KLKFO----- 155
DB 221 AQUALGLGKHNYCRNPDGDAKPWCHLVKNRLTWEYCDVPSCSTGLRQYSPQFRKGG 280
QY 156 FTTTENQWFAAIYRRH-RGGSVTVCGGSLISPCWVISATHCFIDYPKKEDYIVVLGRS 214
DB 281 PADTASHPWQAIIAKHRSRSGERFLCGGILISSCWLSAAHCFQERFPPHLLTVILGRT 340
QY 215 RLNSNTOEMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIOTICLPS 274
DB 341 YRVVPGEEQKFEVEKYIVHKEFDDT--YNDIALQLKSDSRCAQESSVVRTVCLPP 398
QY 275 MYNDPQFCTSCEITGFGKENSTDVLYPEOLKMTVKLISHRECOQPHYGVSEVTTKMLCA 334
DB 399 ADLQLPDWTCELSGKHEALSFFYSERLKEAHRVLYPSSRCTSQHLLNRTVTDNMLCA 458
QY 335 AD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFL 388
DB 459 GDRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGQKDPVPGVYTKVTNYL 518
QY 389 PWIRSHTK 396
DB 519 DWIRDNR 526

RESULT 31
US-10-432-842-1
Sequence 1, Application US/10432842
Publication No. US20040071707A1
GENERAL INFORMATION:
APPLICANT: Aranya Manosroi
APPLICANT: Jiradej Manosroi
APPLICANT: Chatchai Tayapiwatana
APPLICANT: Friedrich Goetz
APPLICANT: Rolf-Guenther Werner
TITLE OF INVENTION: Methods for Large Scale Production of Recombinant
TITLE OF INVENTION: DNA-derived tpa or K2S Molecules
FILE REFERENCE: 0652.2190001
CURRENT APPLICATION NUMBER: US/09/987,455
CURRENT FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/268,574
PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: GB 0027779.8
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 19
LENGTH: 527
TYPE: PRT
ORGANISM: Homo sapiens
US-09-987-455-19

Query Match 38.0%; Score 858.5; DB 10; Length 527;
Best Local Similarity 37.5%; Pred. NO. 4.5e-67; Indels 97; Gaps 10;
Matches 183; Conservative 56; Mismatches 152;

QY 3 ELHQP-SNCD---CLNGGTCVSNKYSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHGY 58
DB 42 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPGPGAGKCEIDTRATCYEDQGISY 100
QY 59 RGASTDTMGRPCLPWNASATVLOQTYHAHRSALQGLGKHNYCRNPDNRPRKCYVQVG 118
DB 101 RGTWSTAESGAECTNWNSSALAQKPYSGRRPDALRLGLGNHNYCRNPDNRDSKPCWYVFK 160
QY 119 LKPLVQECMVHDCADG----- 134
DB 161 KYSSEFCSTPACSEGNSDCYFGNGSAVRGTHSLTESGASCLPWNMILIGKYVTAQNP 220
QY 135 -----KLKFO----- 155
DB 221 AQUALGLGKHNYCRNPDGDAKPWCHLVKNRLTWEYCDVPSCSTGLRQYSPQFRKGG 280
QY 156 FTTTENQWFAAIYRRH-RGGSVTVCGGSLISPCWVISATHCFIDYPKKEDYIVVLGRS 214
DB 281 PADTASHPWQAIIAKHRSRSGERFLCGGILISSCWLSAAHCFQERFPPHLLTVILGRT 340
QY 215 RLNSNTOEMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIOTICLPS 274
DB 341 YRVVPGEEQKFEVEKYIVHKEFDDT--YNDIALQLKSDSRCAQESSVVRTVCLPP 398
QY 275 MYNDPQFCTSCEITGFGKENSTDVLYPEOLKMTVKLISHRECOQPHYGVSEVTTKMLCA 334
DB 399 ADLQLPDWTCELSGKHEALSFFYSERLKEAHRVLYPSSRCTSQHLLNRTVTDNMLCA 458
QY 335 AD-----PWKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFL 388
DB 459 GDRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGQKDPVPGVYTKVTNYL 518
QY 389 PWIRSHTK 396
DB 519 DWIRDNR 526

RESULT 31
US-10-432-842-1
Sequence 1, Application US/10432842
Publication No. US20040071707A1
GENERAL INFORMATION:
APPLICANT: Veronica A. CARROLL
APPLICANT: Adrian L. HARRIS
APPLICANT: Roy BICKNELL
APPLICANT: Pat PRICE
TITLE OF INVENTION: MODULATION OF CELL GROWTH
FILE REFERENCE: 117-450 / N.79507A SER
CURRENT APPLICATION NUMBER: US/10/432,842
CURRENT FILING DATE: 2003-09-27
PRIOR APPLICATION NUMBER: PCT/GB01/05244
PRIOR FILING DATE: 2001-11-28
PRIOR APPLICATION NUMBER: GB 0029001.5
PRIOR FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: MS Word
SEQ ID NO 1

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; LENGTH: 527
; TYPE: PRT
; ORGANISM: Homo sapiens
; 10-432-842-1
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; Query Match      38.0%; Score 858.5; DB 12; Length 527;
; est Local Similarity 37.5%; Pred. No. 4.5e-67;
; atches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
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; 3 ELHQP-SNCD---CLNGGTCVSNKYFNSIHWNCNPKKFGGQHCEDKSKTCYEGNGHFY 58
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; 59 RGKASTDTMGRPCLPWNISATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRPRPCVYQVG 118
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; 119 LKPLVQECMVHDCADG----- 134
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; 161 GKYSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNMSMILIGKYVTAQNP 220
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; 135 -----KLKFO----- 155
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; 221 AALGLGKHNYCRNPDGAKPWCHLVKNRRLTWECYDVPCSTCGLRQYSQPFRIKGG 280
; : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
; 156 FTTENOPWFAAIYRRH--RGGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLG 214
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; 281 FADIASHPWQAIAI FAKHRRSPGERFLCGGILISSCWILSAHCFQERPPPHLTVILGR 340
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; RESULT 33
; US-09-969-271-7
; Sequence 7, Application US/09969271
; Patent No. US20020098179A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));
; APPLICANT: Pfizer Limited (GB and EP (GB) only)
; TITLE OF INVENTION: Pharmaceutical Combinations
; FILE REFERENCE: PCS10951APME
; CURRENT APPLICATION NUMBER: US/09/969,271
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 0025473.0
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-969-271-7
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; Query Match      38.0%; Score 858.5; DB 9; Length 562;
; Best Local Similarity 37.5%; Pred. No. 4.9e-67;
; Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
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; 3 ELHQP-SNCD---CLNGGTCVSNKYFNSIHWNCNPKKFGGQHCEDKSKTCYEGNGHFY 58
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; 77 QCHSVPVKSCSEPRCFNGGTCQOALYFSDP--VCCPEGFAGKCCEDTRATCYEDQGISY 135
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; 59 RGKASTDTMGRPCLPWNISATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRPRPCVYQVG 118
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; 136 RGTWSTAESGAECTNWNSSALAAQKPYSGRRPDALRLGLGNHNYCRNPDNRDPSKPCVYFKA 195
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; 119 LKPLVQECMVHDCADG----- 134
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; 196 GKYSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNMSMILIGKYVTAQNP 255
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; 10-360-101-203
; Sequence 203, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 203
; LENGTH: 527
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of alteplase
; 10-360-101-203
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; Query Match      38.0%; Score 858.5; DB 15; Length 527;
; est Local Similarity 37.5%; Pred. No. 4.5e-67;
; atches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;

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QY 215 RLNSNTGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKGRCQAQPSRTIOTICLPS 274
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QY 335 AD-----POWKT-DSCQDGGPLVCSLQGRMTLTGIVSMGRGCAKDKFQVYTRVSHFL 388
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QY 389 PWIRSHTK 396
Db 554 DWIRDNR 561
RESULT 35
US-10-411-037-26
; Sequence 26, Application US/10411037
; Publication No. US2004004346A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 562
; TYPE: PRT
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Best Local Similarity 37.5%; Pred. No. 4.9e-67;
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QY 3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGGHCHEIDKSKTCYEGNGHFY 58
Db 77 QCHSVPVKSCSBRFCNGTCCQALYFSDP-VCQCEGFGAGKCCHEIDTRATCYEDQGISY 135
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QY 215 RLNSNTGEMKFEVENLILHKDYSADTLAHNDIALLKIRSKGRCQAQPSRTIOTICLPS 274
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QY 335 AD-----POWKT-DSCQDGGPLVCSLQGRMTLTGIVSMGRGCAKDKFQVYTRVSHFL 388
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QY 389 PWIRSHTK 396
Db 554 DWIRDNR 561
US-974-298-145
; Sequence 145, Application US/09974298
; Publication No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/236,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 145
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 1001470CD1
US-974-298-145
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Best Local Similarity 37.5%; Pred. No. 4.9e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
QY 3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGGHCHEIDKSKTCYEGNGHFY 58
Db 77 QCHSVPVKSCSBRFCNGTCCQALYFSDP-VCQCEGFGAGKCCHEIDTRATCYEDQGISY 135
QY 59 RKGASTDTMGRCLPWNSTVLYQTYHAHRSDALQGLGKHNCRNPNRREPWCYVQVG 118
Db 136 RGTWSTAESGAECTNWNSSALAKPKYSGRRPDAIRLGLGNHNYCRNPNRDRSKPCYVKA 195
QY 119 LKPLVQECNVHDCADG----- 134
Db 196 GKYSSFCSTPACSEGNPCYFGNGSAYRGTHSLTESGASCLRWNSMILIGKYVTAQNP 255
QY 135 -----KLKQ-----CG-QKTLRPRFKIIGGE 155
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QY 389 PWIRSHTK 396
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RESULT 35
US-10-411-037-26
; Sequence 26, Application US/10411037
; Publication No. US2004004346A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE OF INVENTION: GALACTOSIDASE A
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-26
Query Match 38.0%; Score 858.5; DB 12; Length 562;
Best Local Similarity 37.5%; Pred. No. 4.9e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
QY 3 ELHQVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGGHCHEIDKSKTCYEGNGHFY 58
Db 77 QCHSVPVKSCSBRFCNGTCCQALYFSDP-VCQCEGFGAGKCCHEIDTRATCYEDQGISY 135
QY 59 RKGASTDTMGRCLPWNSTVLYQTYHAHRSDALQGLGKHNCRNPNRREPWCYVQVG 118
Db 136 RGTWSTAESGAECTNWNSSALAKPKYSGRRPDAIRLGLGNHNYCRNPNRDRSKPCYVKA 195
QY 119 LKPLVQECNVHDCADG----- 134
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; sequence 26, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Deftrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
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; PRIOR APPLICATION NUMBER: US 60/391,777
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; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
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; LENGTH: 562
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; ORGANISM: Homo sapiens
; 10-411-026-26
Query Match 38.0%; Score 858.5; DB 12; Length 562;
Best Local Similarity 37.5%; Pred. No. 4.9e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
C 3 ELHQP-SNCD---CLNGGTCVSNKYFSNTHWCNCPKFGGQHCCEIDKSKTCYEGNGHPY 58
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C 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKNNYCRNPNRRRPPWCYVQVG 118
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RESULT 37
US-10-193-656-8
; Sequence 8, Application US/10193656
; Publication No. US20030096733A1
; GENERAL INFORMATION:
; APPLICANT: NY, Tor
; APPLICANT: HOLMDAHL, Rikard
; APPLICANT: Li, Jinan
; TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
; FILE REFERENCE: 3810/1J577-US3
; CURRENT APPLICATION NUMBER: US/10/193,656
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/304,461
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/304,490
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,182
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P00750
; DATABASE ENTRY DATE: 1986-07-21
; RELEVANT RESIDUES: (1)...(562)
US-10-193-656-8
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Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
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QY 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKNNYCRNPNRRRPPWCYVQVG 118
Db 136 RGTWSTAESGAECTNWNSSALAQPYSGRRPDAIRLGLGNHNYCRNPNDRDRSKPCYVFXA 195
QY 119 LKPLVQECNVHDCADG----- 134

196 GKYSSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNMSILIGKVYTAQNP 255
135 -----KLKFO-----CG-QKTLRPRFKIIGGE 155
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156 FTTIENQWFAIYRRH-RGGSVTVVCGGSLISPCWISATHCFIDYPKKEDYIVVLGRS 214
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215 RLNSNTGEMKFEVENLILHKDYSADTLAHNDIALKIRSKRCAQPSRTIOTICLPS 274
376 YRVVPGEEQKFEVEKYIVHKEFDDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPP 433
275 MYNDPQGTSCITGFKENSTDYLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCA 334
434 ADLQLPDWTCELSGYCKHEALSPFYSERLKEAHRVLPSSRCTSQHLLNRTVTDNMLCA 493
335 AD-----POWKT-DSCOGDSGGPLVCSLQGRMTLTGIVSWGRCALKDQPGVTVRVSHFL 388
494 GDTSGGPOANLHDACQDGGPLVCLNDGRMTLVGLIISWGLCGQKQDVGVTYKVTNYL 553
389 PWIRSHTK 396
554 DWIRDNR 561

LT 38
US 0-443-701-4
; quence 4, Application US/10443701
; blication No. US20030199016A1
; NERAL INFORMATION:
; PPLICANT: Xu, Yuan
; TLE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS
; ILE REFERENCE: P178981
; URRENT APPLICATION NUMBER: US/10/443,701
; URRENT FILING DATE: 2003-05-21
; RIOR APPLICATION NUMBER: US/09/703,695
; RIOR FILING DATE: 2000-11-01
; RIOR APPLICATION NUMBER: US 60/163,607
; RIOR FILING DATE: 1999-11-04
; UMBER OF SEQ ID NOS: 4
; Q ID NO 4
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US 0-443-701-4

ery Match 38.0%; Score 858.5; DB 14; Length 562;
st Local Similarity 37.5%; Pred. No. 4.9e-67;
atches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;

3 ELHOVP-SNCD--CLNGGTCSNKNYPSNIHWCNCPKFGGHCCEIDKSKTCYEGNGHFY 58
77 QCHSVPVKSCSEPRCFNGTQQALYFSDP-VCOCPGPGAGKCEIDTRATCYEDQGISY 135
59 RGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPMCVYQVG 118
136 RGTWSTAESGAECTWNSSALAKQPYSGRRPDALRLGLGNHNYCRNPNDRDSKPCWYVFXA 195
119 LKPLVQECWHDCCADG----- 134
196 KYISSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNMSILIGKVYTAQNP 255

135 -----KLKFO-----CG-QKTLRPRFKIIGGE 155
256 AQALGLGKHNYCRNPDGAKPWCHLVKRLTWEYCDVPCSTCGLRQYSQPOFRKGG 315
156 FTTIENQWFAIYRRH-RGGSVTVVCGGSLISPCWISATHCFIDYPKKEDYIVVLGRS 214
316 FADIASHPWQAIAFAKRRSPGERFLCGGILISSCWILSAHCFQERFPPHLLTVILGRT 375

215 RLNSNTGEMKFEVENLILHKDYSADTLAHNDIALKIRSKRCAQPSRTIOTICLPS 274
376 YRVVPGEEQKFEVEKYIVHKEFDDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPP 433
275 MYNDPQGTSCITGFKENSTDYLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCA 334
434 ADLQLPDWTCELSGYCKHEALSPFYSERLKEAHRVLPSSRCTSQHLLNRTVTDNMLCA 493
335 AD-----POWKT-DSCOGDSGGPLVCSLQGRMTLTGIVSWGRCALKDQPGVTVRVSHFL 388
494 GDTSGGPOANLHDACQDGGPLVCLNDGRMTLVGLIISWGLCGQKQDVGVTYKVTNYL 553
389 PWIRSHTK 396
554 DWIRDNR 561

RESULT 39
US-10-410-962-26
; Sequence 26, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Necose Technologies, Inc.
; APPLICANT: DePrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Caryn
; TITLE OF INVENTION: GLYCOCONJUGATE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 26
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-26

Query Match 38.0%; Score 858.5; DB 16; Length 562;
Best Local Similarity 37.5%; Pred. No. 4.9e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;

3 ELHOVP-SNCD--CLNGGTCSNKNYPSNIHWCNCPKFGGHCCEIDKSKTCYEGNGHFY 58
77 QCHSVPVKSCSEPRCFNGTQQALYFSDP-VCOCPGPGAGKCEIDTRATCYEDQGISY 135
59 RGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPMCVYQVG 118
136 RGTWSTAESGAECTWNSSALAKQPYSGRRPDALRLGLGNHNYCRNPNDRDSKPCWYVFXA 195
119 LKPLVQECWHDCCADG----- 134
196 KYISSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNMSILIGKVYTAQNP 255
135 -----KLKFO-----CG-QKTLRPRFKIIGGE 155

256 AQAALGLGKHNYCRNPDGDAKWPCHLVKRLTWEYCDVPSCTCGLRQYSQPOFRKGGGL 315
156 FTTIENQPFARAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGES 214
316 FADIASHPWQAIAFAKRRSPGERFICGGIILSSCWILSAHCFQERFPPHHLTUVILGRT 375
215 RLNSNTGEMKFEVENILHKDYSADTLAHNDIALKIRSKRGCAQPSRTIQTICLPS 274
376 YRVVPGESEKFEVEKIYVHKFPDDT--YNDNIALQLKSDSRCAQSSVVRTVCLPP 433
275 MYNDPQGTSCBITGFGKENSTDYLYPEQLKMTVVKLISHRECOQHYTGSEVTTMCLCA 334
434 ADLQLPDWTCELSGYKHEALSPFYSERLKEAHRVLYPSSRCTSQHLLNRTVTDNMLCA 493
335 AD-----PQWKT-DSCQDGGPLVCSLQGRMTLTGIVSMGRGCAKDKPGVYTRVSHFL 388
494 GDRSGGPGQANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 553
389 PWIRSHTK 396
554 DWIRDNMR 561

ULT 40
10-411-049-26
Sequence 26, Application US/10411049
Publication No. US20040082026A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Howe, Caryn
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
FILE REFERENCE: 040853-01-5055
CURRENT APPLICATION NUMBER: US/10/411,049
PRIOR FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR FILING DATE: 2001-10-19
PRIOR APPLICATION NUMBER: US 60/387,292
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: US 60/404,249
PRIOR FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 60/407,527
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn version 3.2
SEQ ID NO 26
LENGTH: 562
TYPE: PRT
ORGANISM: Homo sapiens
10-411-049-26

Query Match 38.08; Score 858.5; DB 16; Length 562;
Best Local Similarity 37.5%; Pred. No. 4.9e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
3 ELHQVP--SNCD---CLNGGTCVSNKYFSNIHWNCNCPKFGQCHCEIDKSKTCYEGNGHFY 58
77 QCHSVPVKSCSEPRCFNGTCCQALYFSDF-VQCPGFGAGKCCEDTATCYEDQGISY 135
59 RGKASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRPRPWCYVQVG 118

Db 136 RGTWSTAEGSAECTNWNSSALLAQKPYSGRRPDALRLGLGNHNYCRNPDNRDPSKWCYVFK 195
QY 119 LKPLVQECMVHDCADG-----KLKFO-----CG-QKTLRPRFKIIGGE 155
Db 196 KYSSSEFCSTFACSEGNSDCYFGNGSAVRGTHSITSGASCLPWNMILLIKSVYTAQNP 255
QY 135 -----KLKFO-----CG-QKTLRPRFKIIGGE 155
Db 256 AQAALGLGKHNYCRNPDGDAKWPCHLVKRLTWEYCDVPSCTCGLRQYSQPOFRKGGGL 315
QY 156 FTTIENQPFARAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGES 214
Db 316 FADIASHPWQAIAFAKRRSPGERFICGGIILSSCWILSAHCFQERFPPHHLTUVILGRT 375
QY 215 RLNSNTGEMKFEVENILHKDYSADTLAHNDIALKIRSKRGCAQPSRTIQTICLPS 274
Db 376 YRVVPGESEKFEVEKIYVHKFPDDT--YNDNIALQLKSDSRCAQSSVVRTVCLPP 433
QY 275 MYNDPQGTSCBITGFGKENSTDYLYPEQLKMTVVKLISHRECOQHYTGSEVTTMCLCA 334
Db 434 ADLQLPDWTCELSGYKHEALSPFYSERLKEAHRVLYPSSRCTSQHLLNRTVTDNMLCA 493
QY 335 AD-----PQWKT-DSCQDGGPLVCSLQGRMTLTGIVSMGRGCAKDKPGVYTRVSHFL 388
Db 494 GDRSGGPGQANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 553
QY 389 PWIRSHTK 396
Db 554 DWIRDNMR 561

RESULT 41
US-09-880-503-4
Sequence 4, Application US/09880503
Patent No. US20020131954A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-503-4

Query Match 35.1%; Score 793; DB 9; Length 135;
Best Local Similarity 100.0%; Pred. No. 5.1e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQVP--SNCDCLNGGTCVSNKYFSNIHWNCNCPKFGQCHCEIDKSKTCYEGNGHFYRG 60
Db 1 SNELHQVP--SNCDCLNGGTCVSNKYFSNIHWNCNCPKFGQCHCEIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
Db 61 KASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK 135
Db 121 PLVQECMVHDCADGK 135

RESULT 42
US-09-984-186-12
Sequence 12, Application US/09984186


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; Patent No. US20020151011A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;
; 9-984-186-12
;
; Query Match 35.1%; Score 793; DB 9; Length 138;
; Best Local Similarity 100.0%; Pred. No. 5.3e-62;
; Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SNELHQPNSCCLNGGTCVSNKYFSNHWNCNPKKFGQCHCEIDKSKTCYEGNGHFYRG 60
; DE 4 SNELHQPNSCCLNGGTCVSNKYFSNHWNCNPKKFGQCHCEIDKSKTCYEGNGHFYRG 63
;
; QY 61 KASTDTMGRPCLPWNSATVLQOTYHAHRSALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
; DE 64 KASTDTMGRPCLPWNSATVLQOTYHAHRSALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 123
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; QY 121 PLVQECMVHDCADGK 135
; DE 124 PLVQECMVHDCADGK 138
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; RESULT 44
; US-10-237-708-12
; Sequence 12, Application US/10237708
; Publication No. US20030036170A1
; GENERAL INFORMATION:

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; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,667
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;
; US-10-237-667-12
;
; Query Match 35.1%; Score 793; DB 14; Length 138;
; Best Local Similarity 100.0%; Pred. No. 5.3e-62;
; Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 SNELHQPNSCCLNGGTCVSNKYFSNHWNCNPKKFGQCHCEIDKSKTCYEGNGHFYRG 60
; DE 4 SNELHQPNSCCLNGGTCVSNKYFSNHWNCNPKKFGQCHCEIDKSKTCYEGNGHFYRG 63
;
; QY 61 KASTDTMGRPCLPWNSATVLQOTYHAHRSALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
; DE 64 KASTDTMGRPCLPWNSATVLQOTYHAHRSALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 123
;
; QY 121 PLVQECMVHDCADGK 135
; DE 124 PLVQECMVHDCADGK 138
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; RESULT 44
; US-10-237-708-12
; Sequence 12, Application US/10237708
; Publication No. US20030036170A1
; GENERAL INFORMATION:

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APPLICANT: Fleer, Reinhard
            Fournier, Alain
            Guitton, Jean-Dominique
            Jung, Gerard
            Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
                    PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
                    CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION: <UNKNOWN>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
10-237-708-12

Query Match          35.1%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
DB 4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 63
QY 61 KASDTMTGRPCLPNSATVLCQTYHAHRSALQLGLGKHNCRPNDRRRPWCYVOVGLK 120
DB 64 KASDTMTGRPCLPNSATVLCQTYHAHRSALQLGLGKHNCRPNDRRRPWCYVOVGLK 123
QY 121 PLVQECMVHDCADGK 135
DB 124 PLVQECMVHDCADGK 138

RESULT 46
US-10-237-866-12
; Sequence 12, Application US/10237866
; Publication No. US20030036172A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain

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Guillon, Jean-Dominique
Jung, Gerard
Yeh, Patricia
Yeh, Patricia
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,871
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph. D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US 0-237-871-12
Query Match 35.1%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 60
DE 4 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 63
QY 61 KASTDTMGRPCLPWNSATVLTQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLK 120
DI 64 KASTDTMGRPCLPWNSATVLTQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLK 123
QY 121 PLVQECMVHDCADGK 135
DI 124 PLVQECMVHDCADGK 138

US 0-237-624-12
Query Match 35.1%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 60
DI 4 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 63
QY 61 KASTDTMGRPCLPWNSATVLTQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLK 120
DI 64 KASTDTMGRPCLPWNSATVLTQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLK 123
QY 121 PLVQECMVHDCADGK 135
DI 124 PLVQECMVHDCADGK 138

US 0-237-536-12
Query Match 35.1%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 60
DI 4 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 63
QY 61 KASTDTMGRPCLPWNSATVLTQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLK 120
DI 64 KASTDTMGRPCLPWNSATVLTQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLK 123
QY 121 PLVQECMVHDCADGK 135
DI 124 PLVQECMVHDCADGK 138

Jung, Gerard
Yeh, Patricia
Yeh, Patricia
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph. D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:

US-10-237-624-12
Query Match 35.1%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 4 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 63
QY 61 KASTDTMGRPCLPWNSATVLTQTYHAHRSALQGLGKHNYCRPNDRRPPWCYVQVGLK 120
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QY 121 PLVQECMVHDCADGK 135
DB 124 PLVQECMVHDCADGK 138

US-10-237-536-12
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Best Local Similarity 100.0%; Pred. No. 5.3e-62;
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QY 1 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 60
DB 4 SNELHQPESNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 63
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DB 124 PLVQECMVHDCADGK 138

RESULT 48
US-10-702-536-12
; Sequence 12, Application US/10702536
; Publication No. US20040086976A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guillon, Jean-Dominique
; Jung, Gerard

Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/702,536
FILING DATE: 07-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-702-536-12
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Best Local Similarity 100.0%; Pred. No. 5.3e-62;
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D 4 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 63
Q 61 KASDTMTGRCLPWN SATVLQOYTHAHS DALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
D 64 KASDTMTGRCLPWN SATVLQOYTHAHS DALQLGLGKHNYCRNPNRRPWCYVQVGLK 123
Q 121 PLVQECMVHDCADGK 135
D 124 PLVQECMVHDCADGK 138
K ULT 49
U 10-702-636-12
Sequence 12, Application US/10702636
Publication No. US20040086977A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/702,536
FILING DATE: 07-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-702-536-12
Query Match 35.1%; Score 793; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 5.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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D 4 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 63
Q 61 KASDTMTGRCLPWN SATVLQOYTHAHS DALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
D 64 KASDTMTGRCLPWN SATVLQOYTHAHS DALQLGLGKHNYCRNPNRRPWCYVQVGLK 123
Q 121 PLVQECMVHDCADGK 135
D 124 PLVQECMVHDCADGK 138
K ULT 49
U 10-702-636-12
Sequence 12, Application US/10702636
Publication No. US20040086977A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice

;; CURRENT FILING DATE: 2001-06-13
;; RIOR APPLICATION NUMBER: US 60/212,847
;; RIOR FILING DATE: 2000-06-20
;; NUMBER OF SEQ ID NOS: 18
;; SOFTWARE: Patentin Ver. 2.1
;; 2 ID NO 8
;; LENGTH: 143
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US 9-880-503-8

37y Match 35.13; Score 793; DB 9; Length 143;
st Local Similarity 100.0%; Pred. No. 5.5e-62;
tches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 KASTDTMGRPCLPWSATVLOQTYHAHRS DALQLGLGKHN YCRNPDNRREPWCYQVGLK 120
DE 61 KASTDTMGRPCLPWSATVLOQTYHAHRS DALQLGLGKHN YCRNPDNRREPWCYQVGLK 120
QY 121 PLVQECMVHDCADGK 135
DE 121 PLVQECMVHDCADGK 135

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(protein - protein search, using sw model

on: May 25, 2004, 14:48:05 ; Search time 27.9027 Seconds
(without alignments)
745.636 Million cell updates/sec

le: US-09-880-503-6

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imum DB seq length: 2000000000

t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*

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5: /cgn2_6/ptodata/2/iaa/PTCUS COMB.pep.*

6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

ult No.	Score	Query Match	Length	DB ID	Description
1	2243.5	99.4	430	6	Patent No. 5219569-2
2	2243	99.4	411	1	Sequence 1, Appl
3	2243	99.4	411	1	Sequence 18, Appl
4	2243	99.4	411	1	Sequence 18, Appl
5	2243	99.4	431	4	Sequence 1, Appl
6	2243	99.4	431	6	Patent No. 5188829
7	2240	99.2	411	4	Sequence 2, Appl
8	2240	99.2	430	1	Sequence 3, Appl
9	2219	98.3	411	3	Sequence 1, Appl
10	2219	98.3	411	2	Sequence 46, Appl
11	1965	87.1	432	2	Sequence 47, Appl
12	1964	87.0	365	1	Sequence 83, Appl
13	1964	87.0	365	1	Sequence 83, Appl
14	1964	87.0	393	2	Sequence 24, Appl
15	1964	87.0	393	3	Sequence 24, Appl
16	1964	87.0	393	3	Sequence 25, Appl
17	1466.5	65.0	306	2	Sequence 45, Appl
18	1466.5	65.0	331	2	Sequence 46, Appl
19	1382	61.2	253	3	Sequence 73, Appl
20	1374	60.9	254	2	Sequence 49, Appl
21	983	43.6	200	4	Sequence 73, Appl
22	867.5	38.4	477	2	Sequence 51, Appl
23	865.5	38.3	527	2	Sequence 39, Appl
24	859.5	38.1	527	6	Patent No. 5520313
25	858.5	38.0	527	1	Sequence 16, Appl
26	858.5	38.0	527	5	Sequence 2, Appl
27	858.5	38.0	527	6	Patent No. 5185259

28	856.5	38.0	562	2	US-08-811-949-43	Sequence 43, Appl
29	856.5	38.0	562	2	US-08-560-098A-30	Sequence 50, Appl
30	856.5	38.0	562	2	US-08-883-795A-58	Sequence 38, Appl
31	856.5	38.0	562	4	US-09-703-695A-4	Sequence 4, Appl
32	856.5	38.0	562	6	5185259-3	Patent No. 5185259
33	858.5	38.0	562	6	5200340-2	Patent No. 5200340
34	858.5	38.0	562	6	5344773-2	Patent No. 5344773
35	851.5	37.7	562	6	5244676-5	Patent No. 5244676
36	825	36.6	157	3	US-08-142-590B-25	Sequence 25, Appl
37	808	35.8	355	2	US-08-811-949-59	Sequence 59, Appl
38	803	35.6	437	2	US-08-811-949-51	Sequence 51, Appl
39	800	35.4	437	2	US-08-811-949-57	Sequence 57, Appl
40	799	35.4	208	4	US-09-101-272G-98	Sequence 98, Appl
41	796	35.3	472	2	US-08-811-949-63	Sequence 63, Appl
42	793	35.1	138	2	US-08-797-689-12	Sequence 12, Appl
43	793	35.1	138	4	US-09-984-186-12	Sequence 12, Appl
44	793	35.1	437	2	US-08-811-949-55	Sequence 55, Appl
45	792	35.1	437	2	US-08-811-949-49	Sequence 49, Appl
46	791	35.0	355	2	US-08-811-949-47	Sequence 47, Appl
47	790	35.0	356	1	US-08-427-640-8	Sequence 8, Appl
48	788	34.9	194	4	US-09-101-272G-80	Sequence 80, Appl
49	788	34.9	201	4	US-09-101-272G-96	Sequence 96, Appl
50	786	34.8	378	4	US-09-553-498-10	Sequence 10, Appl
51	786	34.8	378	4	US-09-618-869-10	Sequence 10, Appl
52	784	34.7	355	1	US-08-137-116-1	Sequence 1, Appl
53	784	34.7	355	1	US-08-217-618-1	Sequence 1, Appl
54	784	34.7	355	1	US-08-427-640-2	Sequence 2, Appl
55	784	34.7	355	1	US-08-217-616-1	Sequence 1, Appl
56	784	34.7	355	1	US-08-217-616-1	Sequence 1, Appl
57	784	34.7	355	2	US-08-811-949-45	Sequence 45, Appl
58	784	34.7	355	3	US-08-794-528-1	Sequence 1, Appl
59	784	34.7	355	6	5232356-1	Patent No. 5232356
60	781	34.6	355	2	US-08-811-949-53	Sequence 53, Appl
61	780	34.6	389	2	US-08-811-949-67	Sequence 67, Appl
62	779	34.5	355	1	US-08-427-640-6	Sequence 6, Appl
63	779	34.5	389	2	US-08-811-949-65	Sequence 65, Appl
64	769.5	34.1	356	1	US-08-427-640-4	Sequence 4, Appl
65	766.5	34.0	354	2	US-08-811-949-61	Sequence 61, Appl
66	765.5	33.9	347	2	US-08-811-949-1	Sequence 1, Appl
67	726.5	32.2	655	1	US-08-148-910-12	Sequence 12, Appl
68	726.5	32.2	655	1	US-08-448-937A-12	Sequence 12, Appl
69	645	28.6	546	6	5200340-6	Patent No. 5200340
70	633.5	28.1	326	4	US-09-411-977-3	Sequence 3, Appl
71	583	25.8	383	2	US-08-558-269-6	Sequence 6, Appl
72	583	25.8	383	3	US-09-410-882-6	Sequence 6, Appl
73	565.5	25.1	253	2	US-09-027-337-8	Sequence 8, Appl
74	565.5	25.1	253	4	US-09-644-600-8	Sequence 8, Appl
75	565.5	25.1	253	4	US-09-654-600A-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
5219569-2
; Patent No. 5219569
; APPLICANT: ELABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
; GORDON A.
; TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,858
; FILING DATE: 16-AUG-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 725,468
; FILING DATE: 22-APR-1985
; SEQ ID NO:2:
; LENGTH: 430
5219569-2

Query Match 99.4%; Score 2243.5; DB 6; Length 430;
Best Local Similarity 98.3%; Pred. No. 4.3e-188;
Matches 403; Conservative 0; Mismatches 0; Indels 7; Gaps 1;

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21 SNELHVPNSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 80
61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRRPWCYVQVGLK 120
81 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRRPWCYVQVGLK 140
121 PLVQECMVHDCADGK-----LAFQCGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 173
141 PLVQECMVHDCADGKPPPELAFQCGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 200
174 GGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKEFEVENLIL 233
201 GGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKEFEVENLIL 260
234 HKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPOFGTSCEITGFGK 293
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294 NSTDLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPQWKTDCSQGDSGGPLV 353
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354 CSLOQRMTLTGIVSWGRGKALDKRPGVYTRVSHFLPWIRSHTKENGIAL 403
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RE LT 2
US 8-087-163-1
; Sequence 1, Application US/08087163
; Patent No. 5472632
; GENERAL INFORMATION:
; APPLICANT: Liu, Jian-Ning
; APPLICANT: Gurewicz, Victor
; TITLE OF INVENTION: PRO-UKINASE MUTANTS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/087,163
; FILING DATE: 07/02/93
; CLASSIFICATION: 514
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fasse, J. Peter
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04353/003001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411
; TYPE: amino acid
; STRANDEDNESS: N/A
; TOPOLOGY: N/A
; 8-087-163-1

Query Match 99.4%; Score 2243; DB 1; Length 411;
Best Local Similarity 98.1%; Pred. No. 4.4e-188;
Matches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
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DB 1 SNELHVPNSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRRPWCYVQVGLK 120
DB 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK-----LAFQCGOKTLRPRFKIIGGEFTTIENQWFAAIYRRH 172
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QY 173 RGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQGMKEFEVENLIL 232
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DB 241 LHKDYSADTLAHNDIALKIRSKGRCAQPSRTIQTICLPSMYNDPOFGTSCEITGFGK 300
QY 293 ENSTDLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPQWKTDCSQGDSGGPL 352
DB 301 ENSTDLYPEQLKMTVVKLISHRECOQPHYGVSEVTTKMLCAADPQWKTDCSQGDSGGPL 360
QY 353 VCSLOQRMTLTGIVSWGRGKALDKRPGVYTRVSHFLPWIRSHTKENGIAL 403
DB 361 VCSLOQRMTLTGIVSWGRGKALDKRPGVYTRVSHFLPWIRSHTKENGIAL 411

RESULT 3
US-08-286-748B-18
; Sequence 18, Application US/08286748B
; Patent No. 5759542
; GENERAL INFORMATION:
; APPLICANT: Victor Gurewicz
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
; TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
; TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,748B
; FILING DATE: August 5, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: J. Peter Fasse
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 04547/013001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:


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OTHER INFORMATION:
NAME/KEY: misc.feature
LOCATION: (20)...()
OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)
9-101-272G-1

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tches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

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QY 173 RGGSVTYVCGSLISPCWVISATHCFIDYPKKEDIYVYLGSRNSNTQGMKFEVENLI 232
Df 201 RGGSVTYVCGSLISPCWVISATHCFIDYPKKEDIYVYLGSRNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 292
Df 261 LHKDYSADTLAHHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 320
QY 293 ENSTDYLYPEOLKMTVVVKLIASHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 352
Df 321 ENSTDYLYPEOLKMTVVVKLIASHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 380
QY 353 VCSLQGRMTLTGIVSWGRGCALDKPGVYTVRVSHELFWIRSHTKBEENGLAL 403
Df 381 VCSLQGRMTLTGIVSWGRGCALDKPGVYTVRVSHELFWIRSHTKBEENGLAL 431

RE UT 6
51 929-1
Pf Ant No. 5188829
; APPLICANT: KOBAYASHI, YO-ICHI, OMORI, MUNEKI; YAMADA, CHIKAKO
; TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/340,007
; FILING DATE: 18-AUG-1988
; ID NO.1:
; LENGTH: 431.
51 829-1

ery Match 99.4%; Score 2243; DB 6; Length 431;
st Local Similarity 98.1%; Pred. No. 4.7e-188;
tches 403; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQPVSNCDCNLGGTGVSNKYFSNHWNCNCPKFGGQHCEDKSKTCYEGNGHFYRG 60
Df 21 SNELHQPVSNCDCNLGGTGVSNKYFSNHWNCNCPKFGGQHCEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDRRRPWCYVQVGLK 120
Df 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDRRRPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGBEFTTIENQFWFAAIYRRH 172
Df 141 PLVQECMVHDCADGKPKSSPPEELKFQCGQKTLRPRFKIIGBEFTTIENQFWFAAIYRRH 200
QY 173 RGGSVTYVCGSLISPCWVISATHCFIDYPKKEDIYVYLGSRNSNTQGMKFEVENLI 232
Df 201 RGGSVTYVCGSLISPCWVISATHCFIDYPKKEDIYVYLGSRNSNTQGMKFEVENLI 260
QY 233 LHKDYSADTLAHHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 292

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Db 261 LHKDYSADTLAHHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 320
QY 293 ENSTDYLYPEOLKMTVVVKLIASHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 352
Df 321 ENSTDYLYPEOLKMTVVVKLIASHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 380
QY 353 VCSLQGRMTLTGIVSWGRGCALDKPGVYTVRVSHELFWIRSHTKBEENGLAL 403
Df 381 VCSLQGRMTLTGIVSWGRGCALDKPGVYTVRVSHELFWIRSHTKBEENGLAL 431

RESULT 7
US-09-403-736-2
; Sequence 2, Application US/09403736
; Patent No. 6638502
; GENERAL INFORMATION:
; APPLICANT: Aventis S.A.
; APPLICANT: LI, Hong
; APPLICANT: LU, He
; APPLICANT: GRISCELLI, Frank
; APPLICANT: OPOLON, Paule
; APPLICANT: SORIA, Claudine
; APPLICANT: RAGOT, Thierry
; APPLICANT: LEGRAND, Yves
; APPLICANT: SORIA, Jeanette
; APPLICANT: MABILLAT, Christelle
; APPLICANT: FERRICAUDET, Michel
; APPLICANT: YEH, Patrice
; TITLE OF INVENTION: Adenovirus-Mediated Intratumoral Delivery Of An Angiogenesis Anta
; FILE REFERENCE: A2778A-US
; CURRENT APPLICATION NUMBER: US/09/403,736
; CURRENT FILING DATE: 1999-10-26
; PRIOR APPLICATION NUMBER: PCT/EP98/02491
; PRIOR FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 60/044,980
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: humanurokinase
US-09-403-736-2

Query Match 99.2%; Score 2240; DB 4; Length 411;
Best Local Similarity 97.8%; Pred. No. 8.1e-185;
Matches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

QY 1 SNELHQPVSNCDCNLGGTGVSNKYFSNHWNCNCPKFGGQHCEDKSKTCYEGNGHFYRG 60
Df 1 SNELHQPVSNCDCNLGGTGVSNKYFSNHWNCNCPKFGGQHCEDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDRRRPWCYVQVGLK 120
Df 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRNPDRRRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK-----LKFCGQKTLRPRFKIIGBEFTTIENQFWFAAIYRRH 172
Df 121 PLVQECMVHDCADGKPKSSPPEELKFQCGQKTLRPRFKIIGBEFTTIENQFWFAAIYRRH 180
QY 173 RGGSVTYVCGSLISPCWVISATHCFIDYPKKEDIYVYLGSRNSNTQGMKFEVENLI 232
Df 181 RGGSVTYVCGSLISPCWVISATHCFIDYPKKEDIYVYLGSRNSNTQGMKFEVENLI 240
QY 233 LHKDYSADTLAHHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 292
Df 241 LHKDYSADTLAHHNDIALLKIRSKGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFGK 300
QY 293 ENSTDYLYPEOLKMTVVVKLIASHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 352
Df 301 ENSTDYLYPEOLKMTVVVKLIASHRECQPHYGVSEVTTKMLCAADPQWKTDSCQDSGGPL 360

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353 VCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
 361 VCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

UNIT 8

07-942-157A-3
 Sequence 3, Application US/07942157A
 Patent No. 5648253
 GENERAL INFORMATION:
 APPLICANT: Wei, Cha-Mer
 TITLE OF INVENTION: Inhibitor-Resistant Urokinase
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kilpatrick & Cody
 STREET: 1100 Peachtree Street Suite 2800
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30309-4530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/942,157A

FILING DATE: 19920908
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/631673
 FILING DATE: 20-DEC-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Pabst, Patrea L.
 REGISTRATION NUMBER: 31,284
 REFERENCE/DOCKET NUMBER: TSI108Cont.

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404)815-6508

TELEFAX: (404)815-6555

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 430 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..19

OTHER INFORMATION: /label= peptide

OTHER INFORMATION: /note= "WAP signal"

FEATURE:

NAME/KEY: Modified-site

LOCATION: 198..203

OTHER INFORMATION: /label= modified

OTHER INFORMATION: /note= "six amino acids deleted in mutant"

07-942-157A-3

Query Match 99.2%; Score 2240; DB 1; Length 430;
 Best Local Similarity 97.8%; Pred. No. 8.6e-188;
 Matches 402; Conservative 1; Mismatches 0; Indels 8; Gaps 1;

1 SNELHQPNSCCLNGGTCVSNKYFSNIHCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60

20 SNELHQPNSCCLNGGTCVSNKYFSNIHCNCPKFGGQHCIDKSKTCYEGNGHFYRG 79

61 KASDTMGRPCLPWNATVLQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120

80 KASDTMGRPCLPWNATVLQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 139

121 PLVQECMVHDCADGK-----LKFCQCKTLRPRFKIIGGEFTTIENQPFPAIYRRH 172

Query Match 99.8%; Score 2233; DB 3; Length 411;
 Best Local Similarity 97.8%; Pred. No. 3.3e-187;
 Matches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

1 SNELHQPNSCCLNGGTCVSNKYFSNIHCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60

61 KASDTMGRPCLPWNATVLQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120

121 PLVQECMVHDCADGK-----LKFCQCKTLRPRFKIIGGEFTTIENQPFPAIYRRH 172

Query Match 99.8%; Score 2233; DB 3; Length 411;
 Best Local Similarity 97.8%; Pred. No. 3.3e-187;
 Matches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

1 SNELHQPNSCCLNGGTCVSNKYFSNIHCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60

61 KASDTMGRPCLPWNATVLQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120

121 PLVQECMVHDCADGK-----LKFCQCKTLRPRFKIIGGEFTTIENQPFPAIYRRH 172

Db 140 PLVQECMVHDCADGKFPSPPEELKFCQCKTLRPRFKIIGGEFTTIENQPFPAIYRRH 199
 QY 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQEMKFEVENLI 232
 Db 200 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQEMKFEVENLI 259
 QY 233 LHKDYSADTLAHHNDIALALKIRSKGRCAQPSRTIQTICLPSMYNDPQGTSCETGFGK 292
 Db 260 LHKDYSADTLAHHNDIALALKIRSKGRCAQPSRTIQTICLPSMYNDPQGTSCETGFGK 319
 QY 293 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPQWKTDSQQGDSGGPL 352
 Db 320 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPQWKTDSQQGDSGGPL 379
 QY 353 VCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFLPWIRSHTKENGLAL 403
 Db 380 VCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFLPWIRSHTKENGLAL 430

RESULT 9

US-09-181-816-1
 ; Sequence 1, Application US/09181816
 ; Patent No. 6277818
 ; GENERAL INFORMATION:
 ; APPLICANT: MAZAR, Andrew P.
 ; APPLICANT: JONES, Terence R.
 ; TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
 ; TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR
 ; FILE REFERENCE: 329042000300 SIDN 1-7
 ; CURRENT APPLICATION NUMBER: US/09/181,816
 ; CURRENT FILING DATE: 1998-10-29
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-181-816-1

Query Match 98.9%; Score 2233; DB 3; Length 411;
 Best Local Similarity 97.8%; Pred. No. 3.3e-187;
 Matches 402; Conservative 0; Mismatches 1; Indels 8; Gaps 1;

QY 1 SNELHQPNSCCLNGGTCVSNKYFSNIHCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60

Db 1 SNELHQPNSCCLNGGTCVSNKYFSNIHCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60

QY 61 KASDTMGRPCLPWNATVLQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120

Db 61 KASDTMGRPCLPWNATVLQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120

QY 121 PLVQECMVHDCADGK-----LKFCQCKTLRPRFKIIGGEFTTIENQPFPAIYRRH 172

Db 121 PLVQECMVHDCADGK-----LKFCQCKTLRPRFKIIGGEFTTIENQPFPAIYRRH 180

QY 173 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQEMKFEVENLI 232

Db 181 RGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRSLNSNTQEMKFEVENLI 240

QY 233 LHKDYSADTLAHHNDIALALKIRSKGRCAQPSRTIQTICLPSMYNDPQGTSCETGFGK 292

Db 241 LHKDYSADTLAHHNDIALALKIRSKGRCAQPSRTIQTICLPSMYNDPQGTSCETGFGK 300

QY 293 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPQWKTDSQQGDSGGPL 352

Db 301 ENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCAADPQWKTDSQQGDSGGPL 360

QY 353 VCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFLPWIRSHTKENGLAL 403

Db 361 VCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFLPWIRSHTKENGLAL 411

RESULT 10

US 8-560-098A-48
 Query 48: Application US/08560098A
 Patent No. 5976841
 GENERAL INFORMATION:
 APPLICANT: WNEUDT, Stephan
 APPLICANT: HEINZEL-WIELAND, Regina
 APPLICANT: STEFFENS, Gerd Josef
 TITLE OF INVENTION: Proteins having Fibrinolytic and
 TITLE OF INVENTION: Coagulation-inhibiting Properties
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/560,098A
 FILING DATE: 17-NOV-1995
 PRIOR APPLICATION NUMBER: P 44 40 892.7
 FILING DATE: 17-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D.
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 148/42448
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 411 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 8-560-098A-48

Query Match 98.3%; Score 2219; DB 2; Length 411;
 Best Local Similarity 97.3%; Pred. No. 5.6e-186;
 Matches 400; Conservative 0; Mismatches 3; Indels 8; Gaps 1;
 1 SNELHVPNSDCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHPIRG 60
 1 SNELHVPNSDCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHPIRG 60
 61 KASDTMGRPCLPNSATVLQOTYHAHRSALQGLGKHNYCRPNRRPWCYVQVGLK 120
 61 KASDTMGRPCLPNSATVLQOTYHAHRSALQGLGKHNYCRPNRRPWCYVQVGLK 120
 121 PLVQECMVHDCADK-----LKFCGQKTLRPFKIIIGGEFTTIENQFWFAALYRRH 172
 121 PLVQECMVHDCADK-----LKFCGQKTLRPFKIIIGGEFTTIENQFWFAALYRRH 180
 173 RGGSVTVVCGGSLSPCWVISAHCIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 232
 181 RGGSVTVVCGGSLSPCWVISAHCIDYPKKEDYIVLGRSLNSNTQGMKFEVENLI 240
 233 LHKDYSADTLAHNDIALLKIRSEGRCAQPSRTIOTICLPMSYNDPQFGTSCITGFGK 292
 241 LHKDYSADTLAHNDIALLKIRSEGRCAQPSRTIOTICLPMSYNDPQFGTSCITGFGK 300
 293 ENSDYLYPEOLKMTVVKLISHRECQPHYGVSVTTKMLCAADPQWKTDSCQDGGPL 352
 301 ENSDYLYPEOLKMTVVKLISHRECQPHYGVSVTTKMLCAADPQWKTDSCQDGGPL 360
 353 VCSLQGRMTLTGIVSWGRGCKALDKPGVYTRVSHFLPWIRSHTKENGIAL 403

Db 361 VCSLQGRMTLTGIVSWGRGCKALDKPGVYTRVSHFLPWIRSHTKENGIAL 411
 RESULT 11
 US-08-560-098A-47
 Sequence 47: Application US/08560098A
 Patent No. 5976841
 GENERAL INFORMATION:
 APPLICANT: WNEUDT, Stephan
 APPLICANT: HEINZEL-WIELAND, Regina
 APPLICANT: STEFFENS, Gerd Josef
 TITLE OF INVENTION: Proteins having Fibrinolytic and
 TITLE OF INVENTION: Coagulation-inhibiting Properties
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/560,098A
 FILING DATE: 17-NOV-1995
 PRIOR APPLICATION NUMBER: P 44 40 892.7
 FILING DATE: 17-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D.
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 148/42448
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 432 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-560-098A-47

Query Match 87.1%; Score 1965; DB 2; Length 432;
 Best Local Similarity 90.5%; Pred. No. 9.5e-164;
 Matches 361; Conservative 8; Mismatches 16; Indels 14; Gaps 2;
 QY 13 CLNGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHPIRGKASTDTMGRPCL 72
 Db 40 CVTGEPTKPSHNNNGDFFEEIPEY-----LQISKTCYEGNGHPIRGKASTDTMGRPCL 93
 QY 73 PWSATVLQOTYHAHRSALQGLGKHNYCRPNRRPWCYVQVGLKPLVQECMVHDC 132
 Db 94 PWSATVLQOTYHAHRSALQGLGKHNYCRPNRRPWCYVQVGLKPLVQECMVHDC 153
 QY 133 DCK-----LKFCGQKTLRPFKIIIGGEFTTIENQFWFAALYRRHGGSVTVVCGGS 184
 Db 154 DGKFPSPPEELKFCGQKTLRPFKIIIGGEFTTIENQFWFAALYRRHGGSVTVVCGGS 213
 QY 185 LISPQCVWISAHCIDYPKKEDYIVLGRSLNSNTQGMKFEVENLIHKDYADTLAH 244
 Db 214 LISPQCVWISAHCIDYPKKEDYIVLGRSLNSNTQGMKFEVENLIHKDYADTLAH 273
 QY 245 HNDIALLKIRSEGRCAQPSRTIOTICLPMSYNDPQFGTSCITGFGKENSTDYLYPEOL 304
 Db 274 HNDIALLKIRSEGRCAQPSRTIOTICLPMSYNDPQFGTSCITGFGKENSTDYLYPEOL 333

C 305 KMTVVKLISHRECOPHYGSEVTTKMLCAADPOWKTDSQCGDSGGPLVCSLQGRMTLTG 364
| | | | |
E 334 KMTVVKLISHRECOPHYGSEVTTKMLCAADPOWKTDSQCGDSGGPLVCSLQGRMTLTG 393
| | | | |
C 365 IVSWGRGKALDKPGVYTRVSHFLPWIRSHTKENGLAL 403
| | | | |
E 394 IVSWGRGKALDKPGVYTRVSHFLPWIRSHTKENGLAL 432
| | | | |
F JUL 12
| 08-093-741-83
| sequence 83, Application US/08093741
| Patent No. 5681721
| GENERAL INFORMATION:
| APPLICANT: STEPPENS, GERT J.
| APPLICANT: WENDT, STEPHAN
| APPLICANT: SCHNEIDER, JOHANNES
| APPLICANT: HEINZEL-WIELAND, REGINA
| APPLICANT: SAUNDERS, DEREK J.
| TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
| TITLE OF INVENTION: INHIBITING EFFECT
| NUMBER OF SEQUENCES: 83
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
| STREET: 1200 G Street, N. W. Suite 700
| CITY: Washington, D.C.
| COUNTRY: U.S.
| ZIP: 20005
| COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC compatible
| OPERATING SYSTEM: PC-DOS/MS-DOS
| SOFTWARE: Patent In Release #1.0, Version #1.25
| CURRENT APPLICATION DATA:
| APPLICATION NUMBER: US/08/093,741
| FILING DATE: 20-JUL-1993
| CLASSIFICATION: 435
| PRIOR APPLICATION DATA:
| APPLICATION NUMBER: DE P43 23 754.1
| FILING DATE: 15-JUL-1993
| ATTORNEY/AGENT INFORMATION:
| NAME: EVANS, Joseph D.
| REGISTRATION NUMBER: 26,269
| REFERENCE/DOCKET NUMBER: 148/41345
| TELEPHONE: (202)628-8800
| TELEFAX: (202)628-8844
| INFORMATION FOR SEQ ID NO: 83:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 365 amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| 08-093-741-83
|
| Query Match 87.0%; Score 1964; DB 1; Length 365;
| Best Local Similarity 97.8%; Pred. No. 9.4e-164;
| Matches 357; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
|
C 47 SKTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPD 106
| | | | |
D 1 SKTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPD 60
| | | | |
C 107 NRRRPWCYVQVGLKPLVQECWHDGADGK-----LKFCQCKTLRPFKLIIGSEFTT 158
| | | | |
D 61 NRRRPWCYVQVGLKPLVQECWHDGADGKPKSPPEELKFQCGQKTLRPFKLIIGSEFTT 120
| | | | |
C 159 IENQWPFAIYRRHGGSVTYVCGSLISPCWVISAATHCFIDYPKKEDYIVVLGSRSLNS 218
| | | | |
D 121 IENQWPFAIYRRHGGSVTYVCGSLISPCWVISAATHCFIDYPKKEDYIVVLGSRSLNS 180
| | | | |
C 219 NTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSEGRCAQPSRTIQTICLPSMYND 278
| | | | |

DB 181 NTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSEGRCAQPSRTIQTICLPSMYND 240
| | | | |
QY 279 POFGSCETITGFKENSTDYLYPEOLKMTVVKLISHRECOPHYGSEVTTKMLCAADPO 338
| | | | |
DB 241 POFGSCETITGFKENSTDYLYPEOLKMTVVKLISHRECOPHYGSEVTTKMLCAADPO 300
| | | | |
QY 339 WKTDSCQDSGGPLVCSLQGRMTLTGIVSWGRGKALDKPGVYTRVSHFLPWIRSHTKEE 398
| | | | |
DB 301 WKTDSCQDSGGPLVCSLQGRMTLTGIVSWGRGKALDKPGVYTRVSHFLPWIRSHTKEE 360
| | | | |
QY 399 NGLAL 403
| | | | |
DB 361 NGLAL 365
| | | | |
RESULT 13
US-08-720-012-83
| Sequence 83, Application US/08720012
| Patent No. 5747291
| GENERAL INFORMATION:
| APPLICANT: STEPPENS, GERT J.
| APPLICANT: WENDT, STEPHAN
| APPLICANT: SCHNEIDER, JOHANNES
| APPLICANT: HEINZEL-WIELAND, REGINA
| APPLICANT: SAUNDERS, DEREK J.
| TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
| TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
| TITLE OF INVENTION: INHIBITING EFFECT
| NUMBER OF SEQUENCES: 83
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
| STREET: 1200 G Street, N. W. Suite 700
| CITY: Washington, D.C.
| COUNTRY: U.S.
| ZIP: 20005
| COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC compatible
| OPERATING SYSTEM: PC-DOS/MS-DOS
| SOFTWARE: Patent In Release #1.0, Version #1.25
| CURRENT APPLICATION DATA:
| APPLICATION NUMBER: US/08/720,012
| FILING DATE: 27-SEP-1996
| CLASSIFICATION: 435
| PRIOR APPLICATION DATA:
| APPLICATION NUMBER: US 08/093,741
| FILING DATE: 20-JUL-1993
| APPLICATION NUMBER: DE P43 23 754.1
| FILING DATE: 15-JUL-1993
| ATTORNEY/AGENT INFORMATION:
| NAME: EVANS, Joseph D.
| REGISTRATION NUMBER: 26,269
| REFERENCE/DOCKET NUMBER: 148/41345
| TELECOMMUNICATION INFORMATION:
| TELEPHONE: (202)628-8800
| TELEFAX: (202)628-8844
| INFORMATION FOR SEQ ID NO: 83:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 365 amino acids
| TYPE: amino acid
| TOPOLOGY: linear
| US-08-720-012-83
|
| Query Match 87.0%; Score 1964; DB 1; Length 365;
| Best Local Similarity 97.8%; Pred. No. 9.4e-164;
| Matches 357; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
|
QY 47 SKTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPD 106
| | | | |
DB 1 SKTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPD 60
| | | | |
QY 107 NRRRPWCYVQVGLKPLVQECWHDGADGK-----LKFCQCKTLRPFKLIIGSEFTT 158
| | | | |

DE 61 NRRPWCYVQVGLKPLVQECWVHDCADGKPPPEELKFCQGTLPFRPKIIGGEFTT 120
QY 159 IENQWFAAIYRRHRGGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYVLSRLNS 218
DE 121 IENQWFAAIYRRHRGGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYVLSRLNS 180
QY 219 NTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGRCAPSRITQICLPSMYND 278
DE 181 NTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGRCAPSRITQICLPSMYND 240
QY 279 POFGTSCEITGFGKENSIDYLPKQKMTVVKLISHRECOQPHYVYGVSEVITKMLCAADPO 338
DE 241 POFGTSCEITGFGKENSIDYLPKQKMTVVKLISHRECOQPHYVYGVSEVITKMLCAADPO 300
QY 339 WKTDCQDSDGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 398
DE 301 WKTDCQDSDGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 360
QY 399 NGLAL 403
DE 361 NGLAL 365

RE LT 14
US 3-560-098A-44
; Sequence 44, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WNEBNT, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 3-560-098A-44

ery Match 87.0%; Score 1964; DB 2; Length 393;
st Local Similarity 97.8%; Pred No. 1e-163;
tches 357; Conservative 0; Mismatches 0; Indels 8; Gaps 1;
47 SKTYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPD 106

Db 2 SKTYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPD 61
QY 107 NRRPWCYVQVGLKPLVQECWVHDCADGK-----LKFCQGTLPFRPKIIGGEFTT 158
Db 62 NRRPWCYVQVGLKPLVQECWVHDCADGKPPPEELKFCQGTLPFRPKIIGGEFTT 121
QY 159 IENQWFAAIYRRHRGGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYVLSRLNS 218
Db 122 IENQWFAAIYRRHRGGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYVLSRLNS 181
QY 219 NTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGRCAPSRITQICLPSMYND 278
Db 182 NTQGMKFEVENLILHKDYSADTLAHNDIALLKIRSKEGRCAPSRITQICLPSMYND 241
QY 279 POFGTSCEITGFGKENSIDYLPKQKMTVVKLISHRECOQPHYVYGVSEVITKMLCAADPO 338
Db 242 POFGTSCEITGFGKENSIDYLPKQKMTVVKLISHRECOQPHYVYGVSEVITKMLCAADPO 301
QY 339 WKTDCQDSDGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 398
Db 302 WKTDCQDSDGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE 361
QY 399 NGLAL 403
Db 362 NGLAL 366

RESULT 15
US-08-967-024C-24
; Sequence 24, Application US/08967024C
; Patent No. 6133011
; GENERAL INFORMATION:
; APPLICANT: WNEBNT, Stephan
; APPLICANT: STEFFENS, Gerd Josef
; APPLICANT: JANOSHA, Elke
; APPLICANT: HEINZEL-WIELAND, Regina
; TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/967,024C
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 42 665.8
; FILING DATE: 30-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42444
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-967-024C-24

```
Query Match          87.0%; Score 1964; DB 3; Length 393;
Best Local Similarity 97.8%; Pred. No. 1e-163;
Matches 357; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

47 SKTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQLGLGKHNYCRNPD 106
2 SKTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQLGLGKHNYCRNPD 61
107 NRRRPWCYVQVGLKPLVQECWVHDCADGK-----LKFCQCGKTLRPRFKIIGGEFTT 158
62 NRRRPWCYVQVGLKPLVQECWVHDCADGK-----LKFCQCGKTLRPRFKIIGGEFTT 121
159 IENQPFMAAAYRRHRGGSVTVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRRLNS 218
122 IENQPFMAAAYRRHRGGSVTVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRRLNS 181
219 NTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIOTICLPSMYND 278
182 NTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIOTICLPSMYND 241
279 PQFGTSCIEITGFGKENSVDLYPEQLKMTVVKLISHRECQCPHYGSEVTTKMLCAADPQ 338
242 PQFGTSCIEITGFGKENSVDLYPEQLKMTVVKLISHRECQCPHYGSEVTTKMLCAADPQ 301
339 WKTDSCQSGGGLVCSLOGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKKEE 398
302 WKTDSCQSGGGLVCSLOGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKKEE 361
399 NGLAL 403
362 NGLAL 366

ULT 16
US-09-880-503-6.ra1
Sequence 25, Application US/08967024C
Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: WENNDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOSHA, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
```

```
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-024C-25

Query Match          87.0%; Score 1964; DB 3; Length 393;
Best Local Similarity 97.8%; Pred. No. 1e-163;
Matches 357; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

47 SKTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQLGLGKHNYCRNPD 106
2 SKTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQLGLGKHNYCRNPD 61
107 NRRRPWCYVQVGLKPLVQECWVHDCADGK-----LKFCQCGKTLRPRFKIIGGEFTT 158
62 NRRRPWCYVQVGLKPLVQECWVHDCADGK-----LKFCQCGKTLRPRFKIIGGEFTT 121
159 IENQPFMAAAYRRHRGGSVTVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRRLNS 218
122 IENQPFMAAAYRRHRGGSVTVCGGSLISPCWVISATHCFIDYPKKEDYIVYLGSRRLNS 181
219 NTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIOTICLPSMYND 278
182 NTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCACQPSRTIOTICLPSMYND 241
279 PQFGTSCIEITGFGKENSVDLYPEQLKMTVVKLISHRECQCPHYGSEVTTKMLCAADPQ 338
242 PQFGTSCIEITGFGKENSVDLYPEQLKMTVVKLISHRECQCPHYGSEVTTKMLCAADPQ 301
339 WKTDSCQSGGGLVCSLOGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKKEE 398
302 WKTDSCQSGGGLVCSLOGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKKEE 361
399 NGLAL 403
362 NGLAL 366

RESULT 17
US-08-560-098A-45
Sequence 45, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WENNDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
```

TELEPHONE: (202) 628-8844
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 45:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 306 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-560-098A-45

Query Match 65.0%; Score 1466.5; DB 2; Length 306;
 Best Local Similarity 91.1%; Pred. No. 2.3e-120;
 Matches 275; Conservative 6; Mismatches 12; Indels 9; Gaps 3;

103 RNPONRRRP-WCYVQVGLKPLVQECMVHDCADGKLFQCCGQKTLRPRFKIIGGEFTTIE 161
 13 RNPNDKYEPPFWEDEKSG-PMSS-----PPELKFQCCGQKTLRPRFKIIGGEFTTIE 64
 162 QPWFPAAYRRHRGGSVTVVCGGSLISPCWVISATFCFIDYPKKEDYIVVLRGRSLNSNTQ 221
 65 QPWFPAAYRRHRGGSVTVVCGGSLISPCWVISATFCFIDYPKKEDYIVVLRGRSLNSNTQ 124
 222 GEMKFEVENLILHKDYADTLAHNDIALKIRSKGRCQAPSTTICTICLPSMYNDPQF 281
 125 GEMKFEVENLILHKDYADTLAHNDIALKIRSKGRCQAPSTTICTICLPSMYNDPQF 184
 282 GTSCEITGFGKENSVDLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTKMLCAADPQWKT 341
 185 GTSCEITGFGKENSVDLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTKMLCAADPQWKT 244
 342 DSCQDGGGLVCSLQGRMTLTGIVSWGRGKALKDQKPGVYTRVSHFLPWIRSHTKENGL 401
 245 DSCQDGGGLVCSLQGRMTLTGIVSWGRGKALKDQKPGVYTRVSHFLPWIRSHTKENGL 304
 402 AL 403
 305 AL 306

US-560-098A-46
 Query Match 65.0%; Score 1466.5; DB 2; Length 306;
 Best Local Similarity 91.1%; Pred. No. 2.3e-120;
 Matches 275; Conservative 6; Mismatches 12; Indels 9; Gaps 3;

103 RNPONRRRP-WCYVQVGLKPLVQECMVHDCADGKLFQCCGQKTLRPRFKIIGGEFTTIE 161
 13 RNPNDKYEPPFWEDEKSG-PMSS-----PPELKFQCCGQKTLRPRFKIIGGEFTTIE 64
 162 QPWFPAAYRRHRGGSVTVVCGGSLISPCWVISATFCFIDYPKKEDYIVVLRGRSLNSNTQ 221
 65 QPWFPAAYRRHRGGSVTVVCGGSLISPCWVISATFCFIDYPKKEDYIVVLRGRSLNSNTQ 124
 222 GEMKFEVENLILHKDYADTLAHNDIALKIRSKGRCQAPSTTICTICLPSMYNDPQF 281
 125 GEMKFEVENLILHKDYADTLAHNDIALKIRSKGRCQAPSTTICTICLPSMYNDPQF 184
 282 GTSCEITGFGKENSVDLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTKMLCAADPQWKT 341
 185 GTSCEITGFGKENSVDLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTKMLCAADPQWKT 244
 342 DSCQDGGGLVCSLQGRMTLTGIVSWGRGKALKDQKPGVYTRVSHFLPWIRSHTKENGL 401
 245 DSCQDGGGLVCSLQGRMTLTGIVSWGRGKALKDQKPGVYTRVSHFLPWIRSHTKENGL 304
 402 AL 403
 305 AL 306

TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 331 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-560-098A-46

Query Match 65.0%; Score 1466.5; DB 2; Length 331;
 Best Local Similarity 91.1%; Pred. No. 2.6e-120;
 Matches 275; Conservative 6; Mismatches 12; Indels 9; Gaps 3;

103 RNPONRRRP-WCYVQVGLKPLVQECMVHDCADGKLFQCCGQKTLRPRFKIIGGEFTTIE 161
 13 RNPNDKYEPPFWEDEKSG-PMSS-----PPELKFQCCGQKTLRPRFKIIGGEFTTIE 64
 162 QPWFPAAYRRHRGGSVTVVCGGSLISPCWVISATFCFIDYPKKEDYIVVLRGRSLNSNTQ 221
 65 QPWFPAAYRRHRGGSVTVVCGGSLISPCWVISATFCFIDYPKKEDYIVVLRGRSLNSNTQ 124
 222 GEMKFEVENLILHKDYADTLAHNDIALKIRSKGRCQAPSTTICTICLPSMYNDPQF 281
 125 GEMKFEVENLILHKDYADTLAHNDIALKIRSKGRCQAPSTTICTICLPSMYNDPQF 184
 282 GTSCEITGFGKENSVDLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTKMLCAADPQWKT 341
 185 GTSCEITGFGKENSVDLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTKMLCAADPQWKT 244
 342 DSCQDGGGLVCSLQGRMTLTGIVSWGRGKALKDQKPGVYTRVSHFLPWIRSHTKENGL 401
 245 DSCQDGGGLVCSLQGRMTLTGIVSWGRGKALKDQKPGVYTRVSHFLPWIRSHTKENGL 304
 402 AL 403
 305 AL 306

US-08-944-483-73
 Sequence 73, Application US/08944483
 Patent No. 6232456
 GENERAL INFORMATION:
 APPLICANT: COHEN, MAURICE
 APPLICANT: COLPITTS, TRACEY L.
 APPLICANT: FRIEDMAN, PAULA N.
 APPLICANT: GRANADOS, EDWARD N.
 APPLICANT: KLASS, MICHAEL R.
 APPLICANT: RUSSELL, JOHN C.
 APPLICANT: STEWART, KENT D.
 APPLICANT: STROUPE, STEVEN D.
 TITLE OF INVENTION: NOVEL SERINE PROTEASE REAGENTS
 TITLE OF INVENTION: AND METHODS USEFUL FOR DETECTING AND TREATING DISEASES
 NUMBER OF SEQUENCES: 76
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/944,483
 FILING DATE:
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6183.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6232456e
US-944-483-73

Query Match 61.2%; Score 1382; DB 3; Length 253;
Best Local Similarity 100.0%; Pred. No. 4.4e-113;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

151 IIGGEFTTIENQPFFAAIYRRHGGSVTYVCGSLISPCWVISATHCFIDYPKEDYIV 210
1 IIGGEFTTIENQPFFAAIYRRHGGSVTYVCGSLISPCWVISATHCFIDYPKEDYIV 60

211 LGRSLNSNTQGMKFEVENLIHLKDYSDATLAHNDIALLKIRSKEGRCAQPSRTIQT 270
61 LGRSLNSNTQGMKFEVENLIHLKDYSDATLAHNDIALLKIRSKEGRCAQPSRTIQT 120

271 CLPSMYNDPFGTSCETITGFGKENSVDLYPEQLKMTVVKLIHSHRECCQPHYGVSEVTT 330
121 CLPSMYNDPFGTSCETITGFGKENSVDLYPEQLKMTVVKLIHSHRECCQPHYGVSEVTT 180

331 MLCRAADPQWKTDCQGDGSGPLVCSLQGRMTLTGIVSWGRCALDKKPGVYTVRSHFLP 390
181 MLCRAADPQWKTDCQGDGSGPLVCSLQGRMTLTGIVSWGRCALDKKPGVYTVRSHFLP 240

391 IRSHTKEENGLAL 403
241 IRSHTKEENGLAL 253

US-944-483-73

Query Match 60.9%; Score 1374; DB 2; Length 254;
Best Local Similarity 99.2%; Pred. No. 2.2e-112;
Matches 252; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

150 KIIGGEFTTIENQPFFAAIYRRHGGSVTYVCGSLISPCWVISATHCFIDYPKEDYIV 209
1 KIIGGEFTTIENQPFFAAIYRRHGGSVTYVCGSLISPCWVISATHCFIDYPKEDYIV 60

210 YLGRSLNSNTQGMKFEVENLIHLKDYSDATLAHNDIALLKIRSKEGRCAQPSRTIQT 269
61 YLGRSLNSNTQGMKFEVENLIHLKDYSDATLAHNDIALLKIRSKEGRCAQPSRTIQT 120

270 ICLPSMYNDPFGTSCETITGFGKENSVDLYPEQLKMTVVKLIHSHRECCQPHYGVSEVTT 329
121 ICLPSMYNDPFGTSCETITGFGKENSVDLYPEQLKMTVVKLIHSHRECCQPHYGVSEVTT 180

330 KMLCAADPQWKTDCQGDGSGPLVCSLQGRMTLTGIVSWGRCALDKKPGVYTVRSHFLP 389
181 KMLCAADPQWKTDCQGDGSGPLVCSLQGRMTLTGIVSWGRCALDKKPGVYTVRSHFLP 240

390 WIRSHTKEENGLAL 403
241 WIRSHTKEENGLAL 254

US-09-101-272G-73

Query Match 43.6%; Score 983; DB 4; Length 200;
Best Local Similarity 95.6%; Pred. No. 2.5e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

1 SNELHQVPSNCDCLNGTGVSNKYFNSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 60
21 SNELHQVPSNCDCLNGTGVSNKYFNSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 80

US-09-101-272G-73

Query Match 43.6%; Score 983; DB 4; Length 200;
Best Local Similarity 95.6%; Pred. No. 2.5e-78;
Matches 172; Conservative 0; Mismatches 0; Indels 8; Gaps 1;

1 SNELHQVPSNCDCLNGTGVSNKYFNSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 60
21 SNELHQVPSNCDCLNGTGVSNKYFNSNIHWCNCPKFGQHCIDKSKTCYEGNGHYRG 80

QY 61 KASDTNMGRCPLPWNSTVLTQYTHAHSRDLQGLGKHNCRPNDRRRPWCYVQVGLK 120
 DB 81 KASDTNMGRCPLPWNSTVLTQYTHAHSRDLQGLGKHNCRPNDRRRPWCYVQVGLK 140
 QY 121 PLVQECNVHDCADGK-----LKPCGCKTLRPRFKIIGGFTTIENQPHFAIYRHH 172
 DE 141 PLVQECNVHDCADGKPPSPBELKPCGCKTLRPRFKIIGGFTTIENQPHFAIYRHH 200

RE 22
 US 3-560-098A-51
 ; Quence 51, Application US/08560098A
 ; Tent No. 5978841
 ; GENERAL INFORMATION:
 ; APPLICANT: WENDET, Stephan
 ; APPLICANT: HEINZEL-WIELAND, Regina
 ; APPLICANT: STEFFENS, Gerd Josef
 ; TITLE OF INVENTION: Proteins having Fibrinolytic and
 ; TITLE OF INVENTION: Coagulation-inhibiting Properties
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
 ; STREET: 1200 G Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/560,098A
 ; FILING DATE: 17-NOV-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: P 44 40 892.7
 ; FILING DATE: 17-NOV-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: EVANS, Joseph D.
 ; REGISTRATION NUMBER: 26,269
 ; REFERENCE/DOCKET NUMBER: 148/42448
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-8800
 ; TELEFAX: (202) 628-8844
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 477 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; 8-560-098A-51
 ;
 ; Query Match 38.4%; Score 867.5; DB 2; Length 477;
 ; Best Local Similarity 43.7%; Pred. No. 9.4e-58;
 ; Matches 178; Conservative 60; Mismatches 148; Indels 21; Gaps 9;
 ;
 ; 3 ELHQVP----SNCDLNGGTCVANKYFNSNTHWNCNPKFGGHCIDKSKTCYEGNGHPY 58
 ; 78 QCHTVPVKSCSELRCFNGGTCWQAASFDF-VQCPCPKGYTGKQCEVDTHATCYKDGVTY 136
 ;
 ; 59 RGRKASTDTMGRCPLPWNSTVLTQYTHAHSRDLQGLGKHNCRPNDRRRPWCYVQV 118
 ; 137 RGTWSTSESAQCINMNSNLTARTYNGRSDAITLGLGNHNYCRPNDRNNKFCWCVIKA 196
 ; 119 LKPLVQECNVHDCADGKLFQCG-QKTLRPRFKIIGGFTTIENQPHFAIYRHHRGG- 176
 ; 197 SKFILECSPVPCS---KATCGLRKYKEPOLHSTGGLFTDITSHPWQAAIIPAQRSSG 252
 ; 177 VTYVCGSLSPCWVIGATHCFTD-YPKKEDIYVIGRSLNNTQGENKFEVENILHK 235
 ; 253 ERFICGGILLISSCWLVTAACHFOBRYPQHLRWV-LGRTYRVKPGKEBOTFEVEKCI 311

QY 236 DYSADTLAHNDIALKIRSKRGCAQPSRTIOTICLPSMYNDPQFCTSCITGFGKENS 295
 DB 312 EFDDDT--YNDIALLOKSGSPQCAQESDVRAICLPEANLQLPDWTECELSGVGXHS 369
 QY 296 TDYLYPQLKMTVVKLISHRECOQPHYGVSEVITKMLCAADPOWKT-----DSCQDSDG 349
 DB 370 SSFPYSEQLKEGHVRLYPSRCSKFLFNKTVTKNMLCAGDTSRSGEIHFNWHDACQDSDG 429
 QY 350 GPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPFWIRSHK 396
 DB 430 GPLVCRNDNEMTLGIISWGVGCGEKDIPGVYTKVNYLGNIRDNMR 476

RESULT 23
 US-08-811-949-39
 ; Sequence 39, Application US/08811949
 ; Patent No. 5840533
 ; GENERAL INFORMATION:
 ; APPLICANT: NIMA, MINEO
 ; APPLICANT: SAITO, YOSHIMASA
 ; APPLICANT: SASAKI, HITOSHI
 ; APPLICANT: HAYASHI, MASAKO
 ; APPLICANT: NOTANI, JOUJI
 ; APPLICANT: KOBAYASHI, MASAKAZU
 ; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
 ; NUMBER OF SEQUENCES: 67
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
 ; ADDRESSEE: P.C.
 ; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 ; CITY: ARLINGTON
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22202
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/811,949
 ; FILING DATE: 05-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: OBLON, NORMAN F.
 ; REGISTRATION NUMBER: 24,618
 ; REFERENCE/DOCKET NUMBER: 18-966-0
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-413-3000
 ; TELEFAX: 703-413-2220
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 527 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-811-949-39
 ;
 ; Query Match 38.3%; Score 865.5; DB 2; Length 527;
 ; Best Local Similarity 37.7%; Pred. No. 1.6e-67;
 ; Matches 184; Conservative 56; Mismatches 151; Indels 97; Gaps 10;
 ;
 ; 3 ELHQVP-SNCD---CLNGGTCVSNKYFNSNTHWNCNPKFGGHCIDKSKTCYEGNGHPY 58
 ; 42 QCHSVFVKSCSEPRCFNGGTCQQAALYFSDF-VQCPEGPAGKCECIDTRATCYEDQGISY 100
 ;
 ; 59 RGRKASTDTMGRCPLPWNSTVLTQYTHAHSRDLQGLGKHNCRPNDRRRPWCYVQV 118
 ; 101 RGTWSTAESGAECTNWNSSALAAQFPYSGRRPDAIRLGLGNHNYCRPNDRDSKPCWYFKA 160
 ; 119 LKPLVQECNVHDCADG-----
 ;

161 GYSSSEPCSTPACSEGNDCYFGNGSAYRGTHSLTBSGASCLPWNMSMLIGKYTAQNP 220
135 -----XKFEQ-----CG-OKTLRPRFKLIGGE 155
221 AQAALGLKHNKYNCRNPDGAKPWCHVKNRRLTWYCDVPCSTCGRQYQOPFRILGGL 280
156 FTTIENQWFAAIYRRH-RGGSVTVYCGGLSPCWISATHCFIDYPKKEDYIVYLG 214
281 FADIASHPWQAAI FAKHRRSPGERFLCGGLISSCWILSAAHCFQERFPFHLLTVILGRT 340
215 RLNSNTQCEMKFEVENILHKDYSADTLAHHNDIALKIRSKGRCACQPSRTIOTICLPS 274
341 YRVVPGEEQKFEVEKYIVHKEPDDT--YDNDIALQLKSSRCAQESSVVRTVCLPP 398
275 MYNDPQGTSCETITGFKENSTDYLYPEQLKMTVWKLISHRECOQPHYGVSEVTTMCLCA 334
399 ADLQLPDWTCELSGKGHEALSPFYSERLKEAHRVLPSSRCTSOHLNLRITVDNMLCA 458
335 AD-----POWKT-DSOQDGGPLVCSLQGRMTLTGIVSWGRGCALDKPKGVYTRVSHFL 388
459 GDRSGGPOANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGOKDVPGVYTKVTNYL 518
389 PWIRSHTK 396
519 DWIRDNR 526
RESULT 25
US-07-609-510B-16
Sequence 16, Application US/07609510B
Patent No. 5326700
GENERAL INFORMATION:
APPLICANT: Berg et al.
TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue F
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN.
COUNTRY: U.S.A.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
FILING DATE: 19901106
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-609-510B-16

Query Match 38.1%; Score 859.5; DB 6; Length 527;
Best Local Similarity 37.7%; Pred. No. 5.3e-67;
Matches 184; Conservative 54; Mismatches 153; Indels 97; Gaps 10;
3 ELHQP-SNCD---CLNGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHY 58
42 QCHSVVPKSCSEPRCFNGTCQQAALYFSDP-VCOCEGFAKCCCEIDTRATCYEDQGISY 100
59 RGKASTDTMGRPCLPWN SATVLQOYTHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVG 118
101 RGTWSTAESGAECTWNSSALAAQKPYSGRRPDAIRLGLGNHNYCRNPNDRDPSKWCYVKA 160
119 LKPLVQECWVHDCADG-----LKFEQ-----CG-OKTLRPRFKLIGGE 155
161 GYSSSEPCSTPACSEGNDCYFGNGSAYRGTHSLTBSGASCLPWNMSMLIGKYTAQNP 220
140 -----XKFEQ-----CG-OKTLRPRFKLIGGE 155
221 AQAALGLKHNKYNCRNPDGAKPWCHVKNRRLTWYCDVPCSTCGRQYQOPFRILGGL 280
156 FTTIENQWFAAIYRRH-RGGSVTVYCGGLSPCWISATHCFIDYPKKEDYIVYLG 214
281 FADIASHPWQAAI FAKHRRSPGERFLCGGLISSCWILSAAHCFQERFPFHLLTVILGRT 340

215 RLNSNTQCEMKFEVENILHKDYSADTLAHHNDIALKIRSKGRCACQPSRTIOTICLPS 274
341 YRVVPGEEQKFEVEKYIVHKEPDDT--YDNDIALQLKSSRCAQESSVVRTVCLPP 398
275 MYNDPQGTSCETITGFKENSTDYLYPEQLKMTVWKLISHRECOQPHYGVSEVTTMCLCA 334
399 ADLQLPDWTCELSGKGHEALSPFYSERLKEAHRVLPSSRCTSOHLNLRITVDNMLCA 458
335 AD-----POWKT-DSOQDGGPLVCSLQGRMTLTGIVSWGRGCALDKPKGVYTRVSHFL 388
459 GDRSGGPOANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGOKDVPGVYTKVTNYL 518
389 PWIRSHTK 396
519 DWIRDNR 526
RESULT 25
US-07-609-510B-16
Sequence 16, Application US/07609510B
Patent No. 5326700
GENERAL INFORMATION:
APPLICANT: Berg et al.
TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue F
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN.
COUNTRY: U.S.A.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,510B
FILING DATE: 19901106
CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 527 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-609-510B-16

Query Match 38.0%; Score 858.5; DB 1; Length 527;
Best Local Similarity 37.5%; Pred. No. 6.5e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
3 ELHQP-SNCD---CLNGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHY 58
42 QCHSVVPKSCSEPRCFNGTCQQAALYFSDP-VCOCEGFAKCCCEIDTRATCYEDQGISY 100
59 RGKASTDTMGRPCLPWN SATVLQOYTHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVG 118
101 RGTWSTAESGAECTWNSSALAAQKPYSGRRPDAIRLGLGNHNYCRNPNDRDPSKWCYVKA 160
119 LKPLVQECWVHDCADG-----LKFEQ-----CG-OKTLRPRFKLIGGE 155
161 GYSSSEPCSTPACSEGNDCYFGNGSAYRGTHSLTBSGASCLPWNMSMLIGKYTAQNP 220
135 -----XKFEQ-----CG-OKTLRPRFKLIGGE 155
221 AQAALGLKHNKYNCRNPDGAKPWCHVKNRRLTWYCDVPCSTCGRQYQOPFRILGGL 280
156 FTTIENQWFAAIYRRH-RGGSVTVYCGGLSPCWISATHCFIDYPKKEDYIVYLG 214
281 FADIASHPWQAAI FAKHRRSPGERFLCGGLISSCWILSAAHCFQERFPFHLLTVILGRT 340

QY 215 RLNNTQEMKFEVENLILHKDYSADTLAHNDIALKIRSKGRCAQPSRTIOTICLPS 274
DE 341 YRVVFGBEEQKFEVEKYIVHKEFDDDT--YNDIALQLKSDSSRCQAQSSVVRTVCLPP 398
QY 275 MYNDPQFGTSCHEITGFCOKENSTDYLYPEQLKMTVVKLISHRECOQPHYGSEVTTKMLCA 334
DE 399 ADLQLPDWTCELSGYGKHEALSPFYSERLKEAHRVLYPSSRCTSQHLLNRTVTDNMLCA 458
QY 335 AD---POWKT--DSCOGDSGGPLVCSLQGRMTLTGIVSMGRGCAKDKPGVYTRYSHFL 388
DE 459 GDTSGGPPQANLHDACQDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 518
QY 389 PWIRSHTK 396
DE 519 DWIRDNR 526
RE UT 26
PC US91-01025A-2
; quence 2, Application PC/TUS9101025A
; SERIAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER-READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01025A
; FILING DATE: 19910214
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/486,657
; FILING DATE: 1 March 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 454P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; US91-01025A-2
; Query Match 38.0%; Score 858.5; DB 5; Length 527;
; Best Local Similarity 37.5%; Pred. No. 6.5e-67;
; Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
QY 3 ELHQVP-SNCD---CLNGGTCVSNKYFNSIHWNCNPKFKGQHCIDKSKTCYEGNGHFY 58
DE 42 QCHSVFVKSCSEPRCFNGGTCCQALYFSDF--VCQCEPGFAGKCCCEIDTRATCYEDQGISY 100
QY 59 RGKASTDTMGRCPLPWN SATVLQOTYHAHRSDALQLGLGKHNCRNPNRRPWCYQVG 118
DE 101 RGTWSTASGAECTNWNSSALAAQKPYSGRRPDAIRLGLGNHNYCRNPDSDKPCWYFKA 160
QY 119 LKPLVQECMVHDCADG-----KLKFO-----CG-OKTLPKRIIGGE 155
DE 221 AQAALGLGKHNCRNPDGDAKFWCHLVKNRRLTWEPVSCSTGLRQYSQPFRIKGL 280
QY 156 FTTIENQPFWFAAIYRRH-RGGSVTYVCGSLTSPCWVISATHCFIDYPKKEDIYVILGRS 214

DB 161 GKYSEFCSTPACSEGNSDCYFGNGSAVRGTHSLTESGASCLPWNSMLIGKVYTAQNPS 220
QY 135 -----KLKFO-----CG-OKTLPKRIIGGE 155
DB 221 AQAALGLGKHNCRNPDGDAKFWCHLVKNRRLTWEPVSCSTGLRQYSQPFRIKGL 280
QY 156 FTTIENQPFWFAAIYRRH-RGGSVTYVCGSLTSPCWVISATHCFIDYPKKEDIYVILGRS 214
DB 281 FADIASHPWQAARIAKHPERSGFERFLCGGILISSCWILSAAHCFQERPPPHLTVILGRT 340
QY 215 RLNNTQEMKFEVENLILHKDYSADTLAHNDIALKIRSKGRCAQPSRTIOTICLPS 274
DB 341 YRVVFGBEEQKFEVEKYIVHKEFDDDT--YNDIALQLKSDSSRCQAQSSVVRTVCLPP 398
QY 275 MYNDPQFGTSCHEITGFCOKENSTDYLYPEQLKMTVVKLISHRECOQPHYGSEVTTKMLCA 334
DB 399 ADLQLPDWTCELSGYGKHEALSPFYSERLKEAHRVLYPSSRCTSQHLLNRTVTDNMLCA 458
QY 335 AD---POWKT--DSCOGDSGGPLVCSLQGRMTLTGIVSMGRGCAKDKPGVYTRYSHFL 388
DB 459 GDTSGGPPQANLHDACQDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYL 518
QY 389 PWIRSHTK 396
DB 519 DWIRDNR 526
RESULT 27
5185259-8
; Patent No. 5185259
; APPLICANT: GOEDDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
; VEHAER, GORDON A.
; TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
; ACTIVATOR
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/489,855
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 12,694
; FILING DATE: 09-FEB-1987
; APPLICATION NUMBER: 483,052
; FILING DATE: 07-APR-1983
; APPLICATION NUMBER: 398,003
; FILING DATE: 14-JUL-1982
; APPLICATION NUMBER: 374,860
; FILING DATE: 05-MAY-1982
; SEQ ID NO:8:
; LENGTH: 527
5185259-8
Query Match 38.0%; Score 858.5; DB 6; Length 527;
Best Local Similarity 37.5%; Pred. No. 6.5e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
QY 3 ELHQVP-SNCD---CLNGGTCVSNKYFNSIHWNCNPKFKGQHCIDKSKTCYEGNGHFY 58
DB 42 QCHSVFVKSCSEPRCFNGGTCCQALYFSDF--VCQCEPGFAGKCCCEIDTRATCYEDQGISY 100
QY 59 RGKASTDTMGRCPLPWN SATVLQOTYHAHRSDALQLGLGKHNCRNPNRRPWCYQVG 118
DB 101 RGTWSTASGAECTNWNSSALAAQKPYSGRRPDAIRLGLGNHNYCRNPDSDKPCWYFKA 160
QY 119 LKPLVQECMVHDCADG-----KLKFO-----CG-OKTLPKRIIGGE 155
DB 161 GKYSEFCSTPACSEGNSDCYFGNGSAVRGTHSLTESGASCLPWNSMLIGKVYTAQNPS 220
QY 135 -----KLKFO-----CG-OKTLPKRIIGGE 155
DB 221 AQAALGLGKHNCRNPDGDAKFWCHLVKNRRLTWEPVSCSTGLRQYSQPFRIKGL 280
QY 156 FTTIENQPFWFAAIYRRH-RGGSVTYVCGSLTSPCWVISATHCFIDYPKKEDIYVILGRS 214

QY 59 RGKASTDTMGRPCLPWNSATVLOOTYHAHSDALQOLGLGKHNYCRNPNRRPKCYVOVG 118
DB 136 RGTWSTAESGAECNTWNSALLAQKPYSGRRPDATRLGLGNHNYCRNPDROSKPWCYVFK 195
QY 119 LKPLVQECMVHDCADG----- 134
DB 196 KYSSEFCSTPACSEGNDCVFGNGSAVRGTHSLTESGASCLPWNSMLIGKVYTAQNP 255
QY 135 -----KLKFO-----CG-OKTLPFRKIIGGE 155
DB 256 AALGLGKHNYCRNPDGAKPWCHLVKNRRLTWEYCDVPSCSTGLRQYQOPRIKGL 315
QY 156 FTTIENOPWFAAIYRRH-RGGSVTVYVCGSLISPCWVISATHCFIDYPKKEDYIVYLGRS 214
DB 316 FADIASHPWQAAIAFAKHRRSPGERFLCGGILISSCWILSAACFOERPPPHLTVILGRT 375
QY 215 RLNSNTQGMKFEVENILHKDYADTLAHNDIALKIRSKGRCACQPSRTIOTICLPS 274
DB 376 YRVVPGEEQKFEVEKYIVHKEFDDT--YDNDIALQLKSDSSRCQAQESSVVRVTCVLP 433
QY 275 MYNDPQFGTSCITGFGKENSTDYLYPEOLKMTVVKLIHRECOQPHYVGVSEVTTKMLCA 334
DB 434 ADLQLPDWTCELSGYGKEALSFFYSERLKEAHVRLYPSRCTSQHLLNRTVTDNMLCA 493
QY 335 AD-----PWKT-DSQCGSDGGPLVCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFL 388
DB 494 GDRSGGPQANLHDACQSDGGPLVCLNDGRMTLVGIISWGLGCGQXDPVGYTKVTNYL 553
QY 389 PWIRSHTK 396
DB 554 DWIRDNR 561

RESULT 29
US-08-560-098A-50
; Sequence 50, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WENDET, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid

I 281 FADIASHPWQAAIAFAKHRRSPGERFLCGGILISSCWILSAACFOERPPPHLTVILGRT 340
C 215 RLNSNTQGMKFEVENILHKDYADTLAHNDIALKIRSKGRCACQPSRTIOTICLPS 274
I 341 YRVVPGEEQKFEVEKYIVHKEFDDT--YDNDIALQLKSDSSRCQAQESSVVRVTCVLP 398
C 275 MYNDPQFGTSCITGFGKENSTDYLYPEOLKMTVVKLIHRECOQPHYVGVSEVTTKMLCA 334
I 399 ADLQLPDWTCELSGYGKEALSFFYSERLKEAHVRLYPSRCTSQHLLNRTVTDNMLCA 458
C 335 AD-----PWKT-DSQCGSDGGPLVCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFL 388
I 459 GDRSGGPQANLHDACQSDGGPLVCLNDGRMTLVGIISWGLGCGQXDPVGYTKVTNYL 518
C 389 PWIRSHTK 396
I 519 DWIRDNR 526

ULT 28
I 08-811-949-43
; sequence 43, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SAKAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-966-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 08-811-949-43

very Match 38.0%; Score 858.5; DB 2; Length 562;
set Local Similarity 37.5%; Pred. No. 7.1e-87;
atches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
C 3 ELHQVP-SNCD---CLMGGTVCVNKYFSNIHNCNCPKFTGGQHCCEIDKSKTCYEGNGHPY 58
F 77 QCHSVPVKSCSEPCFNGGTCCQALYFSDP-VQCPEGFAGKCCIDTRATCYEDGISY 135

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-560-098A-50

ery Match
; 38.0%; Score 858.5; DB 2; Length 562;
; Local Similarity 37.5%; Pred. No. 7.1e-67;
; Mismatches 152; Indels 97; Gaps 10;
; Conservative 56;

Q 3 ELHQP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGGQCEIDKSKTCYEGNGHYF 58
D 77 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPEGFAGKCEIDTRATCYEDQISY 135
Q 59 RGKASTDTMGPRCLPWNASATVLOQTYHAHRSDALOLGLGKHYCRNPDNRPRPCVQVG 118
D 136 RGTWSTABSGAECTMNSSALAKPYSGRRPDALRLGLGNHNYCRNPDNRDRSKPCVYFKA 195
Q 119 LKPLVQECMVHDCADG----- 134
D 196 GKYSEFCSTPACSEGNDCYFGNGSAVRGTHSLTESGASCLPWNMILIGKVYTAQNP 255
Q 135 -----KLKFO----- 155
D 256 AQAALGLGKHYCRNPDGDAKPCWCHLVKNRLTWECVDPSCSTCGLRQYSQPFRIKGG 315
Q 156 FTTIENQWFAAIYRRH-RGGSVTVCGGSLISPCWISATHCFIDYPKKEDYIVVLGRS 214
D 316 PADIASHPWQAIAFAKRRSPGERFLCGGILISSCWILSAAHCFQERPPPHLTVILGR 375
Q 215 RLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIOTICLPS 274
D 376 YRVVPGEEQKFEVEKIVHKEFDDT--YDNDIALQLKSDSRCAQESSVVRTVCLPP 433
Q 389 PWIRSHTK 396
D 554 DWIRDNR 561

; LT 30
; 8-883-795A-38
; quence 38, Application US/08883795A
; tent No 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcive, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERESKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein (cpa)
; US-08-883-795A-38

Query Match
; 38.0%; Score 858.5; DB 2; Length 562;
; Best Local Similarity 37.5%; Pred. No. 7.1e-67;
; Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;

Q 3 ELHQP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGGQCEIDKSKTCYEGNGHYF 58
D 77 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPEGFAGKCEIDTRATCYEDQISY 135
Q 59 RGKASTDTMGPRCLPWNASATVLOQTYHAHRSDALOLGLGKHYCRNPDNRPRPCVQVG 118
D 136 RGTWSTABSGAECTMNSSALAKPYSGRRPDALRLGLGNHNYCRNPDNRDRSKPCVYFKA 195
Q 119 LKPLVQECMVHDCADG----- 134
D 196 GKYSEFCSTPACSEGNDCYFGNGSAVRGTHSLTESGASCLPWNMILIGKVYTAQNP 255
Q 135 -----KLKFO----- 155
D 256 AQAALGLGKHYCRNPDGDAKPCWCHLVKNRLTWECVDPSCSTCGLRQYSQPFRIKGG 315
Q 156 FTTIENQWFAAIYRRH-RGGSVTVCGGSLISPCWISATHCFIDYPKKEDYIVVLGRS 214
D 316 PADIASHPWQAIAFAKRRSPGERFLCGGILISSCWILSAAHCFQERPPPHLTVILGR 375
Q 215 RLNSNTQGMKFEVENILHKDYSADTLAHNDIALKIRSKGRCQAQPSRTIOTICLPS 274
D 376 YRVVPGEEQKFEVEKIVHKEFDDT--YDNDIALQLKSDSRCAQESSVVRTVCLPP 433
Q 275 MYNDPQFCTSCITGFGKENSTDVLYPEOLKMTVVKLISHRECQCPHYVSEVTKMLCA 334
D 434 ADLQLPDWTCELSGKGHEALSPYSERLKEAHRVLYPSRCTSQHLLNRTVDNMLCA 493
Q 335 AD-----PWKMT-DSCQDGGPLVCSLQGRMTLTGIVSWGRCALKDKPGVYTRVSHFL 388
D 494 GDTREGGQANLHDAQCQDGGPLVCLNDGRMTLVGIISWGLGCGQKDPVGVYTKVTNYL 553
Q 389 PWIRSHTK 396
D 554 DWIRDNR 561

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; RESULT 31
; US-09-703-695A-4
; Sequence 4, Application US/09703695A
; Patent No. 6593097
; GENERAL INFORMATION:
; APPLICANT: Xu, Yuan
; TITLE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS
; FILE REFERENCE: P1788R1
; CURRENT APPLICATION NUMBER: US/09/703,695A
; CURRENT FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: US 60/163,607
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 4
; LENGTH: 562
; TYPE: PRT
; ORGANISM: Homo sapiens

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09-703-695A-4
Query Match 38.0%; Score 858.5; DB 4; Length 562;
est Local Similarity 37.5%; Pred. No. 7.1e-67;
atches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
3 ELHQP-SNCD---CLNGGTCVSNKYFNSIHWNCPCPKFGGQHCIEDSKTCYEGNGHPY 58
77 QCHSVPVKSCSEPRCFNGTCQOALYFSDP-VQCPEGFAGKCEIDTRATCYEDQISY 135
59 RGKASTDTMGRPCLPWNSATVLOQTYHAHSDALQLGLGKHNYCRNPDNRPRPCYQVG 118
136 RGTWSTAESGAECTNWNSSALAKPYSGRPPDAIRLGLGNHNYCRNPDNRDRSKPWCYVKA 195
119 LKPLVQECMVHDCADG-----KLKFK-----CG-OKTLRPRFKIIGGE 155
196 KYSSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPS 255
135 -----KLKFK-----CG-OKTLRPRFKIIGGE 155
256 AQAALGLGKHNYCRNPDGDAKFWCHLVKNRRLTWECYDVPCSTCGLRQYQPFRIKGG 315
156 FTTIENQFWFAAIYRRH-RGGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRS 214
316 FADIASHPWQAALFAKHRRSPGERFLCGGILISSCWILSAAHCFQERPPPHLTVILGRT 375
215 RLNSNTQGENKFVENILHKOYSADTLAHNDIALLKIRSKBGRCAQPSRTIQTICLPS 274
376 YRVVPGEBEOKFEVKYVHKPEDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPP 433
275 MYNDPQGTSCETITGFGKENSTDYLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTTMCA 334
434 ADLQLPDWTCELSGKGHEALSPFYSERLKEAHVLYPSSRCTSQHLLNRVTDNMCA 493
335 AD-----POWKT-DSCGDSGGPLVCSLQGRMTLGTIVSWGRGCAKDKPGVYTRVSHFL 388
494 GDRSGGPQANLHDACQDGGSGPLVCLNDGRMTLVGIISWGLCGGQKQVPGVYTKVTNYL 553
389 PWIRSHTK 396
554 DWIRDNR 561
RESULT 33
5200340-2
; Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
; ACTIVATORS
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/53,412
; FILING DATE: 22-MAY-1987
; SEQ ID NO:2:
; LENGTH: 562
5200340-2
Query Match 38.0%; Score 858.5; DB 6; Length 562;
Best Local Similarity 37.5%; Pred. No. 7.1e-67;
Matches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
3 ELHQP-SNCD---CLNGGTCVSNKYFNSIHWNCPCPKFGGQHCIEDSKTCYEGNGHPY 58
77 QCHSVPVKSCSEPRCFNGTCQOALYFSDP-VQCPEGFAGKCEIDTRATCYEDQISY 135
59 RGKASTDTMGRPCLPWNSATVLOQTYHAHSDALQLGLGKHNYCRNPDNRPRPCYQVG 118
136 RGTWSTAESGAECTNWNSSALAKPYSGRPPDAIRLGLGNHNYCRNPDNRDRSKPWCYVKA 195
119 LKPLVQECMVHDCADG-----KLKFK-----CG-OKTLRPRFKIIGGE 155
196 KYSSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPS 255
135 -----KLKFK-----CG-OKTLRPRFKIIGGE 155
256 AQAALGLGKHNYCRNPDGDAKFWCHLVKNRRLTWECYDVPCSTCGLRQYQPFRIKGG 315
156 FTTIENQFWFAAIYRRH-RGGSVTVYCGGSLISPCWVISATHCFIDYPKKEDYIVYLGRS 214
316 FADIASHPWQAALFAKHRRSPGERFLCGGILISSCWILSAAHCFQERPPPHLTVILGRT 375
215 RLNSNTQGENKFVENILHKOYSADTLAHNDIALLKIRSKBGRCAQPSRTIQTICLPS 274
376 YRVVPGEBEOKFEVKYVHKPEDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPP 433
275 MYNDPQGTSCETITGFGKENSTDYLYPEQLKMTVVKLIHSHRECOQPHYGVSEVTTMCA 334
434 ADLQLPDWTCELSGKGHEALSPFYSERLKEAHVLYPSSRCTSQHLLNRVTDNMCA 493
335 AD-----POWKT-DSCGDSGGPLVCSLQGRMTLGTIVSWGRGCAKDKPGVYTRVSHFL 388
494 GDRSGGPQANLHDACQDGGSGPLVCLNDGRMTLVGIISWGLCGGQKQVPGVYTKVTNYL 553
389 PWIRSHTK 396
554 DWIRDNR 561
ULT 32
5259-3
; Patent No. 5185259
; APPLICANT: GOEDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
; HAR, GORDON A.
; TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
; ACTIVATOR
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/489,855
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 12,694
; FILING DATE: 09-FEB-1987
; APPLICATION NUMBER: 483,052
; FILING DATE: 07-APR-1983
; APPLICATION NUMBER: 398,003
; FILING DATE: 14-JUL-1982
; APPLICATION NUMBER: 374,860
; FILING DATE: 05-MAY-1982
; Q ID NO:3
; LENGTH: 562
5259-3
Query Match 38.0%; Score 858.5; DB 6; Length 562;
est Local Similarity 37.5%; Pred. No. 7.1e-67;
atches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
3 ELHQP-SNCD---CLNGGTCVSNKYFNSIHWNCPCPKFGGQHCIEDSKTCYEGNGHPY 58

QY 215 RLNSNTQGMKFEVENILHDKYSADTLAHNDIALKIRSKGRCQAQPSRTIOTICLPS 274
 DE 376 YRVVPGEEBQKFEVEKIYHKEFDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPP 433
 QY 275 MYNDPQFTSCITGFKENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCA 334
 DE 434 ADLQLPDWTCELSGYGKHEALSPFYSERLKEAHRVLPSSRCTSQHLLNRTVTDNMLCA 493
 QY 335 AD-----POWKT-DSCOGDSGGLVCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFL 388
 DE 494 GDRSGGQANLHDACQDGGGLVCLNDGRMTLVGLISWGLGCGQKDPGVYTKVTNYL 553
 QY 389 PWIRSHTK 396
 DE 554 DWIRDNR 561
 RE LT 34
 53 773-2
 ; Applicant: WEI, CHA-MER, HSIUNG, NANCY; REDDY, VERMURI B.;
 ; ONT, JEFFREY F.; DACKOWSKI, WILLIAM; DOUGLAS, RICHARD;
 ; E, EDWARD S.; PURCELL JR., RICHARD D.; LAU, DAVID TAI-YUI
 ; TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN
 ; IVATOR PRODUCED BY RECOMBIANT DNA
 ; NUMBER OF SEQUENCES: 6
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/782,686
 ; FILING DATE: 01-OCT-1985
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 656,770
 ; FILING DATE: 01-OCT-1984
 ; ID NO:2:
 ; LENGTH: 562
 ; 773-2

ary Match 38.0%; Score 858.5; DB 6; Length 562;
 st Local Similarity 37.5%; Pred. No. 7.1e-67;
 tches 183; Conservative 56; Mismatches 152; Indels 97; Gaps 10;
 QY 3 ELHVP-SNCD---CLNGGTCVSNKYFNSHNCNPKKFGQHCEDKSKTCYEGNGHYF 58
 DE 77 QCHSVPVKSCSEPCFNGGTCQALYFSDP--VCQCEGFAKGCCEIDTRATCYEDQGISY 135
 QY 59 RGKASTDTMGPRCLPWNASATVLOQTYHAHRSADALQLGLGKHNYCRNPNRRPWCYVQVG 118
 DE 136 RGTWSTAESGAECTNWNSSALAQKPYSGRRPDAILRLGKHNYCRNPNDRDSEKPCVYFKA 195
 QY 119 LKPLVQECMVHDCADG----- 134
 DE 196 KYSGSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNNSMILIGKVYTAQNP 255
 QY 135 -----KLKFG-----CG-OKTLRPRFKIIGGE 155
 DE 256 AALGLGKHNYCRNPDGAKPWCVHLKNRLTWECVDPSCSTCGLRQYSPQFRKGG 315
 QY 156 PTTIENQFWFAIYVRH--RGSVTVYCGSLISPCWVISATHCFIDYPKKEDYIVYLGSR 214
 DE 316 FADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSSAAHCFQERFPFPHLTVILGRT 375
 QY 215 RLNSNTQGMKFEVENILHDKYSADTLAHNDIALKIRSKGRCQAQPSRTIOTICLPS 274
 DE 376 YRVVPGEEBQKFEVEKIYHKEFDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPP 433
 QY 275 MYNDPQFTSCITGFKENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCA 334
 DE 434 ADLQLPDWTCELSGYGKHEALSPFYSERLKEAHRVLPSSRCTSQHLLNRTVTDNMLCA 493
 QY 335 AD-----POWKT-DSCOGDSGGLVCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFL 388
 DE 494 GDRSGGQANLHDACQDGGGLVCLNDGRMTLVGLISWGLGCGQKDPGVYTKVTNYL 553
 QY 389 PWIRSHTK 396
 DE 554 DWIRDNR 561

QY 389 PWIRSHTK 396
 DE 554 DWIRDNR 561
 RESULT 35
 5244676-5
 ; Patent No. 5244676
 ; APPLICANT: BELL, LESLIE D.; MAVER, ERNEST J.; PALMIER, MARK O.
 ; TOLUNAY, H. ESER; WARREN, THOMAS G.; WUN, TZE-CHIN
 ; TITLE OF INVENTION: MODIFIED TISSUE PLASMINOGEN ACTIVATOR
 ; WITH MODIFIED GLYCOSYLATION SITE
 ; NUMBER OF SEQUENCES: 9
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/203,047
 ; FILING DATE: 06-JUN-1988
 ; SEQ ID NO:5:
 ; LENGTH: 562
 ; 5244676-5

Query Match 37.7%; Score 851.5; DB 6; Length 562;
 Best Local Similarity 37.1%; Pred. No. 2.9e-66;
 Matches 181; Conservative 58; Mismatches 152; Indels 97; Gaps 10;
 QY 3 ELHVP-SNCD---CLNGGTCVSNKYFNSHNCNPKKFGQHCEDKSKTCYEGNGHYF 58
 DE 77 QCHSVPVKSCSEPCFNGGTCQALYFSDP--VCQCEGFAKGCCEIDGNSDCYFGSGAY 135
 QY 59 RGKASTDTMGPRCLPWNASATVLOQTYHAHRSADALQLGLGKHNYCRNPNRRPWCYVQVG 118
 DE 136 RGTWSTAESGAECTNWNSSALAQKPYSGRRPDAILRLGKHNYCRNPNDRDSEKPCVYFKA 195
 QY 119 LKPLVQECMVHDCADG----- 134
 DE 196 RRLTWECVDPSCSEGNSDCYFGNGSAYRGTHSLTESGASCLPWNNSMILIGKVYTAQNP 255
 QY 135 -----KLKFG-----CG-OKTLRPRFKIIGGE 155
 DE 256 AALGLGKHNYCRNPDGAKPWCVHLKNRLTWECVDPSCSTCGLRQYSPQFRKGG 315
 QY 156 PTTIENQFWFAIYVRH--RGSVTVYCGSLISPCWVISATHCFIDYPKKEDYIVYLGSR 214
 DE 316 FADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSSAAHCFQERFPFPHLTVILGRT 375
 QY 215 RLNSNTQGMKFEVENILHDKYSADTLAHNDIALKIRSKGRCQAQPSRTIOTICLPS 274
 DE 376 YRVVPGEEBQKFEVEKIYHKEFDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPP 433
 QY 275 MYNDPQFTSCITGFKENSTDYLYPEQLKMTVVKLISHRECCQPHYGSEVTTKMLCA 334
 DE 434 ADLQLPDWTCELSGYGKHEALSPFYSERLKEAHRVLPSSRCTSQHLLNRTVTDNMLCA 493
 QY 335 AD-----POWKT-DSCOGDSGGLVCSLQGRMTLTGIVSWGRGCAKDKPGVYTRVSHFL 388
 DE 494 GDRSGGQANLHDACQDGGGLVCLNDGRMTLVGLISWGLGCGQKDPGVYTKVTNYL 553
 QY 389 PWIRSHTK 396
 DE 554 DWIRDNR 561

RESULT 36
 US-08-142-590B-25
 ; Sequence 25, Application US/08142590B
 ; Patent No. 6120765
 ; GENERAL INFORMATION:
 ; APPLICANT: HIBINO, Tashihiko; TAKAHASHI, Tadahito; HORII, Izumi; and
 ; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston

```
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,590B
FILING DATE: 25-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,318
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-009CP
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
88-142-590B-25

Query Match 36.6%; Score 825; DB 3; Length 157;
Best Local Similarity 91.7%; Pred. No. 1.2e-64;
Matches 144; Conservative 0; Mismatches 5; Indels 8; Gaps 1;

1 SNEHQVPSNCDCLNGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
1 SNEHQVPSNCDCLNGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
61 KASDTMTGRCLPWSATVLOQTYHAHRSALQGLGKHNCRPNRRPWCYVOVGLK 120
61 KASDTMTGRCLPWSATVLOQTYHAHRSALQGLGKHNCRPNRRPWCYVOVGLK 120
121 PLVQECMVHDCADGK-----LKFQCGQKTLRPRF 149
121 PLVQECMVHDCADGKSPSPPELKFQCGQKYLPRF 157

ULT 37
Sequence 59, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-59

Query Match 35.8%; Score 808; DB 2; Length 355;
Best Local Similarity 45.9%; Pred. No. 1e-62;
Matches 163; Conservative 44; Mismatches 132; Indels 16; Gaps 6;

50 CYEGNGHFYRGKASDTMTGRCLPWSATVLOQTYHAHRSALQGLGKHNCRPNRR 109
8 CYFGNGSAYRGTHSLITSGASCLPWSNMLIGKVYTAQNPSAALGLGKHNCRPDGA 67
110 RPYCVQVGLKPLVQECMVHDCADGKLFQCG-----TCGLRQTLRPRFKIGGLFADIASHPWQA 168
68 KPWCHLVKVRRLTWEYCDVPCS-----TCGLRQTLRPRFKIGGLFADIASHPWQA 121
169 YRRH-RGGSVTVYCGSLISPCWISATHCFIDYPKKEDYIVYLGSRSLNSNTGEMKFE 227
122 FAKHRRSPGERFLCGGLISSCWILSAACFCQERFPFPHLTVILGRTVYVVGEEQKFE 181
228 VENILKHDYSADTLAHNDIALKIRSKGRCQAPSTTQICLPSMYNDPQFGTSCEI 287
182 VEKIVHKEFDDT--DYNDIALQLKSDSRCSQESSVVRTVCLPADLQLPDWTCECL 239
288 TGFGENSTDYLYPEQLKMTVVKLIHSHRECOQPHYGSEVTTKMLCAAD-----PWKKT- 341
240 SGYKHEALSFPYSERLKEAHVRLYPSRCTSOHLNRTVTDNMLCAGDTRSGGPOANLH 299
342 DSCOGDSGGPLVCSLOGRMILTGIIVSGRGCALKDKFQGVYTRVSHFLPWIRSHTK 396
300 DACQDSGGPLVCLNDGRMTLVGIISWGLCGQKDVFGVYTKVTNYLDWIRDNR 354

RESULT 38
US-08-811-949-51
Sequence 51, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
```


SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/811,949
 FILING DATE: 05-MAR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-966-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 51:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 9-811-949-51

Query Match 35.6%; Score 803; DB 2; Length 437;
 Best Local Similarity 43.0%; Pred. No. 3.7e-62;
 Matches 164; Conservative 51; Mismatches 144; Indels 22; Gaps 8;

30 WCNCPK--KFGQRCET---DKSKTCYEGNGHFGYRGKASTDTMGRPCLPWNSATVLQOT 83
 64 WCYVFKAGKYSSEFCSTPACSEGNDCYFGNGSAYRGTHSLTSGASCLPWNMILIGKV 123
 84 YHAHRSALQGLGKHNYCRNPDRRPWCYVQVGLKPLVQECMVHDCADGLKFCQG-Q 142
 124 YTAQNPQAQALGLGKHNYCRNPDPDAPKFWCHLVKNRLTWECYCDVPSCS-----TCGLR 177
 143 KTLRPRKIIIGGETTIENOPFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDY 201
 178 QYSPQRIIGGLFADTASHFWQAAIFAKHRRSPGERFLCGGILISSCWILSAHCFQER 237
 202 PKEDYIYVLRSLNNTQGMKFEVENILHKYSDATLAHNDIALKIRSGRCA 261
 238 FPPHLLTVILGRTYRVVPGEEQKFEVEKYIVHKEFDDDT--YNDIALQLKSDSRCA 295
 262 QPSRTIOTICLPMSYNDPQGTSCETITGFGKENSTDYLYPEQLKMTVVKLISHRECOQPH 321
 296 QESSVVRIVCLPPADLQLPDWTCELSGYGKHLSFPYSERLKEAHVRLYPSRRTSOH 355
 322 YGSEVTTKMLCAAD-----PQWKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRCALK 375
 356 LLNRTVTDNMLCAGDTRSGGPPQANLHDACQDGGPLVCLNDGRMTLVGLISWGLCGGOK 415
 376 DKPGVYTVRSHFLPWIRSHTK 396
 416 DVPGVYTKVNYLDWIRDNR 436

LT 39
 9-811-949-57
 Quence 57, Application US/08811949
 Tent No. 584533
 GENERAL INFORMATION:
 APPLICANT: NIWA, MINEO
 APPLICANT: SAITO, YOSHIMASA
 APPLICANT: SASAKI, HITOSHI
 APPLICANT: HAYASHI, MASAKO
 APPLICANT: NOTANI, JOUJI
 APPLICANT: KOBAYASHI, MASAKAZU
 TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
 NUMBER OF SEQUENCES: 67
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
 ADDRESSEE: P.C.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA

ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/811,949
 FILING DATE: 05-MAR-1997
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: OBLON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 18-966-0
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-413-3000
 TELEFAX: 703-413-2220
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 437 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-811-949-57

Query Match 35.4%; Score 800; DB 2; Length 437;
 Best Local Similarity 43.0%; Pred. No. 6.7e-62;
 Matches 164; Conservative 50; Mismatches 145; Indels 22; Gaps 8;

30 WCNCPK--KFGQRCET---DKSKTCYEGNGHFGYRGKASTDTMGRPCLPWNSATVLQOT 83
 64 WCYVFKAGKYSSEFCSTPACSEGNDCYFGNGSAYRGTHSLTSGASCLPWNMILIGKV 123
 84 YHAHRSALQGLGKHNYCRNPDRRPWCYVQVGLKPLVQECMVHDCADGLKFCQG-Q 142
 124 YTAQNPQAQALGLGKHNYCRNPDPDAPKFWCHLVKNRLTWECYCDVPSCS-----TCGLR 177
 143 KTLRPRKIIIGGETTIENOPFAAIYRRH-RGGSVTYVCGGSLISPCWVISATHCFIDY 201
 178 QYSPQRIIGGLFADTASHFWQAAIFAKHRRSPGERFLCGGILISSCWILSAHCFQER 237
 202 PKEDYIYVLRSLNNTQGMKFEVENILHKYSDATLAHNDIALKIRSGRCA 261
 238 FPPHLLTVILGRTYRVVPGEEQKFEVEKYIVHKEFDDDT--YNDIALQLKSDSRCA 295
 262 QPSRTIOTICLPMSYNDPQGTSCETITGFGKENSTDYLYPEQLKMTVVKLISHRECOQPH 321
 296 QESSVVRIVCLPPADLQLPDWTCELSGYGKHLSFPYSERLKEAHVRLYPSRRTSOH 355
 322 YGSEVTTKMLCAAD-----PQWKT-DSCQDGGPLVCSLQGRMTLTGIVSWGRCALK 375
 356 LLNRTVTDNMLCAGDTRSGGPPQANLHDACQDGGPLVCLNDGRMTLVGLISWGLCGGOK 415
 376 DKPGVYTVRSHFLPWIRSHTK 396
 416 DVPGVYTKVNYLDWIRDNR 436

RESULT 40
 US-09-101-272G-98
 Sequence 98, Application US/09101272G
 Patent No. 6509445
 GENERAL INFORMATION:
 APPLICANT: Nissin Food Products Co., Ltd.
 TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
 FILE REFERENCE: Q50979
 CURRENT APPLICATION NUMBER: US/09/101,272G
 CURRENT FILING DATE: 1998-07-08
 PRIOR APPLICATION NUMBER: JP 1059/1996
 PRIOR FILING DATE: 1996-01-08
 NUMBER OF SEQ ID NOS: 107
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 98

QY	30	WCNCPK--KFGQHCET----	D	SKTCTYEGNGHFGYRGKASTDTWGRCLPWN	SA	TVLQOT	83
DB	99	WCYVFKAGKYSSEFCSTPACSEGN	S	DCVFGNGSAYRGTHSLTSGASCLPWN	SMILICKV	159	
QY	84	VHAHRS	D	ALQGLGKHNYCRNPNRRPWCYVQVGLKPLVQECMVHDCADGKLKFCQG-Q	142		
DB	159	YTAQNP	S	SAQALGLGKHNYCRNPDGDGAKPWCHVKNRRLTWECYCDVPGCS-----	TCGLR	212	
QY	143	KTLRPRFKI	O	GEFTTIENQWFAAIYVRH-RGGSVTYVCGSLISPCWVISATHCFIDY	201		
DB	213	QYSQPFRIK	G	LPADIAHPWQAIAFAKHRRSPGERFLCGGILISSCWLSAAHCFQER	272		
QY	202	PKEDYIYV	L	GRSLNNTQGMKFEVENLTHKDYSDATLAHNDIALLKIRSKERCA	261		
DB	273	FPFHLT	W	ILGRTVTRVPEBEEQPEVEKYIVHKEFDDT--YNDIALQLKSDSRCA	330		
QY	262	QPSRTIOT	I	CLIPSMYNDPQFGTSCIEITGFKENSTDYLPQLKMTVVKLISHRECOQPH	321		
DB	331	QESSVVRT	V	TCVLPADQLPDWTECELSGYRKEALSFPYSERLKEAHVRLYPSSECTSQH	399		
QY	322	YIGSVV	T	TMILCAAD-----PWKT-DSCQDSDGGLVCSLOGRMTLTGIVSWGRGCALK	375		
DB	391	LLNRTVT	D	NMLCAGDTRSGGPQANLHDACQSDGGLVCLNDGRTVLGIISWGLGCGQK	450		
QY	376	DKPGVTRV	S	HPFLPWIRSHTK	396		
DB	451	DVPGVYTR	V	KNYVLDWIRDNMR	471		
		RESULT 42					
		US-08-797-689-12					
		Sequence 12, Application US/08797689					
		Patent No. 5876969					
		GENERAL INFORMATION:					
		APPLICANT: Fleer, Reinhard					
		APPLICANT: Fournier, Alain					
		APPLICANT: Guitton, Jean-Dominique					
		APPLICANT: Jung, Gerard					
		APPLICANT: Yeh, Patrice					
		TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES					
		TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION					
		TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES					
		NUMBER OF SEQUENCES: 36					
		CORRESPONDENCE ADDRESS:					
		ADDRESSEE: Rhone-Poulenc Rorer Inc.					
		STREET: 500 Arcola Road, 3043					
		CITY: Collegeville					
		STATE: PA					
		COUNTRY: USA					
		ZIP: 19426					
		COMPUTER READABLE FORM:					
		MEDIUM TYPE: Floppy disk					
		COMPUTER: Macintosh					
		OPERATING SYSTEM: System 7.1					
		SOFTWARE: Word 5.1 (Patentin)					
		CURRENT APPLICATION DATA:					
		APPLICATION NUMBER: US/08/797,689					
		FILING DATE: 31-JAN-1997					
		CLASSIFICATION: 435					
		PRIOR APPLICATION DATA:					
		APPLICATION NUMBER: PCT/FR93/00085					
		FILING DATE: 28-JAN-1993					
		ATTORNEY/AGENT INFORMATION:					
		NAME: Smith Ph.D., Julie K.					
		REGISTRATION NUMBER: P-36,619					
		REFERENCE/DOCKET NUMBER: ST92006-US					
		TELECOMMUNICATION INFORMATION:					
		TELEPHONE: (610) 454-3839					

```

TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-880-503-6-rai

Query Match 35.1%; Score 793; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
4 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 63
61 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNCRPNRRPWCYVQVGLK 120
64 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNCRPNRRPWCYVQVGLK 123
121 PLVQECMVHDCADGK 135
124 PLVQECMVHDCADGK 138

LT 43
US 9-984-186-12
Sequence 12, Application US/09984186
Cent No. 6686179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patricia
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESS: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:

```

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SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-984-186-12

Query Match 35.1%; Score 793; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.3e-62;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
4 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 63
61 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNCRPNRRPWCYVQVGLK 120
64 KASDTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNCRPNRRPWCYVQVGLK 123
121 PLVQECMVHDCADGK 135
124 PLVQECMVHDCADGK 138

RESULT 44
US-08-811-949-55
Sequence 55, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-55

Query Match 35.1%; Score 793; DB 2; Length 437;
Best Local Similarity 42.8%; Pred. No. 2.7e-61;
Matches 163; Conservative 50; Mismatches 146; Indels 22; Gaps 8;

```

US-08-811-949-49

Query Match 35.1%; Score 792; DB 2; Length 437;
Best Local Similarity 42.5%; Pred. No. 3.3e-61;
Matches 162; Conservative 52; Mismatches 145; Indels 22; Gaps 8;

QY 30 WCNCPK--KFGGQHCIEI-----DKSKTCYEGNGHYRGKASTDTMGRPCLPWNSATVLOQT 83
DB 64 WCVVFRAGKYSSSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNMSMILIGKV 123
QY 84 YHAHRSDALQGLGKKNYCRNPNRRPWCYVQVGLKPLVQECMVHDCADGKLKFCQG-Q 142
DB 124 YTAQNPSAQAALGKGNKYNCRNPDGDAKPNCHLVKNRRLTWECYDVPSCS-----TCGLR 177
QY 143 KTLRPRFKIIGGFTTIENQPFAPAIYRRH-RGGSVTVYVCGSLISPCWVISATHCFIDY 201
DB 178 QYSQPFQDIKGLFADIAHPWQAALFAKHRRSPGERFLCGGILSSCWILSAAHCFQER 237
QY 202 PKEDYVIVLGRSLNNTQGEKMFVENILHKOYSADTLAHNDIALKIRSKERCA 261
DB 238 FPPHLLTVILGRYRVVPGEEOKFEVYKIVHKEFDDDT--YNDIALQLKSDSRCA 295
QY 262 QPSRTIOTICLPMSYNDPQFGTSCETITGFKENSTDYLYPEOLKMTVVKLIHSHRCQOPH 321
DB 296 QESSVVRTVCLPADLQLPDWTCELSGYGKHEALSPFYSERLKEAHVRLYPSRCTSQH 355
QY 322 YGSEVTTKMLCAAD-----POWKT-DSCQDGGPLVCSLOGRMTLTGIVSWGRCALK 375
DB 356 LLNRTVTDNMLCAGDTRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGQK 415
QY 376 DKPGVTVRSHFLPWIRSHTK 396
DB 416 DVPGVYTKVNYLDWIRDNR 436

RESULT 46

US-08-811-949-47
; Sequence 47, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-966-0
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 49:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-811-949-49

Query Match 35.1%; Score 792; DB 2; Length 437;
Best Local Similarity 42.5%; Pred. No. 3.3e-61;
Matches 162; Conservative 52; Mismatches 145; Indels 22; Gaps 8;

QY 30 WCNCPK--KFGGQHCIEI-----DKSKTCYEGNGHYRGKASTDTMGRPCLPWNSATVLOQT 83
DB 64 WCVVFRAGKYSSSEFCSTPACSEGNDCYFGNGSAYRGTHSLTESGASCLPWNMSMILIGKV 123
QY 84 YHAHRSDALQGLGKKNYCRNPNRRPWCYVQVGLKPLVQECMVHDCADGKLKFCQG-Q 142
DB 124 YTAQNPSAQAALGKGNKYNCRNPDGDAKPNCHLVKNRRLTWECYDVPSCS-----TCGLR 177
QY 143 KTLRPRFKIIGGFTTIENQPFAPAIYRRH-RGGSVTVYVCGSLISPCWVISATHCFIDY 201
DB 178 QYSQPFQDIKGLFADIAHPWQAALFAKHRRSPGERFLCGGILSSCWILSAAHCFQER 237
QY 202 PKEDYVIVLGRSLNNTQGEKMFVENILHKOYSADTLAHNDIALKIRSKERCA 261
DB 238 FPPHLLTVILGRYRVVPGEEOKFEVYKIVHKEFDDDT--YNDIALQLKSDSRCA 295
QY 262 QPSRTIOTICLPMSYNDPQFGTSCETITGFKENSTDYLYPEOLKMTVVKLIHSHRCQOPH 321
DB 296 QESSVVRTVCLPADLQLPDWTCELSGYGKHEALSPFYSERLKEAHVRLYPSRCTSQH 355
QY 322 YGSEVTTKMLCAAD-----POWKT-DSCQDGGPLVCSLOGRMTLTGIVSWGRCALK 375
DB 356 LLNRTVTDNMLCAGDTRSGGPQANLHDACQDGGPLVCLNDGRMTLVGIISWGLGCGQK 415
QY 376 DKPGVTVRSHFLPWIRSHTK 396
DB 416 DVPGVYTKVNYLDWIRDNR 436

RESULT 46

US-08-811-949-47
; Sequence 49, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-966-0
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 49:
; LENGTH: 437 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
8-811-949-47

Query Match 35.0%; Score 791; DB 2; Length 355;
st Local Similarity 44.8%; Pred. No. 3.1e-61;
Matches 159; Conservative 47; Mismatches 133; Indels 16; Gaps 6;

QY 50 CYEGNGHYFGKASTDTMGRPCLPWNSATVLOQTVHAHRSALQGLGKHNYCRNPDR 109
DB 8 CYFGNGSAYGTHSLTESGASCLPWNMILIGVYTAQNPASQALGGLGKHNYCRNPDGDA 67
QY 110 RPKYVQVGLKPLVQECMVHDCADGLKFKQCG-QKTLRPRFKIIGGEFTTIENQWFAAI 168
DB 68 KPWCHLVKRRLTWEYCDVPSCS-----TCGLRQYSQPQFRIIGGLFADIASHPWQAAI 121
QY 169 YRSH-RGGSVTVYVCGSLISPCWVISAHCDFIDYPKKEDYIVYLGSRSLNSNTQEMKPE 227
DB 122 FAKHRSPPGRFLCGGLILISSCWILSAAHCFQERPPPHLTVILGRTYRVVPGEEQKPE 181
QY 228 VENLILHKDYSADTLAHNDIALLKIRSKEGSCAQPSTRTIQTICLPSMYNDPQFGTSCBI 287
DB 182 VEKVIHKEFDDT--YNDNIALQLKSDSRCAQESSVVRTVCLPPADLQLPDWTCECEL 239
QY 288 TFGCKENSTDYLPQOLKMTVVKLISHRECCQPHYGVSEVTTKMLCAAD-----PQWKT- 341
DB 240 SGYKGHEALSPFYSERLKEAHVRLYPSRSTSOHLNRTVTDNMLCAGTSGGPPQANLH 299
QY 342 DSCQGSGLPLVCSLQGRMTLTGIVSWGRGCALDKPGVYTRVSHFLPWIRSHTK 396
DB 300 DACQGSGLPLVCLNDGRMTLVGLIISWGLGCGQKDPGVYTKVNYLDWIRDNR 354

UT 47
US 8-427-640-8
Query Match 35.0%; Score 790; DB 1; Length 356;
st Local Similarity 44.2%; Pred. No. 3.9e-61;

SEQUENCE CHARACTERISTICS:
LENGTH: 356 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
8-427-640-8

Query Match 35.0%; Score 790; DB 1; Length 356;
st Local Similarity 44.2%; Pred. No. 3.9e-61;

US-09-101-272G-80
; Sequence 80, Application US/08427640
; Patent No. 5658788
; GENERAL INFORMATION:
; APPLICANT: Berg et al.
; TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: U.S.A.
; ZIP: 46285.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/427,640
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/689,410
; FILING DATE: 22 APRIL 1991
; INFORMATION FOR SEQ ID NO. 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 356 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; 8-427-640-8

Matches 159; Conservative 49; Mismatches 136; Indels 16; Gaps 6;
QY 45 DKSKTCYEGNGHYFGKASTDTMGRPCLPWNSATVLOQTVHAHRSALQGLGKHNYCRN 104
DB 4 DTRATCYEDOGISYRGTWSTAEAGECTNWNSSALAKQPSGRRPPDAIRLGLGHNHNYCRN 63
QY 105 PDNRPRWCYVQVGLKPLVQECMVHDCADGLKFKQCG-QKTLRPRFKIIGGEFTTIENQ 163
DB 64 PDGDAKPCWCHLVKRRLTWEYCDVPSCS-----TCGLRQYSQPQFRIIGGLFADIASHP 117
QY 164 WFAAIYRSH-RGGSVTVYVCGSLISPCWVISAHCDFIDYPKKEDYIVYLGSRSLNSNTQ 222
DB 118 WQAAIFAKHRSPPGRFLCGGLILISSCWILSAAHCFQERPPPHLTVILGRTYRVVPGEE 177
QY 223 EMKEFEVENLILHKDYSADTLAHNDIALLKIRSKEGSCAQPSTRTIQTICLPSMYNDPQFG 282
DB 178 EQEVEVEKYIVHKEFDDT--YNDNIALQLKSDSRCAQESSVVRTVCLPPADLQLPDW 235
QY 283 TSCILTFGCKENSTDYLPQOLKMTVVKLISHRECCQPHYGVSEVTTKMLCAAD-----P 337
DB 236 TECELSGYKGHEALSPFYSERLKEAHVRLYPSRSTSOHLNRTVTDNMLCAGTSGGPP 295
QY 338 QWKT-DSCQGSGLPLVCSLQGRMTLTGIVSWGRGCALDKPGVYTRVSHFLPWIRSHTK 396
DB 296 QANLHDAQCQGSGLPLVCLNDGRMTLVGLIISWGLGCGQKDPGVYTKVNYLDWIRDNR 355

RESULT 48
US-09-101-272G-80
; Sequence 80, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: QS0979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ATFHI chimeric protein
US-09-101-272G-80

Query Match 34.9%; Score 788; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 2.7e-61;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYFG 60
DB 2 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYFG 61
QY 61 KASTDTMGRPCLPWNSATVLOQTVHAHRSALQGLGKHNYCRNPDRRPPWCYVQVGLK 120
DB 62 KASTDTMGRPCLPWNSATVLOQTVHAHRSALQGLGKHNYCRNPDRRPPWCYVQVGLK 121
QY 121 PLVQECMVHDCADG 134
DB 122 PLVQECMVHDCADG 135

RESULT 49
US-09-101-272G-96
; Sequence 96, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR

FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101.273G
CURRENT FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: JP 1059/1996
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.1
EQ ID NO 96
LENGTH: 201
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ATFHI-CL chimeric protein
09-101-272G-96

Query Match 34.8%; Score 786; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.8e-61;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNEHLQVPSNCDCLNGTGVSNKYFSNIHWCNPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
2 SNEHLQVPSNCDCLNGTGVSNKYFSNIHWCNPKKFGGQHCEIDKSKTCYEGNGHFYRG 61
61 KASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKKNYCRNPNRRRPMCYVQVGLK 120
62 KASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKKNYCRNPNRRRPMCYVQVGLK 121
121 PLVQRCMVHDCADG 134
122 PLVQRCMVHDCADG 135

ULT 50
09-553-498-10
Sequence 10, Application US/09553498
Patent No. 6309861
GENERAL INFORMATION:
APPLICANT: Ambrosius, Dorothee
APPLICANT: Rudolph, Rainer
APPLICANT: Schaeffner, Joerg
APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production of naturally folded and secreted prote
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
NUMBER OF SEQ ID NOS: 10
EQ ID NO 10
LENGTH: 378
TYPE: PRT
ORGANISM: E. coli
09-553-498-10

Query Match 34.8%; Score 786; DB 4; Length 378;
Best Local Similarity 44.8%; Pred. No. 9.3e-61;
Matches 158; Conservative 47; Mismatches 134; Indels 16; Gaps 6;

50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKKNYCRNPNRR 109
31 CYFGNGSAYRGTHSLTESGASCLPWNMSMLIGKVTYTAQNPSPAQLGLGKKNYCRNPDGDA 90
110 RPYCYVQVGLKPLVQRCMVHDCADGKLFQCG-QKTLRPRFKIIGGEFTTIENQPFQAAI 168
91 KPWCCHVLTNRRLTWECYDVPSCS-----TCGLRQVSPQPRIKGGLFADIASHPWQAAI 144
169 YRRH-RGGSVTVYCGGSLISPCWVISATHCFIDYPKKEDIYVTLGRSRLNSNTQGMKFE 227
145 FAKHRSRPFERLCGGILISSCWILSAAHCFQERPPPHLTVLGRTYRVVFGEEEQKFE 204
228 VENLILHKDYSADTLAHNDIALILKIRSKRGCAQPSRTIQICLPFSMYNDPQFGTSCEI 287
205 VEKYIVHKEFDDDT--YDNDIALQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTCEEL 262

QY 288 TGFGENSTDLYPEQLKMTVVKLISHRECQPHYGVSEVTTKMLCAAD-----PQWKT- 341
Db 263 SGYKHEALSPFYSERLKEBAHRLYPSRCTSQHLLNRTVTDNNLCAAGTFRSGGPOANLH 322
QY 342 DSCQGDSCGPLVCSLQGRMTLTGIVSWGRGCALDKFQVYTRVSHFLPWIRSHTK 396
Db 323 DACQGDSCGPLVCLNDGEMTLVGIISWGLGCGQKDFGVYTKVTNYLDWIRDNR 377

Search completed: May 25, 2004, 15:00:06
Job time : 30.9027 secs

GenCore version 5.1.6
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C: protein - protein search, using sw model

R: On: May 25, 2004, 14:47:10 ; Search time 8.27169 Seconds
(without alignments)
1662.947 Million cell updates/sec

T le: US-09-880-503-8

P: ict score: 837

S: ence: 1 SNEHQVPSNCDLNGTGV.....QECMVHDCADGKPSPPPE 143

S: ing table: BLOSUM62

S: hed: 283366 seqs, 96191526 residues

T: al number of hits satisfying chosen parameters: 283366

M: um DB seq length: 0

M: um DB seq length: 2000000000

P: -processing: Minimum Match 0%

D: base : PIR_78:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

File	Score	Query Match	Length	ID	Description
1	837	100.0	431	1 UKHU	u-plasminogen acti
2	757.5	90.5	433	1 UKBAY	u-plasminogen acti
3	625.5	74.7	442	1 UKPG	u-plasminogen acti
4	605	72.3	433	1 JN0560	u-plasminogen acti
5	592	70.7	432	1 S18932	u-plasminogen acti
6	569	68.0	433	1 UKMS	u-plasminogen acti
7	335.5	40.1	477	1 A34369	t-plasminogen acti
8	335.5	40.1	477	1 J30598	t-plasminogen acti
9	334.5	40.0	434	1 A35005	u-plasminogen acti
10	328.5	39.2	291	1 I38098	u-plasminogen acti
11	328.5	39.2	431	1 J30599	t-plasminogen acti
12	328.5	38.2	562	1 UKHUT	t-plasminogen acti
13	325	38.8	559	1 A35029	t-plasminogen acti
14	315.5	37.7	559	1 A39941	t-plasminogen acti
15	310.5	37.1	477	1 J30597	t-plasminogen acti
16	268	32.0	603	2 S28941	coagulation factor
17	265	31.7	558	2 J35878	plasma hyaluronan
18	263.5	31.5	560	1 J34795	plasma hyaluronan
19	262	31.3	655	1 A46688	hepatocyte growth
20	233	27.8	655	1 K2HU12	coagulation factor
21	223	26.6	394	2 J30600	t-plasminogen acti
22	217	25.9	593	2 S45281	coagulation factor
23	169	20.2	685	1 A48289	neurotrophic recep
24	163	19.5	460	2 B61545	plasmin (EC 3.4.21
25	162.5	19.4	4548	1 S00657	apoptein(a) (EC
26	161	19.2	1420	2 A32869	apolipoprotein(a)
27	160	19.1	123	2 A2869	plasmin (EC 3.4.21
28	159.5	19.1	810	2 B30848	plasmin (EC 3.4.21
29	159	19.0	120	2 E61545	plasmin (EC 3.4.21

plasmin (EC 3.4.21)
neurotrophic recep
plasmin (EC 3.4.21)
plasmin (EC 3.4.21)
plasmin (EC 3.4.21)
plasmin (EC 3.4.21)
plasmin (EC 3.4.21)
macrophage-stimula
plasmin (EC 3.4.21)
neurotrophic recep
apolipoprotein(a)
hypothetical prote
macrophage-stimula
hepatocyte growth
hepatocyte growth
hepatocyte growth
hepatocyte growth
plasmin precursor
thrombin (EC 3.4.2
thrombin (EC 3.4.2
xor-related recept
Notch homolog prote
thrombin (EC 3.4.2
hypothetical prote
notch homolog - se
aggreacan precursor
crumbs protein - f
Motch B protein -
glpi protein precu
notch protein homo
notch protein homo
notch protein - fr
Wnt inhibitory fac
protein FilC7, 4 [i
cell-fate determin
MEGFS protein - ra
Motch A protein -
notch-1 protein -
Notch homolog Motc
hypothetical prote
transmembrane prot

ALIGNMENTS

RESULT 1

UKHU

u-plasminogen activator (EC 3.4.21.73) precursor [validated] - human
N;Alternate names: cellular plasminogen activator; urokinase; urokinase-type plasminogen ac
N;Contains: urokinase-type plasminogen activator chain A; urokinase-type plasminogen ac
in form
C;Species: Homo sapiens (man)
C;Date: 17-Dec-1982 #sequence revision 04-Dec-1986 #text change 15-Sep-2000
C;Accession: A00931; I52209; J70102; A37561; I38102; S65783; A37562; A37563; A37564; A3
R;Riccio, A.; Grimaldi, G.; Verde, P.; Sebastiao, G.; Boast, S.; Blasi, F.
Nucleic Acids Res. 13, 2759-2771, 1985
A;Title: the human urokinase-plasminogen activator gene and its promoter.
A;Reference number: A00931; MUID:85215647; PMID:2987867
A;Accession: A00931
A;Molecule type: DNA
A;Residues: 1-431 <RIC>
A;Cross-references: GB:X02419; NID:G37601; PIDN:CAA26268.1; PID:G1834524
A;Note: the authors translated the codon ATG for residue 214 as Ile
R;Nagamine, Y.; Pearson, D.; Grattan, M.
Biochem. Biophys. Res. Commun. 132, 563-569, 1985
A;Title: Exon-intron boundary sliding in the generation of two mRNAs coding for porcine
A;Reference number: I52209; MUID:86050639; PMID:3933505

A; accession: I52209
A; atus: preliminary; translated from GB/EMBL/DBJ
A; molecule type: DNA
A; residues: 145-161 <NAG1>
A; references: GB:K03027; NID:9340174; PIDN:AAA1257.1; PID:9340175
R; Jai, M.; Hiramatsu, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama,
Ge 36, 183-188, 1985
A; title: Molecular cloning of cDNA coding for human preprourokinase.
A; reference number: J70102; MUID:86056954; PMID:2415429
A; accession: J70102
A; molecule type: mRNA
A; residues: 1-213, 'T', 215-431 <NAG2>
A; references: GB:K03026; NID:9340155; PIDN:AA097138.1; PID:9340158; GB:D00244; NID
R; dg, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Biasi, F.
Pr 1, Natl. Acad. Sci. U.S.A. 81, 4727-4731, 1984
A; title: Identification and primary sequence of an unspliced human urokinase poly(A) + RN
A; reference number: A37561; MUID:84272706; PMID:6589620
A; accession: A37561
A; molecule type: mRNA
A; residues: 66-431 <VER>
A; references: GB:D00244; NID:9220138
R; Coss, P.; Cravador, A.; Loriau, R.; Brockly, F.; Colau, B.; Chuchana, P.; van Elsen,
DN 4, 139-146, 1985
A; title: Molecular cloning, sequencing, and expression in Escherichia coli of human prep
A; reference number: I38102; MUID:85203359; PMID:3888571
A; accession: I38102
A; atus: preliminary
A; molecule type: mRNA
A; residues: 1-150, 'W', 152-213, 'I', 215-385, 'C', 387-429, 'V', 431 <JAC>
A; references: EMBL:X02760; NID:935297; PIDN:CAA26535.1; PID:935298
R; Shimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki,
Bi 1, Ann. Biophys. Acta 1293, 83-89, 1996
A; title: Characterization of single chain urokinase-type plasminogen activator with a no
A; reference number: S65783; MUID:96186279; PMID:8652631
A; accession: S65783
A; atus: preliminary
A; molecule type: mRNA
A; residues: 21-140, 'L', 142-213, 'I', 215-431 <YOS>
A; references: EMBL:D11143; NID:9311467; PIDN:BAA01919.1; PID:91199928
R; Izler, W.A.; Steffens, G.J.; Otting, F.; Kim, S.M.A.; Frankus, E.; Flohe, L.
Hc a-Seiler's Z. Physiol. Chem. 363, 1155-1165, 1982
A; title: The primary structure of high molecular mass urokinase from human urine.
A; reference number: A37562; MUID:83055084; PMID:6754569
A; accession: A37562
A; molecule type: protein
A; residues: 21-177 <GUN>
R; Haller, J.; Nick, H.; Rickli, E.E.; Gillesen, D.; Lergier, W.; Studer, R.O.
Eu J. Biochem. 125, 251-257, 1982
A; title: Human low-molecular-weight urinary urokinase. Partial characterization and prel
A; reference number: A37563; MUID:83003608; PMID:6749491
A; accession: A37563
A; molecule type: protein
A; residues: 156-176, 179-193, 'T', 195, 'T', 197-224 <SCH>
R; affens, G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
Hc a-Seiler's Z. Physiol. Chem. 363, 1043-1058, 1982
A; title: The complete amino acid sequence of low molecular mass urokinase from human uri
A; reference number: A37564; MUID:83055039; PMID:6754572
A; accession: A37564
A; molecule type: protein
A; residues: 158-410 <STE>
R; atzer, E.J.; Buko, A.; Menon, G.; Sarin, V.K.
Bi hem. Biophys. Res. Commun. 171, 401-406, 1990
A; title: Carbohydrate composition and presence of a fucose-protein linkage in recombinan
A; reference number: A35689; MUID:90365737; PMID:2393398
A; accession: A35689
A; molecule type: protein
A; residues: 21-30, 'X', 32, 'X', 34-38, 'X', 40-43 <KEN>
A; title: Identification of a fucose and attempt to determine its attachment site
R; Obani, S.A.; Desjardins, J.; Bell, A.W.; Banville, D.; Mazar, A.; Henkin, J.; Goltzm
Bi hem. Biophys. Res. Commun. 173, 1058-1064, 1990
A; title: An amino-terminal fragment of urokinase isolated from a prostate cancer cell li
A; reference number: A36697; MUID:91097529; PMID:2125213
A; accession: A36697

A; molecule type: protein
A; residues: 21-34 <RAB>
R; Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.
submitted to the Brookhaven Protein Data Bank, July 1993
A; reference number: A51255; PDB:KDU
A; contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R; Li, X.; Smith, R.A.G.; Dobson, C.M.
Biochemistry 31, 9562-9571, 1992
A; title: Sequential (1)H NMR assignments and secondary structure of the kringle domain f
A; reference number: A44375; MUID:93003110; PMID:1327118
A; contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
R; Hansen, A.P.; Petros, A.M.; Meadows, R.P.; Nettlesheim, D.G.; Mazar, A.P.; Olejniczak,
submitted to the Brookhaven Protein Data Bank, January 1994
A; reference number: A66822; PDB:1URK
A; contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R; Spraggon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.;
submitted to the Brookhaven Protein Data Bank, July 1995
A; reference number: A66058; PDB:1LMW
A; contents: annotation; X-ray crystallography, 2.5 angstroms, residues 168-175; 179-426
C; comment: This enzyme is found in urine in a high molecular mass form, consisting of A
C; comment: Urokinase-type plasminogen activator proteolytically activates plasminogen, a
C; genetics:
A; gene: GDB:PLAU
A; cross-references: GDB:119497; OMIM:191840
A; map position: 10q24-10q24
A; introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
C; function:
A; description: proteolytically activates plasminogen
A; pathway: fibrinolysis
C; superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C; keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; kringle; serine proteina
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 21-431/Product: urokinase-type plasminogen activator, single chain form #status predic
F; 21-177/Product: urokinase-type plasminogen activator chain A #status experimental <MPA
F; 31-62/Domain: EGF homology <AGF>
F; 70-151/Domain: kringle homology <KRG>
F; 156-177/Product: urokinase-type plasminogen activator chain A1 #status experimental <M
F; 179-431/Product: urokinase-type plasminogen activator chain B #status experimental <MP
F; 179-419/Domain: trypsin homology <TRY>
F; 31-39, 33-51, 53-62, 70-151, 91-133, 122-146, 168-299, 209-225, 217-288, 313-382, 345-361, 372-40
F; 38/Binding site: carbohydrate (Thr) (covalent) #status predicted
F; 178-179/cleavage site: lys-ile (plasmin) #status experimental
F; 224, 275, 376/Active site: His, Asp, Ser #status experimental
F; 322/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 9.5e-68;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNELHQVPSNCDCLNGTCTVSNKYFNSNIHWNCNPKFGGHCIDKSKTCYEGNGHFYRG 60
Db 21 SNELHQVPSNCDCLNGTCTVSNKYFNSNIHWNCNPKFGGHCIDKSKTCYEGNGHFYRG 80

Qy 61 KASDTWTGRCLPWSNATVLQOYTHAHSRDLQGLGKKNYCNPNRRPWCYVQVGLK 120
Db 81 KASDTWTGRCLPWSNATVLQOYTHAHSRDLQGLGKKNYCNPNRRPWCYVQVGLK 140

Qy 121 PLVQECNVHDCADGKPKSPPEE 143
Db 141 PLVQECNVHDCADGKPKSPPEE 163

RESULT 2
UKBAY
u-plasminogen activator (EC 3.4.21.73) precursor - yellow baboon
C; Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C; Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C; Accession: S14687; S05651
R; Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
Nucleic Acids Res, 18, 3411, 1990
A; title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasminoge
A; reference number: S14687; MUID:90287734; PMID:2113276
A; accession: S14687

A Molecule type: mRNA
 A Residues: 1-433 <AUV>
 A Cross-references: EMBL:X51935; NID:G38130; PIDN:CAA36200.1.1; PID:G38131
 C Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
 C Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
 F 1-176/Domain: signal sequence #status predicted <SIG>
 F 1-176/Product: plasminogen activator chain A #status predicted <ACH>
 F 1-176/Domain: EGF homology <EGF>
 F 1-150/Domain: kringle homology <KRG>
 F 1-433/Product: plasminogen activator chain B #status predicted <BCH>
 F 1-421/Domain: trypsin homology <TRY>
 F 1-298,208-224,216-287,315-384,347-363,374-402/Disulfide bonds: #status predicted
 F 3,274,378/Active site: His, Asp, Ser #status predicted
 F 24/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 90.5%; Score 757.5; DB 1; Length 433;
 Best Local Similarity 92.3%; Pred. No. 1.3e-60; Indels 1; Gaps 1;
 Matches 132; Conservative 4; Mismatches 6; Indels 1; Gaps 1;
 Q 1 SNELHGV--PSNCDCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
 D 21 SREL-QVPSDCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 79
 Q 61 YASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDRRRPWCYVQVGLK 120
 D 80 KASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDRRRPWCYVQVGLK 139
 Q 121 PLVQECMVHDCADGKPKSPSPPEE 143
 D 140 QRVCQMVHNCADGKPKSPSPPEE 162
 R JLT 3
 U 3
 U plasminogen activator (EC 3.4.21.73) precursor - pig
 N Alternate names: uPA
 C Species: Sus scrofa domestica (domestic pig)
 C Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
 C Accession: A00932
 R Arginine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
 R ILE: cDNA and gene nucleotide sequence of porcine plasminogen activator.
 A ILE: cDNA and gene nucleotide sequence of porcine plasminogen activator.
 A Reference number: A00932; MUID:85087954; PMID:6096832
 A Accession: A00932
 A Molecule type: DNA
 A Residues: 1-240, 'H', 242-442 <NAG1>
 A Experimental source: kidney cell line LIC-PK1
 A Submitted to the Protein Sequence Database, December 1986
 A Reference number: A37566
 A Contents: annotation; correction to residue 241
 A Notes: 19/3; 31/1; 67/1; 125/2; 165/1; 238/2; 288/1; 335/1; 384/3
 A Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
 C Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
 F 1-20/Domain: signal sequence #status predicted <SIG>
 F 1-188/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
 F 1-64/Domain: EGF homology <EGF>
 F 2-153/Domain: kringle homology <KRG>
 F 90-442/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
 F 90-430/Domain: trypsin homology <TRY>
 F 52/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F 79-310,220-236,228-299,324-393,356-372,383-411/Disulfide bonds: #status predicted
 F 35,286,387/Active site: His, Asp, Ser #status predicted
 Query Match 74.7%; Score 625.5; DB 1; Length 442;
 Best Local Similarity 73.4%; Pred. No. 9.2e-49; Indels 11; Gaps 2;
 Matches 113; Conservative 11; Mismatches 19; Indels 11; Gaps 2;
 Q 1 SNELHGV--PSNCDCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFY 58
 D 21 SHELHGVESGASNGCLNGGCKVSYKYFSNIQRCSCKPKFGQHCIEDTSQTCEGNGHSHY 80

QY 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDRRRPWCYVQV 118
 DB 81 RKGANTNTGRCPLPWSATVLLNTYHAHR PDALQLGLGKHNYCRNPDRRQREWCYVQV 140
 QY 119 LKPLVQECMVHDCADGKPKSPSPPEE 143
 DB 141 LKQLVQECMVHDCADGKPKSPSPPEE 174
 RESULT 4
 UN50560
 u-plasminogen activator (EC 3.4.21.73) precursor - bovine
 N Alternate names: uPA
 C Species: Bos primigenius taurus (cattle)
 C Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
 C Accession: JN0560
 R Xaetzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
 Gene 125, 177-183, 1993
 A Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and indu
 A Reference number: JN0560; MUID:93216119; PMID:8385052
 A Accession: JN0560
 A Molecule type: mRNA
 A Residues: 1-433 <KRA>
 A Cross-references: GB:L03546; NID:G163800; PIDN:AAA51419.1; PID:G163801
 C Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; tr
 C Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
 F 1-20/Domain: signal sequence #status predicted <SIG>
 F 21-179/Product: plasminogen activator chain A #status predicted <MA1>
 F 21-179/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
 F 33-64/Domain: EGF homology <EGF>
 F 72-153/Domain: kringle homology <KRG>
 F 181-433/Product: plasminogen activator chain B #status predicted <MA2>
 F 181-421/Domain: trypsin homology <TRY>
 F 170-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
 F 226,277,378/Active site: His, Asp, Ser #status predicted
 Query Match 72.3%; Score 605; DB 1; Length 433;
 Best Local Similarity 72.4%; Pred. No. 6.3e-47;
 Matches 105; Conservative 14; Mismatches 24; Indels 2; Gaps 1;
 QY 1 SNELHGV--PSNCDCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFY 58
 DB 21 SNEVHKGESGNGCLNGGCKVYKYFSNIQRCSCKPKFGQHCIEDTSQTCEGNGHSHY 80
 QY 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRS DALQLGLGKHNYCRNPDRRRPWCYVQV 118
 DB 81 RKGANDLSGRPCLPWNSATVLLNTYHAHR SDALQLGLGKHNYCRNPDRRQREWCYVQ 140
 QY 119 LKPLVQECMVHDCADGKPKSPSPPEE 143
 DB 141 LKQVQECMVHDCADGKPKSPSPPEE 165
 RESULT 5
 SI8932
 u-plasminogen activator (EC 3.4.21.73) precursor - rat
 N Alternate names: plasminogen activator; urokinase-type; urinary plasminogen activator
 C Species: Rattus norvegicus (Norway rat)
 C Date: 18-Oct-1989 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
 C Accession: S24604; I60186; I53472; SI8932
 R Rabbani, S.A.
 submitted to the EMBL Data Library, April 1992
 A Reference number: S24604
 A Accession: S24604
 A Molecule type: mRNA
 A Residues: 1-15, 'H', 17-23, 'G', 25-331, 'N', 333-432 <RAB>
 A Cross-references: EMBL:X65651; NID:G57456; PIDN:CAA46601.1; PID:G57457
 A Experimental source: tissue kidney
 R Henderson, B.R.; Tansey, W.P.; Phillips, S.M.; Ramshaw, I.A.; Kefford, R.F.
 Cancer Res. 52, 2489-2496, 1992
 A Title: Transcriptional and posttranscriptional activation of urokinase plasminogen ac
 A Reference number: I60186; MUID:92233409; PMID:1568219
 A Accession: I60186

A: atus: preliminary; translated from GB/EMBL/DBSJ
A: lecul type: mRNA
A: sidues: 1-432 <RES>
A: sss-references: EMBL:X63434; NID:g57465; PIDN:CAA45028.1; PID:g57466
A: Desimalntal source: strain Fischer 344; tissue mammary
A: mo, P.; Cassano, S.; Degen, J.; Kessler, C.; Blasi, F.; Rossi, G.
FE lect. 306, 193-198, 1992
A: le: The receptor for the plasminogen activator of urokinase type is up-regulated in
A: ference number: I53472; MUID:92339549; PMID:1321734
A: session: I53472
A: atus: preliminary; translated from GB/EMBL/DBSJ
A: lecul type: DNA
A: sidues: 31-62 <RE2>
A: sss-references: EMBL:X66907; NID:g336200; PIDN:CAA47356.1; PID:g938279
C: etics:
C: e: ufa
C: efamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C: words: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F: 19/Domain: signal sequence #status predicted <SIG>
F: 177/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F: -62/Domain: EGF homology <EGF>
F: 151/Domain: kringle homology <KRG>
F: 9-432/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
F: 3-420/Domain: trypsin homology <TRY>
F: 3-300,210-226,218-289,314-383,346-362,373-401/Disulfide bonds: #status predicted
F: 5,276,377/Active site: His, Asp, Ser #status predicted
A: ry Match 70.7%; Score 592; DB 1; Length 432;
A: Best Local Similarity 75.6%; Pred. No. 9.2e-46;
A: Matches 102; Conservative 10; Mismatches 23; Indels 0; Gaps 0;
QY 9 SNCDCLNGGTCVSNKYFSNIHWCNCPKFGGHCEDKSKTCYEGNGHFPYRGKASTDTMG 68
Db 29 SNCCQNGGVCSYKVFSSIRRCSCPKFKGHCEDTSTCTVHGNGQSYRGKANTDTKG 88
QY 69 RPLCPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDRRRPWCYVQGLKPLVQECMV 128
Db 89 RPLCLMNSPAVLQFYNAHRSALSLGLGKHNYCRNPDRNQRPPWCYVQGLKQFVQECMV 148
QY 129 HDCADGKKPSSPPE 143
Db 149 QDCSLSKKPSSTVDQ 163
RE 126
UK 126
A: asminogen activator (EC 3.4.21.73) precursor - mouse
C: e: Mus musculus (house mouse)
C: e: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C: session: A29420, A24615
A: en, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
B: emistry 26, 8270-8279, 1987
A: le: The murine urokinase-type plasminogen activator gene.
A: ference number: A29420; MUID:88163489; PMID:2831940
A: session: A29420
A: lecul type: DNA
A: sidues: 1-433 <DEG>
A: sss-references: GB:M17922; NID:g202296; PIDN:AAA40539.1; PID:g202297
A: lin, D.; Vassalli, J.D.; Compeigne, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher,
Eu J. Blochem. 148, 225-232, 1985
A: le: Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase
A: ference number: A24615; MUID:85179474; PMID:2985383
A: session: A24615
A: lecul type: mRNA
A: sidues: 1-433 <BEL>
A: sss-references: GB:X02389; NID:g55127; PIDN:CAA26231.1; PID:g55128
C: etics:
C: rons: 19/3; 30/1; 66/1; 124/2; 155/1; 229/2; 279/1; 326/1; 375/3
C: efamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C: words: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F: 20/Domain: signal sequence #status predicted <SIG>
F: -178/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F: -63/Domain: EGF homology <EGF>

F:71-152/Domain: kringle homology <KRG>
F:180-433/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
F:180-421/Domain: trypsin homology <TRY>
F:165-301,211-227,218-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
F:226,277,378/Active site: His, Asp, Ser #status predicted
Query Match 68.0%; Score 569; DB 1; Length 433;
Best Local Similarity 70.4%; Pred. No. 1.1e-43;
Matches 95; Conservative 15; Mismatches 25; Indels 0; Gaps 0;
QY 9 SNCDCLNGGTCVSNKYFSNIHWCNCPKFGGHCEDKSKTCYEGNGHFPYRGKASTDTMG 68
Db 30 SNCCQNGGVCSYKVFSSIRRCSCPKFKGHCEDTSTCTVHGNGDSYRGKANTDTKG 89
QY 69 RPLCPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDRRRPWCYVQGLKPLVQECMV 128
Db 90 RPLCLMNSPAVLQFYNAHRSALSLGLGKHNYCRNPDRNQRPPWCYVQGLKQFVQECMV 149
QY 129 HDCADGKKPSSPPE 143
Db 150 HDCSLSKKPSSTVDQ 164
RESULT 7
A34369
A: t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C: Species: Megaderma lyra
C: Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C: Accession: A34369
R: J. Biol. Chem. 264, 17947-17952, 1989
A: Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin
A: Reference number: A34369; MUID:90036867; PMID:2509450
A: Accession: A34369
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-477 <GAR>
A: Cross-references: GB:J05082; NID:g166080; PIDN:AAA31596.1; PID:g166081
C: Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C: Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F: 1-21/Domain: signal sequence #status predicted <SIG>
F: 22-36/Domain: propeptide #status predicted <PRO>
F: 37-477/Product: plasminogen activator #status predicted <PLA>
F: 42-79/Domain: fibronectin type I repeat homology <1FA>
F: 87-120/Domain: EGF homology <EGF>
F: 128-209/Domain: kringle homology <KRG>
F: 226-471/Domain: trypsin homology <TRY>
F: 42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F: 272,321,428/Active site: His, Asp, Ser #status predicted
Query Match 40.1%; Score 335.5; DB 1; Length 477;
Best Local Similarity 46.3%; Pred. No. 1e-22;
Matches 62; Conservative 17; Mismatches 50; Indels 5; Gaps 2;
QY 3 ELHVP---SNCDCLNGGTCVSNKYFSNIHWCNCPKFGGHCEDKSKTCYEGNGH 58
Db 78 QCHTVPKVKSSELRFCFNGGTCWQAASFDF-VQCQPKGYTGKQCEVDTHATCKDQV 136
QY 59 RGKASTDTMGRCPLPWNASATVLOQTYHAHRSALQGLGKHNYCRNPDRRRPWCYVQ 118
Db 137 RGTWSTSESQAQCINMNSNLLTERTYNGRSDDATILGLGNHNYCRNPDRNNSKPCYV 196
QY 119 LKPLVQSCWVDCA 132
Db 197 SKFILEFCSPVPCS 210
RESULT 8
J50598
A: t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat
N: Alternate names: tissue plasminogen activator
C: Species: Desmodus rotundus (common vampire bat)
C: Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999

```

cession: JS0598
Caetzschnar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Dor
K 3 105, 229-237, 1991
A title: The plasminogen activator family from the salivary gland of the vampire bat Des
A reference number: JS0597; MUID:92039036; PMID:1937019
A accession: JS0598
A clecule type: mRNA
A residues: 1-477 <KEA>
A cross-references: GB:M63988; NID:G166074; PIDN:AAA31593.1; PID:G166075
C superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F -21/Domain: signal sequence #status predicted <SIG>
F -36/Domain: propeptide #status predicted <PRO>
F 7-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
E 7-79/Domain: fibronectin type I repeat homology <lFA>
F 1-120/Domain: EGF homology <EGF>
F 38-209/Domain: kringle homology <KR>
F 36-477/Domain: trypsin homology <TRY>
F 3-72, 70-79, 87-98, 92-109, 111-120, 128-209, 149-191, 180-204, 214-345, 257-273, 265-334, 359-4
F 35, 398/Binding site: carbohydrate (Asn) (covalent) #status predicted
F 25-226/Cleavage site: His-Ser (plasmin) #status predicted
F 72, 321, 428/Active site: His, Asp, Ser #status predicted

very Match          40.1%; Score 335.5; DB 2; Length 477;
st Local Similarity 46.3%; Pred. No. 1e-22;
atches 62; Conservative      17; Mismatches 50; Indels 5; Gaps 2;

Q   3 ELHQVP-----SNCDLNGTCVSNKYFSNIHWCNCPKFGGQHCEIDKSKTVEGNHGY 58
D   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
D   78 QCHTVPVKSCSELRFCNGGTGWOAASFDF-VQQCPKGYTGKQCEVDTHATCYKDQGVTY 136
Q   59 RGRKASTDTMGRCPLPWNASATVLQQTVAHRSDALQLGLGHNYCRPNRRRFPWCVVQVG 118
D   :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
D   137 RGTWSTSESQAQCINNWSNLTRTYNGRESDAITLGLGNHYCRPNDDNSKPWCYVIKA 196
Q   119 LKPLVQECMVHDCA 132
D   :|:|:|:|:|:|:|:|:|:~
D   197 SKFLTECSFVCVS 210

R   JUL 9
U   plasminogen activator (EC 3.4.21.73) precursor - chicken
N   alternate names: uPA
N   species: Gallus gallus (chicken)
C   ate: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999
C   cession: A35005
R   slie, N.D.; Kessler, C.A.; Bell, S.M.; Degen, J.L.
R   Biol. Chem. 265, 1339-1344, 1990
A   title: The chicken urokinase-type plasminogen activator gene.
A   eference number: A35005; MUID:90110185; PMID:2295632
A   atus: preliminary
A   lecle type: mRNA
A   idues: 1-434 <LES>
A   ross-references: GB:J05187; NID:G212858; PIDN:AAA49131.1; PID:G212859
C   perfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C   ywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F   -21/Domain: signal sequence #status predicted <SIG>
F   7-171/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F   7-71/Domain: EGF homology <EGF>
F   9-158/Domain: kringle homology <KR>
F   F3-428/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
F   F3-416/Domain: trypsin homology <TRY>
F   F2-296, 202-218, 210-285, 310-379, 342-358, 369-397/Disulfide bonds: #status predicted
F   17,272,373/Active site: His, Asp, Ser #status predicted

very Match          40.0%; Score 334.5; DB 1; Length 434;
st Local Similarity 54.2%; Pred. No. 1.2e-22;
atches 58; Conservative     14; Mismatches 30; Indels 5; Gaps 2;

Q   11 CDCLINGTCVSNKYFSNIHWCNCPKFGGQHCEIDKSKTVEGNHGYRGKASTDTMGPR 70

```

[illegible]

C; words: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F; 21/Domain: signal sequence #status predicted <SIG>
F; 36/Domain: propeptide #status predicted <PRO>
F; 431/Product: plasminogen activator beta #status predicted <PLA>
F; 74/Domain: EGF homology <EGF>
F; 163/Domain: kringle homology <KR>
F; 0-425/Domain: trypsin homology <TRY>
F; 52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bond
F; 3352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 9-180/Cleavage site: His-Ser (plasmin) #status predicted
F; 5,275,382/Active site: His, Asp, Ser #status predicted
F; 5-361,378-406/Disulfide bonds: #status predicted
F; 39.2%; Score 328.5; DB 2; Length 431;
F; Local Similarity 47.8%; Pred. NO. 4.1e-22;
F; Conservative 16; Mismatches 48; Indels 1; Gaps 1;
QY 9 SNDCCLNGTGVSNKYFNSIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRKASTDTMG 68
Db 42 SELRCFNGGTQCAASFDF-VCQPKGYTGQCEVDTHATCYKQGVYRGTSSTSG 100
QY 69 RPLPNSATVLOOTHARSALQGLGKHYCRNPNRRPWCYVQVGLKPLVQECW 128
Db 101 AQCIWNSLLTRTYNGRSDAITLGLGNHYCRNPNRRPWCYVQVGLKPLVQECW 160
QY 129 HDCA 132
Db 161 PVCS 164
RE 12
UK 1
t- aminogen activator (EC 3.4.21.68) precursor (validated) - human
N; alternate names: t-PA; tissue plasminogen activator
C; species: Homo sapiens (man)
C; 14-Nov-1983 #sequence revision 14-Nov-1993 #text change 08-Dec-2000
C; session: A94004; A23529; JT0562; A93293; S02125; A91343; A93951; A91322; A54645; 160
R; T.; Elgh, P.; Lund, B.
Pr; Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984
A; title: The structure of the human tissue-type plasminogen activator gene: correlation
A; session number: A94004; MUID:84298137; PMID:6089198
A; molecule type: DNA
A; residues: 1-562 <NT>
A; res-references: GB:L00141
A; note: the codon given for residue 93 (ACC) is inconsistent with the authors' translation
R; lezner Degen, S.J.; Rajput, B.; Reich, E.
J. Biol. Chem. 261, 6972-6985, 1986
A; title: The human tissue plasminogen activator gene.
A; session number: A23529; MUID:86196143; PMID:3009482
A; molecule type: DNA
A; residues: 1-562 <DEG>
A; res-references: GB:K03021; NID:G339817; PIDN:AAA98809.1; PID:G339818
R; Igaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuda, S.; Higashio, K.
AG 2. Biol. Chem. 55, 1225-1232, 1991
A; title: Purification and characterization of tissue plasminogen activator secreted by H
A; session number: JT0562; MUID:914291340; PMID:1366681
A; molecule type: mRNA
A; residues: 31-562 <ITA>
A; res-references: DBJ:001096; NID:G220128; PIDN:AAA00881.1; PID:G441174
A; experimental source: embryonic lung fibroblast IMR-90 cells
A; note: part of this sequence, including the amino end of the mature protein, was confir
R; uica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vohar, G.A.; Ward, C.A.; Bennett
Na 3301, 214-221, 1993
A; title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche
A; session number: A93293; MUID:83115262; PMID:6337343
A; molecule type: mRNA
A; residues: 1-562 <PEN>
A; res-references: GB:L00141
A; experimental source: melanoma cells

R;Sasaki, H.; Saito, Y.; Hayaashi, M.; Otsuka, K.; Niwa, M.
Nucleic Acids Res. 16, 5695, 1988
A; title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe
A; reference number: S02125; MUID:88282579; PMID:3133640
A; accession: S02125
A; status: translation not shown
A; molecule type: mRNA
A; residues: 1-562 <SAS>
A; cross-references: EMBL:X07393; NID:G37243; PIDN:CAA30302.1; PID:G37244
A; experimental source: fetal lung cells
R;Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma
FEBS Lett. 189, 145-149, 1985
A; title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen
A; reference number: A91343; MUID:85285620; PMID:3896853
A; accession: A91343
A; molecule type: mRNA
A; residues: 1-38, 'G', '86-433, 'E', 435-562 <KAG>
R;Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983
A; title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ
A; reference number: A93951; MUID:83169656; PMID:6572897
A; accession: A93951
A; molecule type: mRNA
A; residues: 251-358 <EDL>
A; experimental source: melanoma cells
R;Pohl, G.; Kaliström, M.; Bergsdorf, N.; Wallen, P.; Jörnvall, H.
Biochemistry 23, 3701-3707, 1984
A; title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived am
differences.
A; reference number: A90488; MUID:85000468; PMID:6433976
R;Pohl, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jörnvall, H.
FEBS Lett. 168, 29-32, 1984
A; title: Differences between uterine and melanoma forms of tissue plasminogen activator.
A; reference number: A91322; MUID:84158956; PMID:6538514
A; accession: A91322
A; molecule type: protein
A; residues: 33-45; 311-320 <POH>
A; experimental source: uterus
A; note: in the uterus, cleavage of the activation peptide may also occur after 38-Gln
J. Biol. Chem. 261, 14214-14218, 1986
R;Rivon Zonneveld, A.J.; Veerman, H.; Pannekoek, H.
A; reference number: A37567; MUID:87033611; PMID:3021732
R;Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger
EMBO J. 5, 3525-3530, 1986
A; title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen ac
A; reference number: A37568; MUID:87161761; PMID:3030730
A; contents: annotation; fibrin binding site
R;Dodd, I.; Nunn, B.; Robinson, J.H.
Thromb. Haemost. 59, 523-528, 1988
A; title: Isolation, identification and pharmacokinetic properties of human tissue-type p
A; reference number: A60902; MUID:89044681; PMID:3142086
A; contents: annotation; novel forms of expressed recombinant t-PA
R;Harris, T.J.R.; Patel, T.; Marston, F.A.O.; Little, S.; Entage, J.S.; Opdenakker, G.;
Mol. Biol. Med. 3, 279-292, 1986
A; title: Cloning of cDNA coding for human tissue-type plasminogen activator and its expr
A; reference number: A54645; MUID:86284200; PMID:3090401
A; accession: A54645
A; molecule type: mRNA
A; residues: 1-562 <EAR>
A; cross-references: GB:M15518; NID:G190031; PIDN:AAA60111.1; PID:G190032
A; note: parts of this sequence were confirmed by peptide sequencing
R;Reddy, V.B.; Garramone, A.J.; Sasak, H.; Wei, C.
DNA 6, 461-472, 1987
A; title: Expression of human uterine tissue-type plasminogen activator in mouse cells us
A; reference number: 160110; MUID:88054470; PMID:2824147
A; accession: 160110
A; status: translated from GB/EMBL/DBJ
A; molecule type: mRNA
A; residues: 1-562 <RES>
A; cross-references: GB:M18182; NID:G340176; PIDN:AAA36800.1; PID:G340177

Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.
 J Biol. Chem. 260, 11223-11230, 1995
 A title: Isolation and characterization of the human tissue-type plasminogen activator s
 A reference number: 155233; PMID:18528938; PMID:3161893
 A accession: 155232
 A status: preliminary; translated from GB/EMBL/DBJ
 A molecule type: DNA
 A residues: 1-36 <RE2>
 A cross-references: GB:M11890; NID:G339837; PIDN:AAA61213.1; PID:G339839
 C comment: Cleavage by plasmin or trypsin produces two chains held together by a single
 C comment: t-PA converts plasminogen to plasmin by hydrolyzing a single Arg-Val bond. 10
 C comment: t-PA binds chain A of fibrin by kringle 2 and the fibronectin type I repeat.
 C enetics:
 A gene: GDB:PLAT
 A cross-references: GDB:119496; OMIM:173370
 A map position: 8p12-8p12
 A atoms: 24/3; 39/1; 122/1; 180/2; 211/1; 268/2; 297/1; 362/2; 408/1; 455/3; 510
 C superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
 F 23/Domain: signal sequence #status predicted <SIG>
 F 4-32/Domain: propeptide #status predicted <PRO>
 F 3-562/Product: t-plasminogen activator #status experimental <MAT>
 F 3-310/Product: t-plasminogen activator chain A #status experimental <ACH>
 F 1-78/Domain: fibronectin type I repeat homology <IF1>
 F 5-119/Domain: EGF homology <EGF>
 F 27-208/Domain: kringle homology <KR1>
 F 15-296/Domain: kringle homology <KR2>
 F 11-556/Domain: trypsin homology <TRY>
 F 1-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203,215-296,236-278,267-291,299-4
 F 2,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F 19/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F 10-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental
 F 37,406/Active site: His, Asp #status predicted
 F 13/Active site: Ser #status experimental
 Query Match 39.2%; Score 328.5; DB 1; Length 562;
 Best Local Similarity 46.3%; Pred. No. 5.1e-22;
 Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;
 Q 3 ELHQVP-SNCD---CLNGTGVSNKYPFSNIHWNCNPKFGGQHCHIDKSKTCYEGNGHFY 58
 D 77 QCHSVFVRSCEPRFCNGTCQOALYFSDP-VCCQPEGFAGKCCIDTRATCFEGQGIT 135
 C 59 RGKASDTMTGRPCLPWNSATVLQOTVHAHRS DALQLGLGKHNYCRNPDRRRPWCYVQVG 118
 D 136 RGTWSTAESGACTWNSALQAQKYSGRPPAIRLGLGNHNYCRNPDRDSKPCWCVFKA 195
 C 119 LKPLVQECMWHCADG 134
 D 196 GYSSEFCSTPACSEG 211
 R ULT 13
 A 129
 C lasminogen activator (EC 3.4.21.68) precursor - rat
 C ecies: Rattus norvegicus (Norway rat)
 C te: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C ccession: A35029; A31597
 R ang, P.; Ohlsson, M.; Ny, T.
 J Biol. Chem. 265, 2022-2027, 1990
 A title: The structure of the TATA-less rat tissue-type plasminogen activator gene. Spec
 A reference number: A35029; PMID:190130448; PMID:2105315
 A accession: A35029
 A status: preliminary
 A molecule type: DNA
 A residues: 1-559 <PEN>
 A cross-references: GB:M31197; NID:G207429; PIDN:AAA42261.1; PID:G207431; GB:J05226
 F 7, 671-677, 1986
 D 1, T.; Leonardsson, G.; Heueh, A.J.W.
 A title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activato
 A reference number: A31597; PMID:89170114; PMID:3148445
 A accession: A31597

A:Molecule type: mRNA
 A:Residues: 1-379, 'K', 381-559 <NVT>
 A:Cross-references: GB:M23897; NID:G530159; PIDN:AAA1812.1; PID:G530160
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat ho
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F 1-17/Domain: signal sequence #status predicted <SIG>
 F 18-29/Domain: propeptide #status predicted <PRO>
 F 30-559/Product: t-plasminogen activator #status predicted <MAT>
 F 30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
 F 38-75/Domain: fibronectin type I repeat homology <IF1>
 F 83-116/Domain: EGF homology <EGF>
 F 124-205/Domain: kringle homology <KR1>
 F 213-294/Domain: kringle homology <KR2>
 F 309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
 F 309-553/Domain: trypsin homology <TRY>
 F 38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-
 F 149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F 308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
 F 335,404,510/Active site: His, Asp, Ser #status predicted
 Query Match 38.8%; Score 325; DB 1; Length 559;
 Best Local Similarity 44.1%; Pred. No. 1e-21;
 Matches 64; Conservative 15; Mismatches 56; Indels 10; Gaps 3;
 Q 3 ELHQVP-----SNCDCLNGTGVSNKYPFSNIHWNCNPKFGGQHCHIDKSKTCYEGNGHFY 58
 D 74 QCHSVFVRSCEPRFCNGTCQOALYFSDP-VCCQPEGFAGKCCIDTRATCFEGQGIT 132
 Q 59 RGKASDTMTGRPCLPWNSATVLQOTVHAHRS DALQLGLGKHNYCRNPDRRRPWCYVQVG 118
 D 133 RGTWSTAESGACTWNSALQAQKYSGRPPAIRLGLGNHNYCRNPDRDSKPCWCVFKA 192
 Q 119 LKPLVQECMWHCADGKKPSSPPEE 143
 D 193 GYTTTEFCSTPAC-----PKGPTED 212
 RESULT 14
 A29941
 t-plasminogen activator (EC 3.4.21.68) precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A29941; S48205; S48206; S48207
 R:Rickles, R.J.; Darrow, A.L.; Strickland, S.
 J. Biol. Chem. 263, 1563-1569, 1988
 A:Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator m
 A:Reference number: A29941; PMID:88087303; PMID:2826484
 A:Accession: A29941
 A:Molecule type: mRNA
 A:Residues: 1-559 <RIC>
 R:Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A:Title: Characterization of the murine plasma fibrinolytic system.
 A:Reference number: S48202; PMID:95010076; PMID:7523120
 A:Accession: S48205
 A:Molecule type: protein
 A:Residues: 33-37, 'X', 39-40 <LIJ>
 A:Accession: S48207
 A:Molecule type: protein
 A:Residues: 309-316 <LI2>
 A:Accession: S48206
 A:Molecule type: protein
 A:Residues: 33-37, 'X', 39-40 <LIW>
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat ho
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F 1-17/Domain: signal sequence #status predicted <SIG>
 F 18-29/Domain: propeptide #status predicted <PRO>
 F 30-559/Product: t-plasminogen activator #status predicted <MAT>
 F 30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
 F 38-75/Domain: fibronectin type I repeat homology <IF1>
 F 83-116/Domain: EGF homology <EGF>
 F 124-205/Domain: kringle homology <KR1>

coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
NAlternate names: Hageman factor
CSpecies: Cavia porcellus (guinea pig)
CDate: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
CAccession: S28941
R:Samba, U.; Yanamoto, T.; Kuniada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, H.
Biochim. Biophys. Acta 1159, 113-121, 1992
A>Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage site
AReference number: S28941; MUID:93003367; PMID:1390917
AAccession: S28941
AStatus: preliminary
AMolecule type: mRNA
AResidues: 1-603 <SEM>
ACross-references: EMBL:X68615; NID:G49578; PID:CAA48600.1; PID:G49579
CSuperfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
CKeywords: hydrolase; serine proteinase
F146-57/Domain: fibronectin type II repeat homology <PBI>
F134-169/Domain: fibronectin type I repeat homology <EGF>
F177-208/Domain: EGF homology <EGF>
F216-294/Domain: kringle homology <KRG>
F359-597/Domain: trypsin homology <TRY>

Query Match 32.0%; Score 268; DB 2; Length 603;
Best Local Similarity 39.6%; Pred No. 1,4e-16;
Matches 51; Conservative 21; Mismatches 52; Indels 8; Gaps 3;

QY 13 CLNGTCTVSNKYFSNIHWNCNPKFGGQHCEIDKSCTCYEKGNGHYRKGKASTDTWGRPLC 72
||| | : : : : :
DB 182 CLNGGRCLSE--VEGHILCDCPMGVTGPFCDDLTATSCYEGRGVSYRGMAITVSQAKCQ 238
||| | : : : : :
QY 73 PWSNATVLQOITYHAURSD-ALQLGLGKYNCRPNDRRRPWCVVOGLKPLVOECMWHD 131
||| | : : : : :
DB 239 RWAS----EATRYNTAQALRRLGHHFTFCENPDNDTFPCFVMGNLSWEYCDLAQC 294
||| | : : : : :

QY 132 ADGKPSPSPPEE 143
||| | : : : : :
DB 295 QYPPOQTATPHD 306

RESULT 17
JCS878
plasma hyaluronan-binding protein precursor - mouse
CSpecies: Mus musculus (house mouse)
CDate: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999
CAccession: JCS878
R:Hashimoto, K.; Tohe, T.; Sumiya, J.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, N.
Biol. Pharm. Bull. 20, 1127-1130, 1997
A>Title: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyaluronan-bin-
AReference number: JCS878; MUID:98065239; PMID:9401717
AAccession: JCS878
AMolecule type: mRNA
AResidues: 1-558 <HAS>
CComment: This protein acts as serine protease.
CSuperfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsi-
F1-23/Domain: signal sequence #status predicted <Sig>
F124-311/Product: plasma hyaluronan-binding protein large chain #status predicted <MATL>
F175-106/Domain: EGF homology <EG1>
F113-145/Domain: EGF homology <EG2>
F152-185/Domain: EGF homology <EG3>
F192-274/Domain: kringle homology <KRI>
F312-558/Product: plasma hyaluronan-binding protein small chain #status predicted <MATS>
F312-548/Domain: trypsin homology <TRY>

Query Match 31.7%; Score 265; DB 2; Length 558;
Best Local Similarity 41.1%; Pred No. 2,5e-16;
Matches 53; Conservative 19; Mismatches 51; Indels 6; Gaps 4;

QY 13 CLNGTCTVSNKYFSNIHWNCNPKFGGQHCEIDKSCTCYEKGNGHYRKGKASTDTWGRPLC 72
||| | : : : : :
DB 157 CONGGVCSSHRSRFF-TCAPDPQVKGFCEIGPD-DGYVGDSYRGKSVTVNQNFCL 214
||| | : : : : :
QY 73 PWSNATVLQOITYHAURSDALQLGLGKYNCRPNDRRRPWCVVOGLKPLVOE-CWHD 131
||| | : : : : :

[illegible]

RE UT 21

A: session: I60906
A: atus: preliminary; translated from GB/EMBL/DBDJ
A: le: le: DNA
A: le: le: 1-16 <RE2>
A: ss-references: GB:M90078; NID:G178786; PIDN:AAA35547.1; PID:G553188
A: le: apo(a) gene 1 (nomenclature of reference I52415)
A: session: A47233
A: atus: preliminary; translation not shown; translated from GB/EMBL/DBDJ
A: le: le: DNA
A: le: le: 1-16 <RE5>
A: ss-references: GB:M90079; NID:G178784; PIDN:AAA35546.1; PID:G553187
A: le: le: A.
A: le: le: 3113-3118, 1992
A: le: Multiple members of the plasminogen-apolipoprotein(a) gene family associated with
A: le: le: 152415; MUID:92207924; PMID:1554698
A: session: I52415
A: atus: preliminary; translated from GB/EMBL/DBDJ
A: le: le: DNA
A: le: le: 1-16 <RE4>
A: ss-references: GB:M86878; NID:G178782; PIDN:AAA51749.1; PID:G553186
A: le: le: A.
A: le: le: GDB:LPA
A: ss-references: GDB:120699; OMIM:152200
A: le: le: 626-6427
A: le: le: several genes closely linked on chromosome 6 are identical in the first coding e
A: le: le: kringe repeats
A: le: le: apolipoprotein(a); kringe homology; trypsin homology
A: le: le: signal sequence #statu predicted <SIG>
A: le: le: 4548; Product: apolipoprotein(a) #statu experimental <MAT>
A: le: le: 1-105/Domains: kringe homology <KR1>
A: le: le: 2-219/Domains: kringe homology <KR2>
A: le: le: 3-333/Domains: kringe homology <KR3>
A: le: le: 4-447/Domains: kringe homology <KR4>
A: le: le: 5-561/Domains: kringe homology <KR5>
A: le: le: 6-675/Domains: kringe homology <KR6>
A: le: le: 7-789/Domains: kringe homology <KR7>
A: le: le: 8-903/Domains: kringe homology <KR8>
A: le: le: 9-1017/Domains: kringe homology <KR9>
A: le: le: 10-1131/Domains: kringe homology <KR10>
A: le: le: 11-1245/Domains: kringe homology <KR11>
A: le: le: 12-1359/Domains: kringe homology <KR12>
A: le: le: 13-1473/Domains: kringe homology <KR13>
A: le: le: 14-1587/Domains: kringe homology <KR14>
A: le: le: 15-1701/Domains: kringe homology <KR15>
A: le: le: 16-1815/Domains: kringe homology <KR16>
A: le: le: 17-1929/Domains: kringe homology <KR17>
A: le: le: 18-2043/Domains: kringe homology <KR18>
A: le: le: 19-2157/Domains: kringe homology <KR19>
A: le: le: 20-2285/Domains: kringe homology <KR20>
A: le: le: 21-2499/Domains: kringe homology <KR21>
A: le: le: 22-2613/Domains: kringe homology <KR22>
A: le: le: 23-2727/Domains: kringe homology <KR23>
A: le: le: 24-2841/Domains: kringe homology <KR24>
A: le: le: 25-2955/Domains: kringe homology <KR25>
A: le: le: 26-3069/Domains: kringe homology <KR26>
A: le: le: 27-3183/Domains: kringe homology <KR27>
A: le: le: 28-3297/Domains: kringe homology <KR28>
A: le: le: 29-3411/Domains: kringe homology <KR29>
A: le: le: 30-3525/Domains: kringe homology <KR30>
A: le: le: 31-3639/Domains: kringe homology <KR31>
A: le: le: 32-3753/Domains: kringe homology <KR32>
A: le: le: 33-3869/Domains: kringe homology <KR33>
A: le: le: 34-3983/Domains: kringe homology <KR34>
A: le: le: 35-4097/Domains: kringe homology <KR35>
A: le: le: 36-4201/Domains: kringe homology <KR36>
A: le: le: 37-4315/Domains: kringe homology <KR37>

F:4228-4307/Domains: kringe homology <KR38>
F:4328-4541/Domains: trypsin homology <TRY>

Query Match 19.4%; Score 162.5; DB 1; Length 4548;
Best Local Similarity 33.1%; Pred. No. 2.4e-06;
Matches 41; Conservative 12; Mismatches 46; Indels 25; Gaps 7;

QY 27 NIHW--CN---CP-----KKFGQHCEIDKST---CYEGNGHFYRGKASTDIMG 69
DB 3742 NVRWEYCNLTQCPVTSSVLATSTAVSEQAPTQSCPTVQDCYHGDSQSYRGSFSTVTG 3801

QY 70 PCLPWSATVLQOQTYHAHRSALQGLGKKNYCRNPNRRPWCYVQVGLKPLV--QECM 127
DB 3802 TCOSWSMT---PHWHQRTTEYPNGGLTRNYCRNPDAEIRPWCYT---MDPSVRWEYCN 3855

QY 128 VHDC 131
DB 3856 LTQC 3859

RESULT 26
A:32869
A: apolipoprotein(a) (EC 3.4.21.-) - rhesus macaque (fragment)
C:Species: Macaca mulatta (rhesus macaque)
C:Date: 22-Nov-1989 #sequence_revision 22-Nov-1989 #text_change 22-Jun-1999
C:Accession: A32869; A30848
R:Tominson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A:Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A:Reference number: A32869; MUID:99174660; PMID:2925643
A:Accession: A32869
A:Molecule type: mRNA
A:Residues: 1-1420 <TCM>
A:Cross-references: GB:J04635; NID:G342072; PIDN:AAA36833.1; PID:G342073
C:Superfamily: apolipoprotein(a); kringe homology; trypsin homology
C:Keywords: hydrolase; kringe; lipid binding; lipoprotein; serine proteinase
F:50-127/Domains: kringe homology <KR1>
F:164-241/Domains: kringe homology <KR2>
F:278-355/Domains: kringe homology <KR3>
F:392-469/Domains: kringe homology <KR4>
F:506-583/Domains: kringe homology <KR5>
F:620-697/Domains: kringe homology <KR6>
F:726-803/Domains: kringe homology <KR7>
F:840-917/Domains: kringe homology <KR8>
F:954-1031/Domains: kringe homology <KR9>
F:1068-1145/Domains: kringe homology <KR10>
F:1191-1413/Domains: trypsin homology <TRY>

Query Match 19.2%; Score 161; DB 2; Length 1420;
Best Local Similarity 40.9%; Pred. No. 1.2e-06;
Matches 36; Conservative 9; Mismatches 31; Indels 12; Gaps 4;

QY 50 CYEGNGHFYRGKASTDIMGPCLPWSATVLQ--QTYHAHRSALQGLGKKNYCRNPN 107
DB 1068 CYHNGOSYRGTFSTVTGRTCOSWSMTPHQHKRTPENHPNDLTM-----NYCRNPDA 1122

QY 108 RRREWCYVQVGLKPLVQEE--CMVHDCAD 133
DB 1123 DTGWCFT---MDPSVRWEYCNLTQCD 1147

RESULT 27
C61545
A: plasmin (EC 3.4.21.7) precursor - goat (fragments)
N:Alternate names: plasminogen
C:Species: Capra aegagrus hircus (domestic goat)
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C:Accession: C61545
R:Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A:Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61545; MUID:8905015; PMID:3168975
A:Accession: C61545

R.Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A>Title: Structural aspects of the plasminogen of various species.
A'Reference number: A61545; MUID:8905015; PMID:3168975
A'Accession: E61545
A>Status: preliminary
A'Molecule type: protein
A'Residuals: 1-120 <SCH>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog
C:Keywords: hydrolase; serine proteinase
F:37-114/Domain: kringle homology <KR4>

Query Match 19.0%; Score 159; DB 2; Length 120;
Best Local Similarity 38.9%; Pred. No. 2.2e-07;
Matches 37; Conservative 8; Mismatches 32; Indels 18; Gaps 5;

QY 46 KSKTYEGNGHYRGKASDTMGRLPCLPWNSATVLQQTVAHRSDAL-----QLGGLGKN 100
Db 33 KVEQCVHGNGQSYRGTSSTITGRKQSSMT-----PHEHXTPEHFPAGL-TWN 84
QY 101 YGRNFDNRPRPCYQVGLKPLV--QECMVHDCAD 133
Db 85 YCRNPDADKSPCYT---TDPGVRWEFCNLKRLCD 116

RESULT 30
PL50
plasmin (EC 3.4.21.7) precursor - bovine
N:Alternate names: plasminogen
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1987 #sequence revision 28-Apr-1995 #text_change 18-Jun-1999
C:Accession: S45046; A25835; I45961; S03736
R:Bergrund, L.; Andersen, M.D.; Petersen, T.E.
submitted to the EMBL Data Library, May 1994
A:Description: Cloning and characterization of the bovine plasminogen cDNA.
A'Reference number: S45046
A'Accession: S45046
A'Molecule type: mRNA
A'Residuals: 1-812 <BER>
A:Cross-references: EMBL:X79402; NID:G494962; PIDN:CAA55939.1; PID:G494963
A:Experimental source: liver
A:Note: It is uncertain whether Met-1 or Met-8 is the initiator
R:Schaller, J.; Moser, P.W.; Danneberg-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Ric
Eur. J. Biochem. 149, 267-278, 1985
A>Title: Complete amino acid sequence of bovine plasminogen. Comparison with human plas
A'Reference number: A25835; MUID:85203306; PMID:3946532
A'Accession: A25835
A'Molecule type: protein
A'Residuals: 27-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCH>
R:Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A>Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A'Reference number: I45961; MUID:85023311; PMID:6148361
A'Accession: I45961
A>Status: translated from GB/EMBL/DBJ
A'Molecule type: mRNA
A'Residuals: 706-743, 'R', 745-812 <MAL>
A:Cross-references: GB:K02935; NID:G163551; PIDN:AAA30714.1; PID:G163552
R:Brinshulz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.
Eur. J. Biochem. 114, 465-470, 1981
A>Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A'Reference number: S03736; MUID:8121097; PMID:7238497
A'Accession: S03736
A'Molecule type: protein
A'Residuals: 27-83 <BRU>
C:Function:
A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ac
A:Pathway: fibrinolysis
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog
C:Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma
F:18-103/Domain: signal sequence #status predicted <SIG>
F:18-103/Domain: plasminogen-related protein precursor homologov <PIPH>

DB 296 CIRIGIPWADPINKHKKYNTGVDTGTVSVTKSGRCQCPWNS-----QVPHHTFTAL 350
QY 93 QLG--LGGKHYNCRNPDNR--PWCY 114
DB 351 REPFLNGGSHVCNPNCKEAPWCF 375

RESULT 32
PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contains: angiotatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 02-Dec-1994 #text_change 15-Sep-2000
C;Accession: A35229; I52242; A26646; I62738; I84609; S03735; A00929; A04627; A04625; A04
R;Petersen, T.E.; Maritzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6113, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the fibr
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229
A;Molecule type: DNA
A;Residues: 1-810 <P>
A;Cross-references: GB:J05286; GB:M34276; NID:G190064; PIDN:AAA60113.1; PID:G387026
A;Experimental source: leukocyte; lung fibroblast
R;Valcaratti, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; Ta
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen gene in li
A;Reference number: I52242; MUID:91097523; PMID:2268308
A;Accession: I52242
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-16 <NAL>
A;Cross-references: GB:M62890; NID:G190092; PIDN:AAA36454.1; PID:G553613
R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for human pl
A;Reference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
A;Molecule type: mRNA
A;Residues: 1-471,'D',473-810 <FOR>
A;Cross-references: GB:X05199; NID:G35530; PIDN:CRA28931.1; PID:G35531
A;Experimental source: liver
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I62738
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 292-471,'D',473-810 <MAL2>
A;Cross-references: GB:K02922; NID:G190112; PIDN:AAA60124.1; PID:G387031
A;Accession: I84609
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 367-419 <MAL3>
A;Cross-references: GB:K02921; NID:G190110; PIDN:AAA60123.1; PID:G190111
R;Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
A;Molecule type: protein
A;Residues: 20-71,'E',73-76 <BRU>
R;Sottrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
Submitted to the Atlas, July 1977
A;Reference number: A00929
A;Accession: A00929
A;Molecule type: protein
A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
R;Wiman, B.
Eur. J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.

A reference number: A04627; MUID:77225245; PMID:142009
 A accession: A04627
 A molecule type: protein
 A residues: 581-810 <W11>
 A iman, B.; Wallen, P.
 A J. Biochem. 50, 489-494, 1975
 A title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen
 A reference number: A04625; MUID:75093329; PMID:122322
 A accession: A04625
 A molecule type: protein
 A residues: 20-50, 'Q', 'E', '71', 'E', '73-85, 87-100 <W12>
 A iman, B.; Wallen, P.
 A J. Biochem. 58, 539-547, 1975
 A title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen
 A reference number: A04626; MUID:76043692; PMID:126863
 A accession: A04626
 A molecule type: protein
 A residues: 483-507, 'E', 509-604 <W13>
 A obins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
 A Biol. Chem. 248, 1631-1633, 1973
 A title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen
 A reference number: A92125; MUID:73149248; PMID:4694729
 A contents: annotation; active site
 A ontents: annotation; active site
 A roskopf, W.R.; Summaria, L.; Robbins, K.C.
 A Biol. Chem. 244, 3590-3597, 1969
 A title: Studies on the active center of human plasmin. Partial amino acid sequence of a
 A reference number: A92046; MUID:69234739; PMID:4240117
 A contents: annotation; active site
 A ontents: annotation; active site
 A rexler, M.; Vali, Z.; Pathy, L.
 A Biol. Chem. 257, 7401-7406, 1982
 A title: Structure of the omega-amino-carboxylic acid-binding sites of human plasminogen.
 A reference number: A92382; MUID:82213905; PMID:6919539
 A contents: annotation; omega-amino-carboxylic acid binding sites
 A ali, Z.; Pathy, L.
 A Biol. Chem. 259, 13690-13694, 1984
 A title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
 A reference number: A92458; MUID:85054794; PMID:6094526
 A ontents: annotation; fibrin binding site; omega-amino-carboxylic acid binding site
 A ao, Y.; J.J.; Davidson, D.; Schaller, J.; Marri, D.; Soehndel, S.; McCance, S.G.;
 A Biol. Chem. 271, 29461-29467, 1996
 A title: Kringle domains of human angiotensin. Characterization of the anti-proliferative
 A reference number: A58811; MUID:97067211; PMID:8910613
 A contents: annotation
 A ijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
 A Chemistry 37, 4699-4702, 1998
 A title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M
 A reference number: A58812; MUID:9548733; PMID:9548733
 A contents: annotation
 A ulinsky, A.; Mulichak, A.M.
 A reference number: A51341; PDB:1PK4
 A ontents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
 A ulinsky, A.; Wu, T.P.
 A reference number: A51488; PDB:2PK4
 A ontents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
 A ulinsky, A.
 A reference number: A51911; PDB:1PKR
 A ontents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
 A admanabhan, K.; Tulinsky, A.
 A reference number: A52408; PDB:1PMK
 A ontents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
 A ulinsky, A.; Mathews, I.I.
 A reference number: A65244; PDB:1CEA
 A ontents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 A ulinsky, A.; Mathews, I.I.
 A reference number: A65245; PDB:1CEB
 A ontents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181

R; Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
 Biochemistry 30, 10576-10588, 1991
 A title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9
 A reference number: A58819; MUID:92031502; PMID:1657148
 A contents: annotation
 R; Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
 Biochemistry 30, 10589-10594, 1991
 A title: The refined structure of the epsilon-aminocaproic acid complex of human plasmi
 A reference number: A58818; MUID:92031503; PMID:1657149
 A contents: annotation
 R; de Vos, A.M.; Ultsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M
 Biochemistry 31, 270-279, 1992
 A title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2
 A reference number: A39483; MUID:92118803; PMID:1310033
 A contents: annotation; X-ray crystallography, 2.4 angstroms
 R; Stec, B.; Teeter, M.M.; Whilow, M.; Yamano, A.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A reference number: A65980; PDB:1KRN
 A contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
 R; Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A reference number: A65903; PDB:1HPJ
 A contents: annotation; conformation by (1)H-NMR, residues 103-181
 R; Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A reference number: A65804; PDB:1HPK
 A contents: annotation; conformation by (1)H-NMR, residues 103-181
 R; Rejante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 927-937, 1994
 A title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
 A reference number: S43645; MUID:94237157; PMID:8181475
 A contents: annotation; conformation by (1)H-NMR, residues 96-184
 R; Rejante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 939-949, 1994
 A title: Solution structure of the epsilon-amino-hexanoic acid complex of human plasmin
 A reference number: A58817; MUID:94237158; PMID:8181476
 A contents: annotation; conformation by (1)H-NMR
 C comment: Plasminogen is synthesized by the kidney and is present in plasma and many o
 C comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU
 C PIR:FOHUGB).
 C comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately a
 C comment: resulting in two chains connected by two disulfide bonds. Without the inhibitor
 C comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial con
 C comment: Stromelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiotensin. T
 ting solid tumors.
 C Genetics:
 A Gene: GDB:PLG
 A Cross-references: GDB:119498; OMIM:173350
 A Map position: 6q26-6q27
 A Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 52
 C Function:
 A Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ac
 C Pathway: fibrinolysis
 C Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog
 C Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
 P:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 P:1-19/Domain: signal sequence #status predicted <SIG>
 P:20-810/Product: plasminogen #status experimental <PRO>
 P:20-96/Domain: activation peptide #status experimental <APT>
 P:79-466/Product: angiotensin #status experimental <ASr>
 P:97-580, 581-810/Product: plasmin #status experimental <MAT>
 P:97-580/Domain: plasmin chain A #status experimental <CHA>
 P:103-181/Domain: kringle homology <KR1>
 P:185-262/Domain: kringle homology <KR2>
 P:275-352/Domain: kringle homology <KR3>
 P:377-454/Domain: kringle homology <KR4>
 P:481-560/Domain: kringle homology <KR5>
 P:550-580, 581-810/Product: microplasmin #status experimental <MWT>

Query Match 18.7%; Score 156.5; DB 1; Length 810;
 Best Local Similarity 28.5%; Pred. No. 1.9e-06;
 Matches 49; Conservative 22; Mismatches 52; Indels 49; Gaps 12;

QY 5 HOVPSNCDCLNGTCTVSNKYFSN-----IHCNCP-KKFGGQHCHI-----DKS-----47
 DB 308 NRTPEFPCKN-----LDENYCRNPDGKRAPWCHTINSQVRWEYCKIPSCDSFVSTEQIA 363
 QY 48 -----KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHR---SDALQ 93
 DB 364 PTAPPELTVPVQCYGDSQSGTSTTTTITGKCSWS-----MTPHRHOKTPEYFN 418
 QY 94 LGLGKHYCRNPNRRPWCYVQVGLKPLV--OECMVHDCADGKFPS--SPP 141
 DB 419 AGL-TWNYCRNPDADKGPWCFT--TDPVRWEYCNLKKCS-GTEASVVAAP 465
 RE JT 33
 PL main (EC 3.4.21.7) precursor - pig (fragment)
 N:ternate names: plasminogen
 N:acins: miniplasminogen
 C:acins: Sus scrofa domestica (domestic pig)
 C:Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
 C:Accession: S03733; A25834
 R:Galler, J.; Marti, T.; Roessli, S.J.; Kaempfer, U.; Rickli, E.E.
 F1:Analysis 1, 91-102, 1987
 A:Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
 A:Reference number: S03733
 A:Accession: S03733
 A:Molecule type: protein
 A:Residues: 1-560 <SCH>
 R:Insholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
 E:U. Blochem. 114, 465-470, 1981
 A:Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
 A:Reference number: S03735; MUID:81212097; PMID:7238497
 A:Accession: S03737
 A:Molecule type: protein
 A:Residues: 1-57 <BSU>
 R:Galler, J.; Schaller, J.; Rickli, E.E.
 E:U. Blochem. 149, 279-285, 1985
 A:Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.
 A:Reference number: A25834; MUID:85203907; PMID:3846533
 A:Accession: A25834
 A:Molecule type: protein
 A:Residues: 450-790 <MAR>
 C:Action:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Way: fibrinolysis
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringe; plasmin; serine prote
 F:190/Product: plasminogen #status predicted <PRO>
 F:77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
 F:77/Domain: activation peptide #status predicted <APT>
 F:560/Product: plasmin chain A #status predicted <ACH>
 F:162/Domain: kringe homology <KR1>
 F:5-243/Domain: kringe homology <KR2>
 F:5-333/Domain: kringe homology <KR3>
 F:8-435/Domain: kringe homology <KR4>
 F:1-790/Product: miniplasminogen #status experimental <MIN>
 F:1-540/Domain: kringe homology <KR5>
 F:1-783/Domain: trypsin chain B #status experimental <BCH>
 F:1-783/Domain: trypsin homology <TRY>
 F:54,34-42,84-162,105-145,133-157,166-243,169-297,187-226,215-238,256-333,277-316,305
 bonds: #status predicted
 F:2,645,740/Active site: His, Asp, Ser #status predicted
 Query Match 18.5%; Score 155; DB 1; Length 790;
 Best Local Similarity 27.2%; Pred. No. 2.5e-06;
 Matches 44; Conservative 16; Mismatches 56; Indels 46; Gaps 9;
 QY 5 HOVPSNCDCLNGTCTVSNKYFSN-----IHCNCP-KKFGGQHCHI-----DKS-----46
 DB 289 NRTPEFPCKN-----LDENYCRNPDGKRAPWCHTINSQVRWEYCKIPSCGSGTSTTEHLD 344

QY 47 -----SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHR---SDALQ 93
 DB 345 APVPEQTPVAQDCYRGNGESYRGTSSTTTITGKCSWS-----VSMTPRHEKTPGFPN 399
 QY 94 LGLGKHYCRNPNRRPWCYVQVGLKPLV--OECMVHDCAD 133
 DB 400 AGL-TWNYCRNPDADKGPWCFT--TDPVRWEYCNLKKCS 437
 RESULT 34
 PLMS
 N:plasmin (EC 3.4.21.7) precursor - mouse
 N:Contains: angiotensin; plasminogen
 C:Species: Mus musculus (house mouse)
 C:Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
 C:Accession: A38514; S48202; S48203
 R:Degen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
 Genomics 8, 49-61, 1990
 A:Title: Characterization of the cDNA coding for mouse plasminogen and localization of t
 A:Reference number: A38514; MUID:91184812; PMID:2081600
 A:Accession: A38514
 A:Molecule type: mRNA
 A:Residues: 1-812 <DEG>
 R:Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A:Title: Characterization of the murine plasma fibrinolytic system.
 A:Reference number: S48202; MUID:95010076; PMID:7523120
 A:Accession: S48202
 A:Molecule type: protein
 A:Residues: 20-25 <LIJ>
 A:Accession: S48203
 A:Molecule type: protein
 A:Residues: 22-27 <LIJ>
 C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many otl
 C:Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasmin
 e inhibitor, the activation involves also removal of the activation peptide.
 C:Comment: Stromelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiotensin. To
 eful in treating solid tumors.
 C:Function:
 A:Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
 ns the walls of the graafian follicle; also activates the urokinase-type plasminogen act
 A:Pathway: fibrinolysis
 C:Superfamily: plasmin; kringe homology; plasminogen-related protein precursor homology
 C:Keywords: angiotensin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydr
 F:1-96/Domain: plasminogen-related protein precursor homology <PLPH>
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-812/Product: plasminogen #status predicted <PRO>
 F:20-96/Domain: activation peptide #status predicted <APT>
 F:79-466/Product: angiotensin #status predicted <AST>
 F:97-581,582-812/Product: plasmin #status predicted <MAT>
 F:97-581,582-812/Product: plasmin #status predicted <ACH>
 F:103-181/Domain: kringe homology <KR1>
 F:185-262/Domain: kringe homology <KR2>
 F:275-352/Domain: kringe homology <KR3>
 F:377-454/Domain: kringe homology <KR4>
 F:481-560/Domain: kringe homology <KR5>
 F:582-812/Domain: chain B #status predicted <BCH>
 F:582-805/Domain: trypsin homology <TRY>
 F:49-73,53-61,103-181,124-164,152-176,185-362,188-316,206-245,234-257,275-352,296-335,32
 bonds: #status predicted
 F:78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
 F:116,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
 F:581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
 F:624,667,762/Active site: His, Asp, Ser #status predicted
 Query Match 18.5%; Score 155; DB 1; Length 812;
 Best Local Similarity 30.1%; Pred. No. 2.6e-06;
 Matches 40; Conservative 12; Mismatches 55; Indels 26; Gaps 7;
 QY 30 WC-NCPKFGGQHCHIDKSKT-----CYENGHFYRGKASTDTMGRPCLPWNSA 77

D 244 WCFTDPTK-RWEYCDIPCTTPPPSPPTYOCLGRGENVRGTVSVTSVSGTKQWRWS-- 300
Q 78 TVLQOQTYHAHRSDALQGLG--KHNYCRNPDNRPRPWCYVQVGLKPLVQECMVHDCADGK 135
D 301 ---EQTPHRNTPTENFPCKNLBNYCRNPDGETAPWCYT-TDSQLRWEYCEIPSCSSA 356
Q 136 KP-----SSPPEE 143
D 357 SPDQSDSSVPPEE 369

R JLT 35
A 140
P min (EC 3.4.21.7) precursor - chicken (fragment)
N lternate names: plasminogen
C ecies: Gallus gallus (chicken)
C ite: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
R ecession: A60140
R genes: M.; Pattrhy, L.
B him. Biophys. Acta 832, 326-330, 1985
A itle: The kringle 4 domain of chicken plasminogen.
A eference number: A60140; MUID:86077796; PMID:4074753
A ecession: A60140
A lecle type: protein
A sidiues: 1-89 <GE>
A erfamly: plasmin; kringle homology; plasminogen-related protein precursor homology
C ywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase
F -83/Domain: kringle homology <RG>
F -83,27-66,55-78/Disulfide bonds: #status predicted
F y/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 18.4%; Score 154; DB 2; Length 89;
Best Local Similarity 37.4%; Pred. No. 4.8e-07;
Matches 34; Conservative 9; Mismatches 36; Indels 12; Gaps 4;

Q 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLG--KHNYCRN 104
D 3 TEECYQNGSVYRGTSFTITGKGCQAWNS-----MSPHRNKTESHPNADLRQNYCRN 57

Q 105 PDNRPRPWCYVQVGLKPLV--QECMVHDCAD 133
D 58 PDADRSPWCYT---TDPSVRWEYCNLKRCS 85

R JLT 36
I 260
P min (EC 3.4.21.7) precursor - western European hedgehog
C ecies: Erinaceus europaeus (western European hedgehog)
C ite: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C ecession: I46260
R wn, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
J iol. Chem. 270, 24004-24009, 1995
A itle: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein
A eference number: I46259; MUID:96025778; PMID:7592597
A ecession: I46260
A us: preliminary; translated from GB/EMBL/DBJ
A lecle type: mRNA
A sidiues: 1-810 <LAW>
A oss-references: EMBL:U33171; NID:G1046360; PID:G1046361
C erfamly: plasmin; kringle homology; plasminogen-related protein precursor homology
C ywords: hydrolase; serine proteinase
F -96/Domain: plasminogen-related protein precursor homology <PLPH>
F -13-181/Domain: kringle homology <KR1>
F -35-262/Domain: kringle homology <KR2>
F -75-352/Domain: kringle homology <KR3>
F -9-456/Domain: kringle homology <KR4>
F -12-561/Domain: kringle homology <KR5>
F -12-803/Domain: trypsin homology <TR>

Query Match 18.3%; Score 153.5; DB 2; Length 810;
Best Local Similarity 27.3%; Pred. No. 3.5e-06;
Matches 39; Conservative 12; Mismatches 47; Indels 45; Gaps 6;

QY 6 QVPSNCDCLN-----GGTCVSNKYFSNIHW--CNCPKKFGGQHCIDSKT- 49
Db 309 RTENYPCKNLDENYCNPDGEPAPWCFTN--SSVRWFECKIP-----DCVSSASETE 360
QY 50 -----CYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDA 91
Db 361 HSDAPVIVPEQTPVQECYQNGQTYRGTSFTITGKGCQAWNSMRPHRHSKTPENYPD 420
QY 92 LQLGLGHNYCRNPDNRPRPWCY 114
Db 421 ADLTM---NYCRNPDGDKGPWCY 440

RESULT 37
A40522
plasmin (EC 3.4.21.7) precursor - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C/Accession: A40522
R/Kanaias, J.J.; Makker, S.P.
J. Biol. Chem. 266, 10825-10829, 1991
A/Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor
A/Reference number: A40522; MUID:91250378; PMID:1645711
A/Accession: A40522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-169 <KAN>
A/Cross-references: GB:M62832; NID:G206215; PIDN:AAA41884.1; PID:G544488
A/Note: the authors translated the codon TGT for residue 76 as Ala
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F/34-112/Domain: kringle homology <KRG>
F/34-112,55-95,83-107/Disulfide bonds: #status predicted

Query Match 18.2%; Score 152.5; DB 2; Length 169;
Best Local Similarity 30.2%; Pred. No. 1.1e-06;
Matches 42; Conservative 18; Mismatches 32; Indels 47; Gaps 9;

QY 40 QHCEI-----DKS-----KTCYEGNGHFYRGKASTDTMGRPCLPWSAT 78
Db 3 EYCEIFSCGSSVSPDQSDSSVLPEQTPVQECYQNGKSYRGTSFTITGKGCQSW---- 58

QY 79 VLOQTYHAHRSDALQ-----GLGKHNYCRNPDN---RRPWCYVQVGLKPLV--QECMVHDC 132
Db 59 -VSMTPHSHSKTPANFPDSGL-EMNYCRNPDNDQRPWCFT---TDPSVRWEYCNLKRCS 113

QY 133 D-----GKPPSP 140
Db 114 ETGGVAESAIVPQVPSAP 132

RESULT 38
A47136
macrophage-stimulating protein 1 precursor - human
C/Species: Homo sapiens (man)
C/Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_change 18-Jun-1999
C/Accession: A40331; B40331; A47136; A61395
R/Han, S.; Stuart, L.A.; Degen, S.J.F.
Biochemistry 30, 9768-9780, 1991
A/Title: Characterization of the DNFI582 locus on human chromosome 3: identification of
A/Reference number: A40331; MUID:92002016; PMID:1655021
A/Accession: A40331
A/Molecule type: DNA
A/Residues: 1-711 <HAL>
A/Cross-references: GB:M74179
A/Accession: B40331
A/Molecule type: mRNA
A/Residues: 1-711 <HA2>
A/Cross-references: GB:M74178; NID:G183976; PIDN:AAAS0165.1; PID:G183977
R/Yoshimura, T.; Yuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
J. Biol. Chem. 268, 15461-15468, 1993
A/Title: Cloning, sequencing, and expression of human macrophage stimulating protein (M

C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; z;
F:1-33,34-117,118-455/Product: plasminogen (fragments) #status experimental <PRO>
F:1-33/Domain: activation peptide (fragment) #status experimental <APT>
F:34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
F:37-114/Domain: kringle homology <KR4>
F:118-455/Product: miniplasminogen #status experimental <MIN>
F:126-205/Domain: kringle homology <KRS>
F:226-455/Domain: plasmin chain B #status experimental <BCH>
F:226-448/Domain: trypsin homology <TRY>
F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match 17.8%; Score 149; DB 2; Length 455;
Best Local Similarity 34.0%; Pred. No. 5.4e-06;
Matches 36; Conservative 17; Mismatches 39; Indels 14; Gaps 6;

QY 40 QHCEIDKSKTVEGNGHFYRGKASTDTMGRPCLPWNSATV--LQOTVHAHSDALQLGLG 97
Db 28 ESCEA-KVQDCYQDKGESYRGTSITVTGKKQSSWMTPHWHOKTPEKYNADLTW--- 83

QY 98 KNYCRNPDRRRPWCYVOGLKPLV--QECNVHDCADG-KKPSPP 140
Db 84 --NYCRNPDGDKPWCYF---TDPFVRWEFCNLKRCSETVOEPSEP 124

RESULT 40
B45082
Neurotrophic receptor rox2 precursor - human
N:Contains: protein-tyrosine kinase (EC 2.7.1.112)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C:Accession: B45082
R:Maslakowski, P.; Carroll, R.D.
J. Biol. Chem. 267, 26181-26190, 1992
A:Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
A:Reference number: A45082; MUID:93100347; PMID:133494
A:Accession: B45082
A:Molecule type: mRNA
A:Residues: 1-943 <MAS>
A:Cross-references: GB:M97639; NID:g337466; PIDN:AAA60276.1; PID:g337467
A:Note: sequence extracted from NCBI backbone (NCBIP:120918)
C:Genetics:
A:Gene: GDB:NTRKR2
A:Cross-references: GDB:136454
A:Map position: fp21-6p21
C:Superfamily: neurotrophic receptor tor; immunoglobulin homology; kringle homology; pro
C:Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyros
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-337/Product: neurotrophic receptor rox2 #status predicted <MAT>
F:76-137/Domain: immunoglobulin homology <IMM>
F:316-394/Domain: kringle homology <KR3>
F:412-428/Domain: transmembrane #status predicted <TMN>
F:471-753/Domain: protein kinase homology <KIN>
F:479-487/Region: protein kinase ATP-binding motif
F:70,188,318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.7%; Score 148; DB 2; Length 943;
Best Local Similarity 34.3%; Pred. No. 1.2e-05;
Matches 37; Conservative 12; Mismatches 41; Indels 18; Gaps 6;

QY 32 NC-----PKFGGGOHCIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLTQTYH 85
Db 299 NCWRIGTIPAEIRGRVH-----QCYNQSGMDYRTASTTSGHCQCPW--ALQHPHSHH 349

QY 86 AHRSDALQLGLGKHYCRNPDRRR--PWCYVQVGLKPLVQECMVHDC 132
Db 350 LSSDTPPELG-GGHAYCRNPGQEGPWCFTQ-NKNVRMELCDVPSCS 395

RESULT 41
A40332
macrophage-stimulating protein 1 precursor - mouse
N:Alternate names: hepatocyte growth factor-like protein
C:Species: Mus musculus (house mouse)

C Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
C Ccession: A40332; B40332
F Egen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
F Chemistry 30, 9781-9791, 1991
F Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor
F Reference number: A40332; MUID:92002017; PMID:1832957
F Ccession: A40332
F Molecule type: DNA
F Residues: 1-716 <DEG>
F Cross-references: GB:M74180; NID:G193831; PIDN:AAA50166.1; PID:G193832
F Ccession: B40332
F Molecule type: mRNA
F Residues: 1-18, 'P', 20-716 <DEG2>
F Cross-references: GB:M74181; NID:G193833; PIDN:AAA50167.1; PID:G193834
F Ccessions:
C Amino acids: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 459/1; 47
C Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C Keywords: duplication; glycoprotein; growth factor; kringle
F 31/Domain: signal sequence #status predicted <SIG>
F 9-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F 9-483/Domain: alpha chain #status experimental <ACH>
F 10-186/Domain: kringle homology <KR1>
F 91-268/Domain: kringle homology <KR2>
F 92-370/Domain: kringle homology <KR3>
F 79-457/Domain: kringle homology <KR4>
F 94-711/Domain: beta chain #status experimental <BCH>
F 39-709/Domain: trypsin homology <TRY>
F 2,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 17.6%; Score 147.5; DB 1; Length 716;
Best Local Similarity 36.5%; Pred. No. 1.1e-05;
Matches 38; Conservative 11; Mismatches 34; Indels 21; Gaps 7;
C 50 CYEGNGHFYRGKASTDTMGSPCLPWNATVLOQTYHAHR-----SDALQLGLGKKNYCRN 104
D 379 CYHSGEQRGVSKTRKGVQCHWSSET-----PHRQPTPTSAPOAGL-EANFCRN 430
C 105 PD-NRRRPWCYVQVGLKP--LVQCMVHDCADGKFS--SPPEE 143
D 431 PDGDSHGWCYT--LDPDILPYCALQRCDDQPPSILDPDQ 471
F ULT 42
F 518
F Lipoprotein(a) - western European hedgehog (fragment)
C Species: Erinaceus europaeus (western European hedgehog)
C Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C Ccession: T18518
F Iwama, R.M.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
F Biol. Chem. 270, 24004-24009, 1995
F Title: The recurring evolution of Lp(a): Insights from cloning of hedgehog apolipoprotein
F Reference number: I46259; MUID:96025778; PMID:7592597
F Ccession: T18518
F Status: preliminary; translated from GB/EMBL/DBJ
F Molecule type: mRNA
F Residues: 1-2869 <LAW>
F Cross-references: EMBL:U33170; NID:G1046358; PID:G1046359; PIDN:AA48522.1
F Experimental source: liver
F Comment: The lipoprotein Lp(a), a major inherited risk factor for atherosclerosis, con
F apolipoprotein(a).
Query Match 17.6%; Score 147; DB 2; Length 2869;
Best Local Similarity 29.3%; Pred. No. 4e-05;
Matches 39; Conservative 11; Mismatches 61; Indels 22; Gaps 6;
C 19 CVSNKYFSNIHWCNCPKFGQHCIDKSKT-----CYEGNGHFYRGKASTDTMGSP 70
D 2558 CYTNSAMRWYCSIFA-----CESPTPTTEHLVPEQCLGNGENYQGNMAITVSGOP 2611
C 71 CLPWNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRPWCYVQVGLKPLVQCMVHD 130
I 2612 CQGRKOTPHRHYETENVPFSKNL-FG--NYCRNPDEIAPWCYT-TNSAVERWYCSIPT 2667

QY 131 CADGKKPSPPEE 143
DB 2668 C-----ESSSPPE 2676

RESULT 43

T18840

hypochemical protein C01G6.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18840

R:Barks, M.

submitted to the EMBL Data Library, August 1994

A:Reference number: Z19029

A:Accession: T18840

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-806 <WIL>

A:Cross-references: EMBL:Z35595; PIDN:CAA84639.1; GSPDB:GN00020; CESP:C01G6.8

A:Experimental source: clone C01G6

C:Genetics:

A:Gene: CESP:C01G6.8

A:Map position: 2

A:Introns: 36/3; 170/3; 217/3; 636/3; 760/3

Query Match 17.5%; Score 146.5; DB 2; Length 806;

Best Local Similarity 25.1%; Pred. No. 1.5e-05;

Matches 43; Conservative 25; Mismatches 60; Indels 43; Gaps 9;

QY 1 SNELHQVPS-----NCDCLNGTCTVSNKYFSNIH-----WCNPKFGGQHC--- 42

DB 152 SDSNNQIVSIKDKCDVIQNDCEPSELAAQAQHELVDTPKALFPLCSRLSSTSNCPVM 211

QY 43 -----EIDK--SKTCYEGNGHFYRGKASTDTMGSPCLPWNATVLOQTYHAHR 89

DB 212 STALQSSPFAVNRGTHUHCYVNSGTQYEGTVAQTSSSGKQCAPWIDST--SRDFNVHRF 269

QY 90 DALQLGLGKKNYCRNPNRR-RPWCYVQVGLKPLVQ--CMVHDCADGKXP 137

DB 270 PEL---MNSKNYCRNPGGKSRWCY---SKPMGQEYCDVQCPSPDMYP 313

RESULT 44

JC5061

macrophage-stimulating protein 1 precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000

C:Accession: JC5061

R:Ohnishi, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu,

Biochem. Biophys. Res. Commun. 227, 273-280, 1996

A:Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in

A:Reference number: JC5061; MUID:97011126; PMID:8858136

A:Accession: JC5061

A:Molecule type: mRNA

A:Residues: 1-716 <OHS>

A:Cross-references: EMBL:X95096; NID:G1669718; PIDN:CAA64473.1; PID:G1669719

C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor

C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology

C:Keywords: duplication; glycoprotein; growth factor; kringle

F:1-31/Domain: signal sequence #status predicted <SIG>

F:32-488,489-716/Product: macrophage-stimulating protein 1 #status predicted <MAT>

F:32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>

F:110-186/Domain: kringle homology <KR11>

F:191-268/Domain: kringle homology <KR12>

F:292-370/Domain: kringle homology <KR13>

F:379-457/Domain: kringle homology <KR14>

F:489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>

F:489-709/Domain: trypsin homology <TRY>

F:72,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.4%; Score 145.5; DB 1; Length 716;

Best Local Similarity 33.6%; Pred. No. 1.7e-05;

30 WC---NCPKFGGCHCEIDSKTCYEG-----NGHFYRGKASTDTNWRPCLPWSATVLIQ 81
 168 WCVTTRESVRF--QSGI---KSCRAVCVWNGEDYRGVEDVTSRGRCQWDLOPHS 222
 82 QYHAHRSALQGLGRKHNCRPNRPWCYVQVGLKPLVQES--CMVHDCADGKPPSS 139
 223 HPFHPKFPDKAL---KDNVCRNPDASERFWCYT---TDPNVEREPCDLPSCG----PNL 272
 140 PP 141
 273 PP 274
 JT 45
 79
 bocyte growth factor precursor [validated] - human
 N; ternate names: hepatopoietin A; scatter factor
 C; ectes: Homo sapiens (man)
 C; te: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
 C; session: J00333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796; S08
 R; xi, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
 Ge 102, 213-219, 1991
 A; ele: Organization of the human hepatocyte growth factor-encoding gene.
 A; Reference number: J00579; MUID:91340155; PMID:1831432
 A; session: J00579
 A; le: type: DNA
 A; sidues: 1-728 <SEK>
 A; ss-references: DDBJ:D90318
 A; te: the authors translated the codon GAA for residue 662 as Gly
 R; xi, T.; Hagiya, M.; Shimonishi, M.; Nakamura, T.; Shimizu, S.
 su litted to JIPID, March 1991
 A; scription: Organization of the human hepatocyte growth factor-encoding gene.
 A; ference number: J00333
 A; session: J00333
 A; le: type: DNA
 A; sidues: 1-481, 'ET', 484-728 <SE2>
 R; idner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
 Pr . Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
 A; le: Evidence for the identity of human scatter factor and human hepatocyte growth f
 A; ference number: A41140; MUID:91334393; PMID:1831466
 A; session: A41140
 A; le: type: mRNA
 A; sidues: 1-728 <WE1>
 A; ss-references: GB:M73239; NID:9337935; PIDN:AAA4239.1; PID:g184032
 R; ki, T.; Ihara, I.; Sugimura, A.; Shimonishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M
 Bi hem. Biophys. Res. Commun. 172, 321-327, 1990
 A; le: Isolation and expression of cDNA for different forms of hepatocyte growth facto
 A; ference number: A36677; MUID:91025062; PMID:2145836
 A; session: B36677
 A; le: type: mRNA
 A; sidues: 1-728 <SE3>
 A; ss-references: GB:M60718; NID:g184031; PIDN:AAA52648.1; PID:g184032
 A; session: A36677
 A; le: type: mRNA
 A; sidues: 1-161, 167-728 <SE4>
 A; ss-references: EMBL:X16323
 A; perimental source: leukocyte
 R; yazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
 Bi hem. Biophys. Res. Commun. 163, 967-973, 1989
 A; le: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
 A; ference number: A33512; MUID:8932017; PMID:2528952
 A; session: A33512
 A; tus: not compared with conceptual translation
 A; le: type: mRNA
 A; sidues: 1-728 <MIY>
 A; ss-references: GB:M29145; NID:g184041; PIDN:AAA52650.1; PID:g306846
 R; bin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hil
 Pr . Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
 A; le: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
 A; ference number: A39006; MUID:91110540; PMID:1824873
 A; session: A39006

A; Molecule type: mRNA
 A; Residues: 1-161, 167-728 <RUB>
 A; Cross-references: GB:M55379
 A; Experimental source: embryonic lung
 R; Yoshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama, I
 Biochem. Biophys. Res. Commun. 175, 660-667, 1991
 A; Title: Identification of the N-terminal residue of the heavy chain of both native and
 A; Reference number: PH0114; MUID:91207365; PMID:1826837
 A; Accession: PH0114
 A; Molecule type: protein
 A; Residues: 32-43, 53-58 <YOS>
 A; Experimental source: plasma
 R; Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
 J. Cell Biol. 111, 2097-2108, 1990
 A; Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
 A; Reference number: A37796; MUID:91035621; PMID:2146276
 A; Accession: A37796
 A; Molecule type: protein
 A; Residues: 86-91, 1329-344, 356-363, 'XX', 366-370, 425-434, 442-447, 'X', 449-450, 543-546, 'X', 5
 R; Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimonishi, M.; Sugimura, A.; Tashi
 Nature 342, 440-443, 1999
 A; Title: Molecular cloning and expression of human hepatocyte growth factor.
 A; Reference number: S06794; MUID:90066676; PMID:2531289
 A; Accession: S06794
 A; Molecule type: mRNA
 A; Residues: 1-31, 'HK', 34-77, 'N', 79-292, 'V', 294-299, 'W', 301-316, 'A', 318-335, 'K', 337-386, '
 A; Cross-references: EMBL:X16323; NID:g32081; PIDN:CAA34387.1; PID:g32082
 A; Experimental source: liver
 A; Note: the authors translated the codon CAG for residue 727 as Glu
 A; Note: part of this sequence, including the amino end of both the alpha and beta chains
 R; Hartmann, G.; Naldini, L.; Weidner, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birchm
 Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
 A; Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth fact
 A; Reference number: I59214; MUID:93087571; PMID:1280830
 A; Accession: I59214
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 1-288, 'ET', <HAR>
 A; Cross-references: GB:I02931; NID:g184033; PIDN:AAA52649.1; PID:g184034
 R; Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
 Eur. J. Biochem. 197, 15-22, 1991
 A; Title: An alternatively processed mRNA generated from human hepatocyte growth factor g
 A; Reference number: S15443; MUID:91200041; PMID:1826653
 A; Accession: S15443
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-288, 'ET', <MIY>
 A; Cross-references: EMBL:X57574; NID:g32083; PIDN:CAA40802.1; PID:g32084
 R; Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Murakami, A.; Higashio, K.
 Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
 A; Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
 A; Reference number: I52253; MUID:92062058; PMID:1835383
 A; Accession: I52253
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: mRNA
 A; Residues: 161-166 <SHI>
 A; Cross-references: GB:S62561; NID:g237996; PIDN:AAB20169.1; PID:g237997
 C; Genetics:
 A; Gene: GDB:HGF
 A; Cross-references: GDB:I27524; OMIM:142409
 A; Map position: 7q21.1-7q21.1
 A; Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/1; 289/1; 347/2; 390/1; 424/2; 459/1; 48
 C; Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C; Function:
 A; Description: stimulates mitosis of hepatocytes and other cells
 A; Note: does not have proteinase activity
 C; Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyr
 F; 1-31/Domain: signal sequence #status predicted <SIG>
 F; 32-494, 495-728/Product: hepatocyte growth factor #status experimental <WAT>
 F; 32-494/Domain: alpha chain #status experimental <ACH>
 F; 128-206/Domain: kringle homology <KR1>
 F; 211-288/Domain: kringle homology <KR2>

F 05-383/Domain: kringle homology <KR3>
 F 91-469/Domain: kringle homology <KR4>
 F 95-728/Domain: beta chain #status experimental <BCH>
 F 95-716/Domain: trypsin homology <TRY>
 F 2/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
 F 34,402,566,653/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F 87-604/Disulfide bonds: #status predicted
 Query Match 17.3%; Score 144.5; DB 1; Length 728;
 Best Local Similarity 29.6%; Pred. No. 2.1e-05;
 Matches 45; Conservative 13; Mismatches 69; Indels 25; Gaps 10;
 Q 2 NELHQVPSNCDC--LNGGTCVSNKYFSNIHWC-----NCPKKFGGQ--HCEIDSKSCYCE 52
 D 335 HEHDTTPENFKCKDLRENYC-RNPDSGSPWCFTTDPNIRVGYCSQIPNCDMSHGQDCYR 393
 Q 53 GNGHYRGKASTDTMGRCPLPNSATVLOOTYHAH---RSDALQLGLGKHNYCRNP-DNR 108
 D 394 GNGKRYMGNLSQTRSGLTCSMWDXN---MEDLHRHIFWEPDASKL---NENYCRNPDDA 447
 Q 109 RPPWCVVQVGLKPLV--QECMVHDCADGKKPS 138
 D 448 HGPWCYTG---NPLVPWDYCPISRCEGDTTPT 476
 R ULT 46
 I 285
 h atocyte growth factor/scatter factor - chicken (fragment)
 C species: Gallus gallus (chicken)
 C date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
 C accession: I51285
 R Kretz, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
 D alignment 121, 813-824, 1995
 A title: A role for HGF/SF in neural induction and its expression in Hensen's node during
 A reference number: I51285; MUID:95237013; PMID:7720585
 A accession: I51285
 A status: preliminary; translated from GB/EMBL/DBJ
 A molecule type: mRNA
 A residues: 1-411 <STR>
 A cross-references: GB:S77480; NID:9998675; PID:9998676
 A superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 F 24-197/Domain: kringle homology <KR2>
 F 22-279/Domain: kringle homology <KR3>
 F 36-374/Domain: kringle homology <KR3>
 Query Match 17.0%; Score 142; DB 2; Length 411;
 Best Local Similarity 28.4%; Pred. No. 2.1e-05;
 Matches 38; Conservative 18; Mismatches 48; Indels 30; Gaps 7;
 Q 30 WC-----NCPKKFGG-QHCEID-----KSKTCYEGNGHYRGKASTDTMGRCPLPW 74
 D 261 WCYTLDPNTPWEFCAIKTCVGLNSTEAVAEITTCIQGGEGYGTNTWSGLQCORW 320
 Q 75 NSATVLOOTYHAH--SDALQLGLGKHNYCRNPDRRPPWCY-----VQVGLKPLVQECM 127
 D 321 DS-----QPPHQHNTPENFKCKDLRENYCRNPDGSPWCFTTDPNIRVGYCSQIPKCD 375
 Q 128 V---HDCADGKKPS 138
 D 376 VSNEDQCYRGNGKS 389
 R JLT 47
 A 344
 h atocyte growth factor precursor - rat
 N alternate names: hepatoin A; scatter factor
 C species: Rattus norvegicus (Norway rat)
 C date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000
 C accession: A35644; S13211
 R Ashiro, K.; Hagiya, M.; Nishizawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamura
 P 1. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
 A title: Deduced primary structure of rat hepatocyte growth factor and expression of the
 A reference number: A35644; MUID:90222197; PMID:2139229

A;Accession: A35644
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-728 <TAS>
 A;Cross-references: GB:D90102; GB:M32987; NID:9220766; PIDN:BAA14133.1; PID:9220767
 A;Note: the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
 R;Okajima, A.; Miyazawa, K.; Kitamura, N.
 Eur. J. Biochem. 193, 375-381, 1990
 A;Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA du
 A;Reference number: S13211; MUID:91031482; PMID:2146117
 A;Accession: S13211
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-728 <OKA>
 A;Cross-references: EMBL:X54400; NID:956353; PIDN:CAA38266.1; PID:94539554
 A;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C;Function:
 A;Note: stimulates mitosis of hepatocytes and other cells
 A;Note: does not have proteinase activity
 C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
 C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; py
 F;1-32/Domain: signal sequence #status predicted <SIG>
 F;56-495/Product: hepatocyte growth factor #status predicted <MAT>
 F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
 F;129-207/Domain: kringle homology <KR1>
 F;212-289/Domain: kringle homology <KR2>
 F;306-384/Domain: kringle homology <KR3>
 F;392-470/Domain: kringle homology <KR4>
 F;486-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
 F;486-728/Domain: trypsin homology <TRY>
 F;436-719/Domain: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
 F;33/Modified site: pyrrolidone carboxylic acid (Gln) (covalent) #status predicted
 F;295,403,569,656/Binding site: carbohydrate (Asn)
 F;488-607/Disulfide bonds: #status predicted
 Query Match 17.0%; Score 142; DB 1; Length 728;
 Best Local Similarity 28.8%; Pred. No. 3.5e-05;
 Matches 45; Conservative 11; Mismatches 62; Indels 38; Gaps 11;
 QY 5 HOV-PSNCDC--LNGGTCVSNKYFSNIHWC-----NCPKKFGGQHCIEDSK 48
 DB 338 HDITPENFKCKDLRENYC-RNPDSGSPWCFTTDPNIRVGYCSQIPK-----CDVSSGQ 390
 QY 49 TCYEGNGHYRGKASTDTMGRCPLPNSATVLOOTYHAH---RSDALQLGLGKHNYCRNP 105
 DB 391 DCYRGNGKRYMGNLSQTRSGLTCSMWDXN---MEDLHRHIFWEPDASKL---TKNYCRNP 444
 QY 106 -DNRPRPWCVVQVGLKPLV--QECMVHDCADGKKPS 138
 DB 445 DDDAHGWCYTG---NPLVPWDYCPISRCEGDTTPT 477
 RESULT 48
 A60185
 hepatocyte growth factor precursor - mouse
 N;Alternate names: hepatoin A; scatter factor
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 16-Jun-2000
 C;Accession: J02117; PC2064; A60185; S43416; S45521; S1173; S10966; 148758; J00231
 R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
 Biochem. Biophys. Res. Commun. 199, 772-778, 1994
 A;Title: Identification of mouse mammary fibroblast-derived mammary growth factor as he
 A;Reference number: J02117; MUID:94183257; PMID:8135822
 A;Accession: J02117
 A;Molecule type: mRNA
 A;Residues: 1-728 <SAS2>
 A;Cross-references: GB:D10212; NID:9220435; PIDN:BAA01064.1; PID:9220436
 A;Experimental source: fibroblast, COS-1 cell
 A;Note: submitted to JIPID, May 1993
 A;Accession: PC2064
 A;Molecule type: protein
 A;Residues: 456-504 <SAS2>
 R;Rosen, E.M.; Meromsky, L.; Setter, E.; Vinter, D.W.; Goldberg, I.D.
 Proc. Soc. Exp. Biol. Med. 195, 34-43, 1990

```

Qy 49 TCYEGNGHYFGKASTDTMGAPCLPWN SATVLQQTYYAH---RSDALQLGLGKHNYCRNP 105
Db 391 DCYRGNGKYNGLNLSKTRSGLTCSNWDKN---MEDLHRHIFWEPDASKL---NKNYCRNP 444
Qy 106 -DNRRRPMCYQVGLKPLV--QECMVHDCADCKKPS 138
Db 445 DDDAHGPMCYTG---NPLIPWDYCFISRCGDTTPT 477

RESULT 49
151283
hepatocyte growth factor precursor - clawed frog
N:Alternate names: hepatoinetin A: scatter factor
C:Species: Xenopus sp. (clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C:Accession: 151283
R:Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.
Mech. Dev. 49, 123-131, 1995
A:Title: Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus ea
A:Reference number: 151283; MUID:95267690; PMID:7748783
A:Accession: 151283
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-710 <NAK>
A:Cross-references: GB:S77422; NID:9989932; PIDN:AAB34354.1; PID:G9898933
A:Note: the authors' translation for residue 458 (Thr) is inconsistent with the nucleoti
C:Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C:Description:
A:Description: stimulates mitosis of hepatocytes and other cells
A:Note: does not have proteinase activity
C:Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C:Keywords: duplication; glycoprotein; growth factor; heterodimer; kringle
F:42-477, 478-709/Product: hepatocyte growth factor #status predicted <WAT>
F:42-477/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F:115-193/Domain: kringle homology <KR1>
F:198-275/Domain: kringle homology <KR2>
F:289-367/Domain: kringle homology <KR3>
F:375-453/Domain: kringle homology <KR4>
F:478-709/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F:478-700/Domain: hepatocyte growth factor
F:52,128,281,322,379,550,637,666/Binding site: carbohydrate (Asn) (covalent) #status pre
F:470-588/Disulfide bonds: #status predicted

Query Match 16.8%; Score 141; DB 1; Length 710;
Best Local Similarity 29.2%; Pred. NO. 4.2e-05;
Matches 42; Conservative 12; Mismatches 64; Indels 26; Gaps 9;

Qy 4 LHQ-VPSNDCD--LNGGTCVSNKYFSNIHWC-----NCPKFGGGOHCEIDKSKTC 50
Db 320 LHNFTPEYKCKDLSGNYC-RNPDGSESPWCFTDPIRIGHCSQI---KKQASNQOEC 375

Qy 51 YEGNGHFYRGKASTDTMGAPCLPWN SATVLQQTYYAHRS DALQLGLGKHNYCRNPDN-RR 109
Db 376 YYGNGSTYKGLSTRFRFLPCSMWEKNL---QDLKRHTFNEPDVSIQKNYCRNPDNAH 432

Qy 110 RPWCYVQVGLKPLV--QECMVHDC 131
Db 433 GPWCYTD---DPFVPMWYCPISRC 453

RESULT 50
S33879
plasmin precursor - lamprey (fragments)
N:Alternate names: plasminogen
C:Species: Petromyzontidae gen. sp. (lamprey)
C>Date: 02-Dec-1993 #sequence_revision 01-Sep-1995 #text_change 07-Nov-1997
C:Accession: S33879
R:Affolter, M.; Schaller, J.; Rickli, E.E.
Protein Seq. Data Anal. 5, 207-211, 1993
A:Title: Isolation, characterization and partial amino acid sequence of lamprey plasmino
A:Reference number: S33879
A:Accession: S33879
A>Status: preliminary

```

Molecule type: protein
A residues: 1-15;16-34;35-44;45-59;60-76;77-111;111-138;139-158;159-178;179-216;217-236;
C superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
F 1-146/Domain: kringle homology <RR3>

Query Match 16.2%; Score 136; DB 2; Length 336;
Best Local Similarity 30.7%; Pred. No. 6.2e-05;
Matches 31; Conservative 7; Mismatches 41; Indels 22; Gaps 3;

Q 34 PKKFGQHCEIDKSKTCYEGNGHFGYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQ 93
D 71 POSFAG-----LTTACVKGTEGYRGTAALTVSGKACQAWASQT-----PGDVYS 115
C 94 LGLGKHNYCRNPDNRPRPCYVQVGLKPLVQECMVHDCADG 134
D 116 CQGLVSNYCRNPDGKLPWCYT-----TEYCNVPSCITGG 149

Search completed: May 25, 2004, 14:58:36
CPU time : 10.2717 secs

GenCore version 5.1.6
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C protein - protein search, using sw model

Run on: May 25, 2004, 14:43:40 ; Search time 5.51446 Seconds
(without alignments)
1350.274 Million cell updates/sec

Title: US-09-880-503-8

Sequence: 837
1 SNEHLQVNSDCLNGGTCV.....QECMVHPCADKPKSPPEE 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Sequences: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum Match 100%

Maximum Match 100%

Listing first 75 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	837	100.0	431	1 UROK_HUMAN	P00749 homo sapien
2	757.5	90.5	433	1 UROK_PAPCY	P16227 papio cynoc
3	625.5	74.7	442	1 UROK_PIG	P04185 sus scrofa
4	605	72.3	433	1 UROK_BOVIN	Q05589 bos taurus
5	592	70.7	432	1 UROK_RAT	P29598 rattus norv
6	569	68.0	433	1 UROK_MOUSE	P06869 mus musculu
7	335.5	40.1	477	1 URT2_DESRO	P15638 desmodus ro
8	334.5	40.0	434	1 UROK_CHICK	P15120 gallus gall
9	328.5	39.2	431	1 URTB_DESRO	P98121 desmodus ro
10	325	38.8	559	1 TPA_RAT	P19637 rattus norv
11	315.5	37.7	559	1 TPA_MOUSE	P11214 mus musculu
12	310.5	37.1	477	1 URT1_DESRO	P98119 desmodus ro
13	268	32.0	603	1 FA12_CAVPO	Q28198 bos taurus
14	262	31.3	655	1 HGFA_HUMAN	Q04962 cavia porce
15	250.5	29.9	653	1 HGFA_MOUSE	Q07556 mus musculu
16	233	27.8	615	1 FA12_HUMAN	Q07098 mus musculu
17	223	26.6	394	1 URTG_DESRO	P49150 desmodus ro
18	217	25.9	593	1 FA12_BOVIN	P98140 bos taurus
19	216.9	20.2	685	1 ROR1_DROME	Q24488 drosophila
20	162.5	19.4	4548	1 APOA_HUMAN	P08519 homo sapien
21	161	19.2	473	1 KRM1_RAT	Q92454 rattus norv
22	161	19.1	1420	1 APOA_MACMU	P14417 macaca mula
23	159.5	19.1	810	1 PLMN_MACMU	P12545 macaca mula
24	159	19.0	452	1 KRM1_XENLA	Q90990 xenopus lae
25	159	19.0	473	1 KRM1_MOUSE	P09843 mus musculu
26	159	19.0	812	1 PLMN_BOVIN	P06868 bos taurus
27	158.5	18.9	937	1 ROR1_HUMAN	Q01973 homo sapien
28	158.5	18.9	937	1 ROR1_MOUSE	Q92139 mus musculu
29	156.5	18.7	810	1 PLMN_HUMAN	P00747 homo sapien
30	156	18.6	475	1 KRM1_HUMAN	Q96mu8 homo sapien
31	155	18.5	790	1 PLMN_PIG	P06867 sus scrofa

ALIGNMENTS

RESULT 1	UROK_HUMAN	STANDARD;	PRT;	431 AA.
ID	UROK_HUMAN	Q15944; Q16618; Q969W6;		
AC	P00749; Q15944; Q16618; Q969W6;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	20-MAR-1987 (Rel. 04, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)			
DE	(U-plasminogen activator)			
GN	PLAU.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=85215647; PubMed=2987867;			
RA	Riccio A., Grimaldi G., Verde P., Sebastiao G., Boast S., Blasi F.;			
RA	"The human urokinase-plasminogen activator gene and its promoter.";			
RL	Nucleic Acids Res. 13:2759-2771(1985).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Holmes W.E., Pennica D., Blaber M., Rey M.W., Guenzler W.A.,			
RA	Steffens G.J., Heyneker H.L.;			
RT	"Cloning and expression of the gene for pro-urokinase in Escherichia coli."			

34	155	18.5	812	1 PLMN_MOUSE	P20918 mus musculu
35	153.5	18.3	810	1 PLMN_BRIEU	Q29485 erinaceus e
36	152.5	18.2	169	1 PLMN_RAT	Q01177 rattus norv
37	150	17.9	711	1 HGFL_HUMAN	Q8ncw0 homo sapien
38	148.5	17.7	462	1 KRM2_HUMAN	P80009 canis famil
39	148	17.7	333	1 PLMN_CANFA	Q01974 homo sapien
40	148	17.7	943	1 ROR2_HUMAN	Q92138 mus musculu
41	148	17.7	944	1 ROR2_MOUSE	P26928 mus musculu
42	147.5	17.6	716	1 HGFL_MOUSE	Q8k157 mus musculu
43	146.5	17.5	461	1 KRM2_MOUSE	P14210 homo sapien
44	144.5	17.3	728	1 HGF_MOUSE	Q08048 mus musculu
45	142	17.0	728	1 HGF_RAT	P17945 rattus norv
46	136	16.2	325	1 PLMN_PETMA	P33574 petromyzon
47	136	16.2	325	1 THRB_MOUSE	P19221 mus musculu
48	125.5	15.0	618	1 PLMN_SHEEP	P81286 ovis aries
49	124.5	14.9	343	1 PLMN_HUMAN	P00734 homo sapien
50	124	14.8	622	1 THRB_HUMAN	Q9v8k3 drosophila
51	123.5	14.8	724	1 ROR2_DROME	P21783 xenopus lae
52	117	14.0	2524	1 NOTC_XENLA	Q17833 bos taurus
53	115	13.7	625	1 THRB_BOVIN	P00735 mus musculu
54	113.5	13.6	1238	1 JAG2_HUMAN	Q9Y219 homo sapien
55	113	13.3	617	1 THRB_RAT	P18292 rattus norv
56	111	13.3	338	1 PLMN_HORSE	P80010 equus cabal
57	106.5	12.7	2471	1 NTC3_HUMAN	Q04721 homo sapien
58	105.5	12.6	1213	1 JAG3_BRARE	Q90554 brachydanio
59	105.5	12.6	1242	1 JAG1_BRARE	Q90557 brachydanio
60	105.5	12.6	2109	1 PGCA_CHICK	P07898 gallus gall
61	104.5	12.5	2139	1 CRB_DROME	P10040 drosophila
62	103.5	12.4	1321	1 PGCN_HUMAN	Q14594 homo sapien
63	103	12.3	1295	1 GLP1_CAEEL	P13508 caenorhabdi
64	102	12.3	2470	1 NTC2_MOUSE	Q35516 mus musculu
65	102	12.2	618	1 DLL3_HUMAN	Q9NYJ7 homo sapien
66	102	12.2	1202	1 JAG2_RAT	P97607 rattus norv
67	102	12.2	1376	1 CRBH_HUMAN	P82279 homo sapien
68	102	12.2	2531	1 NTC1_RAT	Q07008 rattus norv
69	101.5	12.1	686	1 DLL4_MOUSE	Q9J171 mus musculu
70	101.5	12.1	2556	1 NTC1_HUMAN	P46531 homo sapien
71	101.5	12.1	2703	1 NOTC_DROME	P07207 drosophila
72	101	12.1	379	1 WIF1_HUMAN	Q9Y3W5 homo sapien
73	101	12.1	2471	1 NTC2_RAT	Q9Y3W3 rattus norv
74	101	12.1	3014	1 CLR1_HUMAN	Q99466 homo sapien
75	100	11.9	2003	1 NTC4_HUMAN	

RL Biotechnology 3:923-929(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86056994; PubMed=2415429;
 RA Nagai M., Hiramatsu R., Kaneda T., Hayasuke N., Arimura H.,
 RA Nishida M., Suyama T.,
 RT "Molecular cloning of cDNA coding for human preprothrombinase";
 RL Gene 36:183-188(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85203359; PubMed=3888571;
 RA Jacobs P., Cravador A., Loriau R., Brockly P., Colau B., Chuchana P.,
 RA van Elsen A., Herzog A., Bollen A.,
 RT "Molecular cloning, sequencing, and expression in *Escherichia coli* of
 RT human prethrombinase cDNA";
 RL DNA 4:139-146(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89127526; PubMed=2536903;
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.,
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Sapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 66-431 FROM N.A.
 RX MEDLINE=84272706; PubMed=6589620;
 RA Verde P., Stoppelli M.P., Galeffi P., di Nocera P., Blasi F.,
 RT "Identification and primary sequence of an unspliced human urokinase
 RT poly(A)+ RNA";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4727-4731(1984).
 RN [8]
 RP SEQUENCE OF 21-177.
 RX MEDLINE=83055084; PubMed=6754569;
 RA Gunzler W.A., Steffens G.J., Otting F., Kim S.-M.A., Frankus E.,
 RA Flohe L.,
 RT "The primary structure of high molecular mass urokinase from human
 RT urine. The complete amino acid sequence of the A chain";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1155-1165(1982).
 RN [9]
 RP SEQUENCE OF 156-176 AND 179-224.
 RX MEDLINE=83003608; PubMed=6749491;
 RA Schaller J., Nick H., Rickli E.E., Gillesen D., Lergier W.,
 RA Studer R.O.,
 RT "Human low-molecular-weight urinary urokinase. Partial
 RT characterization and preliminary sequence data of the two polypeptide
 RT chains";
 RL Eur. J. Biochem. 125:251-257(1982).
 RN [10]
 RP SEQUENCE OF 158-410.
 RX MEDLINE=83055099; PubMed=6754572;
 RA Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe L.,

RT "The complete amino acid sequence of low molecular mass urokinase
 RT from human urine";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1043-1058(1982).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=96000858; PubMed=8591045;
 RA Spraggon G., Phillips C., Nowak U.K., Ponting C.P., Saunders D.,
 RA Dobson C.M., Stuart D.I., Jones E.Y.,
 RT "The crystal structure of the catalytic domain of human
 RT urokinase-type plasminogen activator";
 RL Structure 3:681-691(1995).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 159-411.
 RX MEDLINE=20266327; PubMed=10805774;
 RA Sperl S., Jacob U., Arroyo de Prada N., Sturzebecher J., Wilhelm O.G.,
 RA Bode W., Magdolen V., Huber R., Moroder L.,
 RT "(4-aminomethyl)phenylguanidine derivatives as nonpeptidic highly
 RT selective inhibitors of human urokinase";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5113-5118(2000).
 RN [13]
 RP STRUCTURE BY NMR.
 RX MEDLINE=89127526; PubMed=2536903;
 RA Oswald R.B., Bogusky M.J., Bamberger M., Smith R.A.G., Dobson C.M.,
 RT "Dynamics of the multidomain fibrinolytic protein urokinase from two-
 RT dimensional NMR";
 RL Nature 337:579-582(1989).
 RN [14]
 RP STRUCTURE BY NMR OF 67-155.
 RX MEDLINE=93003110; PubMed=1327118;
 RA Li X., Smith R.A.G., Dobson C.M.,
 RT "Sequential 1H NMR assignments and secondary structure of the kringle
 RT domain from urokinase";
 RL Biochemistry 31:9562-9571(1992).
 RN [15]
 RP STRUCTURE BY NMR OF 67-155.
 RX MEDLINE=94149701; PubMed=8107091;
 RA Li X., Bokman A.M., Linas M., Smith R.A.G., Dobson C.M.,
 RT "Solution structure of the kringle domain from urokinase-type
 RT plasminogen activator";
 RL J. Mol. Biol. 235:1548-1559(1994).
 RN [16]
 RP VARIANT LEU-141.
 RX MEDLINE=96186279; PubMed=8652631;
 RA Yoshimoto M., Ushiyama Y., Sakai M., Tamaki S., Hara H., Takahashi K.,
 RA Sawasaki Y., Hanada K.,
 RT "Characterization of single chain urokinase-type plasminogen
 RT activator with a novel amino-acid substitution in the kringle
 RT structure";
 RL Biochim. Biophys. Acta 1293:83-89(1996).
 RN [17]
 RP VARIANT LEU-141.
 RX MEDLINE=97218551; PubMed=9065988;
 RA Conne B., Berczy M., Belin D.,
 RT "Detection of polymorphisms in the human urokinase-type plasminogen
 RT activator gene";
 RL Thromb. Haemost. 77:434-435(1997).
 RN [18]
 RP ERRATUM.
 RA Conne B., Berczy M., Belin D.,
 RL Thromb. Haemost. 78:973-973(1997).
 RN [19]
 RP VARIANT LEU-141.
 RX MEDLINE=97337920; PubMed=9194591;
 RA Turkmen B., Schmitt M., Schmaifeldt B., Trommler P., Hell W.,
 RA Creutzburg S., Graeff H., Magdolen V.,
 RT "Mutational analysis of the genes encoding urokinase-type plasminogen
 RT activator (uPA) and its inhibitor PAI-1 in advanced ovarian cancer";
 RL Electrophoresis 18:686-689(1997).
 CC -!- FUNCTION: Potent plasminogen activator and is clinically used for
 CC therapy of thrombolytic disorders.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: Found in high and low molecular mass forms. Each consists

of two chains, A and B. The high molecular mass form contains a long chain A. Cleavage occurs after residue 155 in the low molecular mass form to yield a short A1 chain.

- PHARMACEUTICAL: Available under the name Abbokinase (Abbott). Used in Pulmonary Embolism (PE) to initiate fibrinolysis.

- SIMILARITY: Belongs to peptidase family S1.

- SIMILARITY: Contains 1 EGF-like domain.

- SIMILARITY: Contains 1 kringle domain.

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EMBL; X02419; CAA26268.1; -
EMBL; M15476; AAA61253.1; -
EMBL; D00244; BAA00175.1; -
EMBL; D11143; BAA01919.1; -
EMBL; X02760; CAA26635.1; -
EMBL; AF377330; AAK33822.1; -
EMBL; BC013375; AAH13575.1; -
EMBL; K03226; AAC97138.1; -
EMBL; K02286; AAA61252.1; -
EMBL; A21571; CAA01559.1; -
EMBL; A18397; CAA01390.1; -
PIR; A00931; UKHU
PDB; 1KDU; 31-OCT-93.

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 5e-74;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNELHGVNSCDLNGGTCVSNKYFSTHWCNCPKFGQCEIDKSKTCYEGNGHYRG 60
21 SNELHGVNSCDLNGGTCVSNKYFSTHWCNCPKFGQCEIDKSKTCYEGNGHYRG 80
61 KASTDTMGRCPLPWNASATVLAQTYHAHRSALQGLGKHNYCRNPDNRRCWCVQVGLK 120
81 KASTDTMGRCPLPWNASATVLAQTYHAHRSALQGLGKHNYCRNPDNRRCWCVQVGLK 140
121 PLVQECMVHDCADGKKPSPEE 143
141 PLVQECMVHDCADGKKPSPEE 163

ULT 2
U: PACY
I: UROK_PAPCY STANDARD; PRT; 433 AA.
P16227;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
PLAU.
Papio cynocephalus (Yellow baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecoidea; Papio.
NCBI_TaxID=9556;
[1]_TaxID=9556;
SEQUENCE FROM N.A.
TISSUE: Thoracic aorta;
MEDLINE=90287734; PubMed=2113276;
Au Y.P.T., Wang T.W., Clowes A.W.;
"Nucleotide and deduced amino acid sequences of baboon urokinase-type plasminogen activator."
Nucleic Acids Res. 18:3411-3411(1990).
- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in plasminogen to form plasmin.

- SUBUNIT: Found in high and low molecular mass forms. Each consists of two chains, A and B. The high molecular mass form contains a long chain A. Cleavage occurs after residue 155 in the low molecular mass form to yield a short A1 chain (By similarity).

- SIMILARITY: Belongs to peptidase family S1.

- SIMILARITY: Contains 1 EGF-like domain.

- SIMILARITY: Contains 1 kringle domain.

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EMBL; X51935; CAA36200.1; -
PIR; S14687; UKBAY.
HSSP; P00749; ILMW.
MEROPS; S01.231; -
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR062209; EGF-like.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR008293; Pept_S1A_uPA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PR00051; kringle; 1.
Pfam; PR00089; trypsin; 1.
PIRSE; PIRSF001144; Urokinase_act; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00181; EGF; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; FALSE_NEG.
PROSITE; PS00026; EGF_3; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS02440; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 433 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 176 CHAIN A (BY SIMILARITY).
FT CHAIN 155 176 SHORT A CHAIN (A1) (BY SIMILARITY).
FT CHAIN 178 433 CHAIN B (BY SIMILARITY).
FT DOMAIN 26 62 EGF-LIKE.
FT DOMAIN 69 150 KRINGLE.
FT DOMAIN 151 177 CONNECTING PEPTIDE.
FT DOMAIN 178 433 SERINE PROTEASE.
FT DISULFID 30 38 BY SIMILARITY.
FT DISULFID 32 50 BY SIMILARITY.
FT DISULFID 52 61 BY SIMILARITY.
FT DISULFID 167 298 INTERCHAIN (BY SIMILARITY).
FT DISULFID 208 224 BY SIMILARITY.
FT DISULFID 216 287 BY SIMILARITY.
FT DISULFID 315 384 BY SIMILARITY.
FT DISULFID 347 363 BY SIMILARITY.
FT DISULFID 374 402 BY SIMILARITY.
FT ACT_SITE 223 223 CHARGE RELAY SYSTEM.
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 378 378 CHARGE RELAY SYSTEM.
FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ SEQUENCE 433 AA; 48595 MW; 816D22DFEDDC8792 CRC64;

Query Match 90.5%; Score 757.5; DB 1; Length 433;
Best Local Similarity 92.3%; Pred. No. 2.6e-66;
Matches 132; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 SNEHQVPSNCDCLNGTGVSNKYFSNIHWNCNPKKFGQHQHCEIDKSKTCYEGNGHFYRG 60
Db 21 SREL-QVPBDCGLNGTGVSNKYFSNIHWNCNPKKFGQHQHCEIDKSKTCYEGNGHFYRG 79
QY 61 KASTDTMGRCPLPWNATVLTQYTHAHRSDALQGLGKINYCRNPNRRRPPWCYVQVGLK 120
Db 80 KASTDTMGRCPLPWNATVLTQYTHAHRSDALQGLGKINYCRNPNRRRPPWCYVQVGLK 139
QY 121 PLVQECWVHDCADGKKPSSPPPE 143
Db 140 QRVOECWVHDCADGKKPSSPPPE 162
RE J.T.3
UR PIG
ID UROK PIG STANDARD; PRT; 442 AA.
AC P04185;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
GN (U-plasminogen activator).
OS Plas (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OG Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=85087954; PubMed=6096832;
RT Nagamine Y., Pearson D., Altus M.S., Reich E.;
RL "cDNA and gene nucleotide sequence of porcine plasminogen activator.";
RN Nucleic Acids Res. 12:9525-9541(1984).
RP REVISION TO 241.
RA Nagamine Y.;
RL Submitted (DEC-1986) to the PIR data bank.
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01648; CAA25806.1; -;
DR EMBL; X02724; CAA26511.1; -;
DR PIR; A00932; UKPG.
DR HSP; P00749; iKDU.
DR MKOPS; S01233; -;
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR008293; Pept_S1A_uPA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PIRSF; PIRSF001144; Utk_plasm_act; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1 SPC; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.

DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 20
FT CHAIN 21 442 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 186 CHAIN A (BY SIMILARITY).
FT CHAIN 190 442 CHAIN B (BY SIMILARITY).
FT DOMAIN 29 65 EGF-LIKE.
FT DOMAIN 72 153 KRINGLE.
FT DOMAIN 154 189 CONNECTING PEPTIDE.
FT DOMAIN 190 442 SERINE PROTEASE.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .).
FT DISULFID 33 41 BY SIMILARITY.
FT DISULFID 35 53 BY SIMILARITY.
FT DISULFID 55 64 BY SIMILARITY.
FT DISULFID 179 310 INTERCHAIN (BY SIMILARITY).
FT DISULFID 220 236 BY SIMILARITY.
FT DISULFID 228 299 BY SIMILARITY.
FT DISULFID 324 393 BY SIMILARITY.
FT DISULFID 356 372 BY SIMILARITY.
FT DISULFID 383 411 BY SIMILARITY.
FT ACT_SITE 235 235 CHARGE RELAY SYSTEM.
FT ACT_SITE 286 286 CHARGE RELAY SYSTEM.
FT ACT_SITE 387 387 CHARGE RELAY SYSTEM.
FT CONFLICT 241 241 Q -> H (IN REF. 1; CAA25806).
FT CONFLICT 242 242 Q -> H (IN REF. 1; CAA26511).
FT CONFLICT 288 288 A -> GS (IN REF. 1; CAA25806).
SQ SEQUENCE 442 AA; 49116 MW; E332FCFP501321EE CRC64;
Query Match 74.7%; Score 625.5; DB 1; Length 442;
Best Local Similarity 73.4%; Pred. No. 1.8e-53;
Matches 113; Conservative 11; Mismatches 19; Indels 11; Gaps 2;
QY 1 SNEHQV--PSNCDCLNGTGVSNKYFSNIHWNCNPKKFGQHQHCEIDKSKTCYEGNGHFY 58
Db 21 SHELHQESGASNGCLNGKGVKYFSNIQRSCPKKFGQHQHCEIDTSOTCEGNGHSY 80
QY 59 RGKASTDTMGRCPLPWNATVLTQYTHAHRSDALQGLGKINYCRNPNRRRPPWCYVQV 118
Db 81 RGKANTNTGRCPLPWNATVLTQYTHAHRSDALQGLGKINYCRNPNRRRPPWCYVQV 140
QY 119 LKPLVQECWVHDCA-----DGKKPSSPPPE 143
Db 141 LKQLVQECWVHDCGSGSHRPAIDYDGNPFPTPEK 174
RESULT 4
UROK_BOVIN
ID UROK_BOVIN STANDARD; PRT; 433 AA.
AC Q05589; Q28209;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
GN (U-plasminogen activator).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=aortic endothelium;
RX MEDLINE=93216119; PubMed=8385052;
RA Kretschmar J., Haendler B., Kojima S., Rifkin D.B.,
RA Schleuning W.-D.;

FT ACT SITE 378 378 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 189 A -> T (IN REF. 2).
SQ SEQUENCE 433 AA; 48730 MW; 4DE1B8D4DA47027A CRC64;

Query Match 72.3%; Score 605; DB 1; Length 433;
Best Local Similarity 72.4%; Pred. No. 1.7e-51;
Matches 105; Conservative 14; Mismatches 24; Indels 2; Gaps 1;

QY 1 SNEHQV--PSNCDCLNGTCTVSNKYFNSNIHWCNCPKFGQGHCEIDSKTCYEGNGHFX 58
DB 21 SNEVHKGESGCGCLNGKGVYKYFNSIQRCSCPKFGQGHCEIDSKTCYQNGHXY 80
QY 59 RGAASDTDTGRCPLPNSATVLTQYHARSALQGLGKHNKYNCRPNRRPWCYVQVG 118
DB 81 RGNARDLSGRFLAWDSPTVLLKMYHARSDAIQLGKHNKYNCRPNRRPWCYVQVG 140
QY 119 LKPLVQECMVHDCADGKPSPPPE 143
DB 141 LKQVQFCVQDCSVGKSPSPSPREK 165

RESULT 5
UOK RAT STANDARD; PRT; 432 AA.
ID UOK RAT
AC P29538;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-plasminogen activator).
GN PLAU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=92233409; PubMed=1568219;
RA Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
RA Kefferd R.F.;
RT "transcriptional and posttranscriptional activation of urokinase
RT plasminogen activator gene expression in metastatic tumor cells";
RL Cancer Res. 52:2489-2496(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Rabbani S.A.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -!- SUBUNIT: Found in high and low molecular mass forms. Each consists
CC of two chains, A and B. The high molecular mass form contains a
CC long chain A. Cleavage occurs after residue 156 in the low
CC molecular mass form to yield a short A1 chain (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X63434; CAA45028.1; -;
DR EMBL; X65651; CAA45601.1; -;
DR PIR; S24604; S18932.
DR HSSP; P00749; ILMW.
DR MEROPS; S01.231; -;
DR InterPro; IPR009003; Cys_Ser_trypsin.

"Bovine urokinase-type plasminogen activator and its receptor:
cloning and induction by retinoic acid.";
Gene 125:177-183(1993).
[2]
SEQUENCE OF 12-433 FROM N.A.
TISSUE=Kidney;
Ravn P., Berglund L., Petersen T.B.;
"Cloning and characterization of the bovine plasminogen activators uPA
and tPA.";
Int. Dairy J. 5:605-617(1995).
C -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
C plasminogen to form plasmin.
C -!- INDUCTION: By retinoic acid.
C -!- SIMILARITY: Belongs to peptidase family S1.
C -!- SIMILARITY: Contains 1 EGF-like domain.
C -!- SIMILARITY: Contains 1 kringle domain.
C -----
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C or send an email to license@isb-sib.ch).
C -----
C EMBL; L03546; AAA51419.1; -;
DR EMBL; X85801; CAA59796.1; -;
DR PIR; J00560; J00560.
DR HSSP; P00749; ILMW.
DR MEROPS; S01.231; -;
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR008293; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PIRSF; PIRSF001144; Urokinase act; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; kringle; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
DR Kringle; EGF-like domain; Signal; Zymogen.
DR SIGNAL; 1 20
F CHAIN 21 433 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
F CHAIN 21 179 CHAIN A (BY SIMILARITY).
F CHAIN 181 433 CHAIN B (BY SIMILARITY).
F DOMAIN 29 65 EGF-LIKE.
F DOMAIN 72 153 KRINGLE.
F DOMAIN 154 180 CONNECTING PEPTIDE.
F DOMAIN 181 433 SERINE PROTEASE.
F DISULFID 33 41 BY SIMILARITY.
F DISULFID 35 53 BY SIMILARITY.
F DISULFID 55 64 BY SIMILARITY.
F DISULFID 170 301 INTERCHAIN (BY SIMILARITY).
F DISULFID 211 227 BY SIMILARITY.
F DISULFID 219 290 BY SIMILARITY.
F DISULFID 315 384 BY SIMILARITY.
F DISULFID 347 363 BY SIMILARITY.
F DISULFID 374 402 BY SIMILARITY.
F ACT_SITE 226 226 CHARGE RELAY SYSTEM (BY SIMILARITY).
F ACT_SITE 277 277 CHARGE RELAY SYSTEM (BY SIMILARITY).

DR InterPro: IPR006209; EGF like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR008293; Pept S1A uPA.
DR InterPro: IPR001354; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00051; kringle; 1.
DR PIRSF: PIRSF001144; Urk plas act; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0018; KRINGLE.
DR ProDom: PD000395; Kringle; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00026; EGF_2; FALSE_NEG.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00021; KRINGLE_2; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 19 POTENTIAL
FT CHAIN 20 432 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 20 177 CHAIN A (BY SIMILARITY).
FT CHAIN 156 177 SHORT A CHAIN (A1) (BY SIMILARITY).
FT CHAIN 179 432 CHAIN B (BY SIMILARITY).
FT DOMAIN 27 63 EGF-LIKE.
FT DOMAIN 70 151 KRINGLE.
FT DOMAIN 152 178 CONNECTING PEPTIDE.
FT DOMAIN 179 432 SERINE PROTEASE.
FT DISULFID 31 39 BY SIMILARITY.
FT DISULFID 33 51 BY SIMILARITY.
FT DISULFID 53 62 BY SIMILARITY.
FT DISULFID 168 300 INTERCHAIN (BY SIMILARITY).
FT DISULFID 210 226 BY SIMILARITY.
FT DISULFID 218 289 BY SIMILARITY.
FT DISULFID 314 383 BY SIMILARITY.
FT DISULFID 346 382 BY SIMILARITY.
FT DISULFID 373 401 BY SIMILARITY.
FT ACT_SITE 225 225 CHARGE RELAY SYSTEM.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 377 377 CHARGE RELAY SYSTEM.
FT CONFLICT 16 16 N -> H (IN REF. 2).
FT CONFLICT 24 24 E -> G (IN REF. 2).
FT CONFLICT 332 332 D -> N (IN REF. 2).
SQ SEQUENCE 432 AA; 47957 MW; 4EB1B96C716244C8 CRC64;

try Match 70.7%; Score 592; DB 1; Length 432;
t Local Similarity 75.6%; Pred. No. 3.1e-50;
ches 102; Conservative 10; Mismatches 23; Indels 0; Gaps 0;

QY 9 SNCCDLGGTCVSNKYFSNIHWCNCPKFGGCHCETDKSKTCYEGNGHYRGKASTDTMG 68
DB 29 SNGCGQGGVGVSVKYFSSIRRCSPKPKGEGHEIDTSKTCYHNGQSGYRGKANTDTG 88
QY 69 RPLCPNWSATVLOQTYAHRSDALQLGLGKHNYCRNPDNRPPWCYVQVGLKPLVQECVW 128
DB 89 RPLCLANSPAVLQQTNAHRSDALSGLGKHNYCRNPDNRPPWCYVQVGLKPLVQECVW 148
QY 129 HDCADGKXSPPEE 143
DB 149 QDCSLSKSPSTVDQ 163

RE T 6
UR MOUSE
ID UROK MOUSE
AC P06869; STANDARD; PRT; 433 AA.
DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-plasminogen activator).
GN PLAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85179474; PubMed=2985383;
RA Belin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y.,
RA Reich E., Kocher H.P., Duvoisin R.M.;
RT "Cloning, nucleotide sequencing and expression of cDNAs encoding
RT mouse urokinase-type plasminogen activator.";
RL Eur. J. Biochem. 148:225-232(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88163459; PubMed=2831940;
RA Degen S.J.F., Heckel J.L., Reich E., Degen J.L.;
RT "The murine urokinase-type plasminogen activator gene.";
RL Biochemistry 26:8270-8279(1987).
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -1- SUBUNIT: Found in high and low molecular mass forms. Each consists
CC of two chains, A and B. The high molecular mass form contains a
CC long chain A. Cleavage occurs after residue 156 in the low
CC molecular mass form to yield a short A1 chain (by similarity).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X02389; CAA26231.1; -;
DR EMBL: M17922; AAA40539.1; -;
DR PIR: A29420; URONS.
DR HSSP: P00749; INDU.
DR MEROPS: S01.231; -;
DR MGD: MGI.97611; Plau.
DR InterPro: IPR009003; Cys Ser trypsin.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR008293; Pept S1A uPA.
DR InterPro: IPR001254; Peptidase S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00051; kringle; 1.
DR Pfam: PF00089; trypsin; 1.
DR PIRSF: PIRSF001144; Urk plas act; 1.
DR PRINTS: PRO0722; CHYMOTRYPSIN.
DR PRINTS: PRO0018; KRINGLE.
DR ProDom: PD000395; Kringle; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00020; TRYPSIN_DOM; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; FALSE_NEG.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00021; KRINGLE_2; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.

F SIGNAL 1 20
 F CHAIN 21 433
 F CHAIN 21 178
 F CHAIN 157 178
 F CHAIN 180 433
 F CHAIN 28 64
 F DOMAIN 71 152
 F DOMAIN 153 179
 F DOMAIN 180 433
 F DISULFID 32 40
 F DISULFID 34 52
 F DISULFID 54 63
 F DISULFID 169 301
 F DISULFID 211 227
 F DISULFID 219 290
 F DISULFID 315 384
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 F ACT SITE 226 226
 F ACT SITE 277 277
 F ACT SITE 378 378
 S SEQUENCE 433 AA; 48268 MW; A99C35F6250443F9 CRC64;

very Match 68.0%; Score 569; DB 1; Length 433;
 est Local Similarity 70.4%; Pred No. 5.3e-48;
 itches 95; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

Q 9 SNCDCLNGTGVSNKYFNIHWCNPKFGQGHCEIDKSKTCYEGNGHFGYRGKASTDTMG 68
 D 30 SNGCQNGGVCSYKYFYFRRIRCSKPRFQGEHCEIDASKTCYHNGSDSYRGKANTDTKG 89
 Q 69 RPLCPNATVLQOYTHAHRSDALQLGLGKKNYCRNPNRPRPCYQVGLKPLVQSCMV 128
 D 90 RPLCAWNAVLQKPYNAHRPDAISLGLGKKNYCRNPNRQKRPWCYQVGLRQVQSCMV 149
 Q 129 HDCADGKFPSPPEE 143
 D 150 HDCSLSKFPSSVDQ 164

R IT 7
 U DESRO STANDARD; PRT; 477 AA.
 I UR2 DESRO STANDARD; PRT; 477 AA.
 A P15638;
 D 01-APR-1990 (Rel. 14, Created)
 D 01-FEB-1996 (Rel. 33, Last sequence update)
 D 28-FEB-2003 (Rel. 41, Last annotation update)
 D Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA
 alpha-2) (BAP-PA) (t-plasminogen activator).
 C Desmodus rotundus (Vampire bat).
 O Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 O Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 O Desmodontinae; Desmodus.
 C NCBI_TaxID=9430;
 R [1]_TaxID=9430;
 R SEQUENCE FROM N.A.
 R TISSUE=Salivary gland;
 R MEDLINE=9203036; PubMed=1937019;
 R Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 R Alagon A., Donner P., Schleuning W.D.;
 R "The plasminogen activator family from the salivary gland of the
 R vampire bat Desmodus rotundus: cloning and expression.";
 R Gene 105:229-237 (1991).
 R [2]
 R SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 R TISSUE=Salivary gland;
 R MEDLINE=9003667; PubMed=2509450;
 R Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
 R Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
 R "Isolation, characterization, and cDNA cloning of a vampire bat
 R salivary plasminogen activator.";
 R J. Biol. Chem. 264:17947-17952 (1989).
 R [3]

RP CHARACTERIZATION.
 RX MEDLINE=93393059; PubMed=1309059;
 RA Schleuning W.D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baidus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of Desmodus rotundus (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403 (1992).
 CC -I- FUNCTION: Probably essential to support the feeding habits of this
 CC exclusively haematophagous animal. Probable potent thrombolytic
 CC agent.
 CC -I- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -I- ENZYME REGULATION: Activity toward plasminogen is stimulated in
 CC the presence of fibrin I.
 CC -I- SUBUNIT: Monomer.
 CC -I- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
 CC and the kringle domain apparently mediates fibrin-induced
 CC stimulation of activity.
 CC -I- SIMILARITY: Belongs to peptidase family S1.
 CC -I- SIMILARITY: Contains 1 EGF-like domain.
 CC -I- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -I- SIMILARITY: Contains 1 kringle domain.
 CC -----
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 CC -----
 DR EMBL; M63988; AAA1593.1; -;
 DR EMBL; J05082; AAA1596.1; -;
 DR PIR; A34369; A34369.
 DR PIR; J05098; J05098.
 DR HSSP; P98119; 1A51.
 DR MEROPS; S01.232; -;
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR000083; Fibrctn1.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00039; fni; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00058; FNI; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 FT Kringle; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 477
 FT DOMAIN 40 82
 FT DOMAIN 83 121
 FT DOMAIN 128 209
 FT DOMAIN 225 477
 FT DOMAIN 225 477

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CC	EMBL; J05187; AAA49131.1; -	CC
CC	EMBL; J05188; AAA49130.1; -	CC
DR	PIR; A35005; A35005.	DR
DR	HSSP; P00763; 1DPO.	DR
DR	MEROPS; S01.231; -	DR
DR	InterPro; IPR009003; Cys Ser trypsin.	DR
DR	InterPro; IPR006209; EGF-like.	DR
DR	InterPro; IPR006210; EGF.	DR
DR	InterPro; IPR000001; Kringle.	DR
DR	InterPro; IPR008293; Pept_S1A_upA.	DR
DR	InterPro; IPR001254; Peptidase_S1.	DR
DR	InterPro; IPR001314; Peptidase_S1A.	DR
DR	Pfam; PF00051; Kringle; 1.	DR
DR	Pfam; PF00083; trypsin; 1.	DR
DR	PISRP; PISRP001144; Utk Plasm act; 1.	DR
DR	PRINTS; PRO0722; CHYMOTRYPSIN.	DR
DR	PRINTS; PRO0018; KRINGLE.	DR
DR	ProDom; PD000395; Kringle; 1.	DR
DR	SMART; SM00181; EGF; 1.	DR
DR	SMART; SM00130; KR; 1.	DR
DR	SMART; SM00020; Tryp_Spc; 1.	DR
DR	PROSITE; PS00022; EGF_1; 1.	DR
DR	PROSITE; PS01186; EGF_2; 1.	DR
DR	PROSITE; PS50028; EGF_3; 1.	DR
DR	PROSITE; PS00021; KRINGLE_1; 1.	DR
DR	PROSITE; PS00070; KRINGLE_2; 1.	DR
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.	DR
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	DR
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	DR
KW	Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;	KW
KW	Kringle; EGF-like domain; Signal; Zymogen.	KW
FT	SIGNAL	FT
FT	CHAIN 21 434	FT
FT	CHAIN 21 171	FT
FT	CHAIN 173 434	FT
FT	DOMAIN 36 72	FT
FT	DOMAIN 79 158	FT
FT	DOMAIN 159 172	FT
FT	DOMAIN 173 434	FT
FT	DISULFID 40 48	FT
FT	DISULFID 42 60	FT
FT	DISULFID 62 71	FT
FT	DISULFID 162 296	FT
FT	DISULFID 202 218	FT
FT	DISULFID 210 285	FT
FT	DISULFID 310 379	FT
FT	DISULFID 342 358	FT
FT	DISULFID 369 397	FT
FT	ACT_SITE 217 217	FT
FT	ACT_SITE 272 272	FT
FT	ACT_SITE 373 373	FT
FT	CARBOHYD 228 228	FT
FT	SEQUENCE 434 AA; 49400 MW; BD881048DD66A55 CRC64;	FT
FT	Query Match	FT
FT	Best Local Similarity 40.0%; Score 334.5; DB 1; Length 434;	FT
FT	Matches 58; Conservative 14; Mismatches 30; Indels 5; Gaps 2;	FT
QY	11 CDCLNGTGVSNKYFSNIHWCNCKPFGQGHCEIDKSKTCYEGNGHFRGKASTDTWGRP 70	QY
DB	40 CQCLNGTGTCTYRFFSQIKRCLCEPGYGLHCEIDTNSICYSGNGEDYRGMAEDP---G 95	DB
QY	71 CLPWSNATVLQ-OTYHAHRSDALQLGLGKHNYCRNPNRRRCVQ 116	QY
DB	96 CLYWDHFSVRWGDYHADLKNALQLGLGKHNYCRNPNRNGSRPCWYTK 142	DB
RESULT 9		RESULT 9
URTB DESRO		URTB DESRO
ID URTB DESRO	STANDARD; PRY; 431 AA.	ID URTB DESRO
AC P98121;		AC P98121;

I 01-FEB-1996 (Rel. 33, Created)
D 01-FEB-1996 (Rel. 33, Last sequence update)
D 28-FEB-2003 (Rel. 41, Last annotation update)
L Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA
beta).
C Desmodus rotundus (Vampire bat).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
C Desmodontinae; Desmodus.
C NCBI_TaxID=9430;
K [1]
R SEQUENCE FROM N.A.
R TISSUE=Salivary gland;
R MEDLINE=9203036; PubMed=1937019;
F Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
F Alagon A., Donner P., Schleuning W.D.;
K "The plasminogen activator family from the salivary gland of the
K vampire bat Desmodus rotundus: cloning and expression.";
K Gene 105:229-237(1991).
K [2]
R CHARACTERIZATION.
R MEDLINE=9333059; PubMed=1309059;
F Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
F Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
R Donner P.;
R "Plasminogen activators from the saliva of Desmodus rotundus (common
R vampire bat): unique fibrin specificity.";
R Ann. N.Y. Acad. Sci. 667:395-403(1992).
C -!- FUNCTION: Probably essential to support the feeding habits of this
C exclusively haematophagous animal. Probable potent thrombolytic
C agent.
C -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
C plasminogen to form plasmin.
C -!- SUBUNIT: Monomer.
C -!- SIMILARITY: Belongs to peptidase family S1.
C -!- SIMILARITY: Contains 1 EGF-like domain.
C -!- SIMILARITY: Contains 1 kringle domain.
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C or send an email to license@isb-sib.ch).
C -----
C EMBL; M63989; AAA31594.1; --
D F01; J80599; J80599.
D HSP; P98119; IAS1.
D MEROPS; S01.239; --
D InterPro; IPR009003; Cys Ser trypsin.
D InterPro; IPR006209; EGF-like.
D InterPro; IPR006210; IEGF.
D InterPro; IPR000001; Kringle.
D InterPro; IPR001254; Peptidase_S1.
D InterPro; IPR001314; Peptidase_S1A.
D Pfam; PF00008; EGF; 1.
D Pfam; PF00051; kringle; 1.
D Pfam; PF00089; trypsin; 1.
D PRINTS; PR00722; CHYMOTRYPSIN.
D PRINTS; PR00018; KRINGLE.
D ProDom; PD000395; Kringle; 1.
D SMART; SM00181; EGF; 1.
D SMART; SM00130; KS; 1.
D SMART; SM00020; Tryp_Spc; 1.
D PROSITE; PS00022; EGF_1; 1.
D PROSITE; PS01186; EGF_2; 1.
D PROSITE; PS00026; EGF_3; 1.
D PROSITE; PS00021; KRINGLE_1; 1.
D PROSITE; PS00070; KRINGLE_2; 1.
D PROSITE; PS00240; TRYPSIN_DOM; 1.
D PROSITE; PS00134; TRYPSIN_HIS; 1.
D PROSITE; PS00135; TRYPSIN_SER; 1.

KW plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Signal; Multigene family.
FT SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 431 SALIVARY PLASMINOGEN ACTIVATOR BETA.
FT DOMAIN 37 75 EGF-LIKE.
FT DOMAIN 82 163 KRINGLE.
FT DOMAIN 179 431 SERINE PROTEASE.
FT ACT_SITE 226 226 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 275 275 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 382 382 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 41 52 BY SIMILARITY.
FT DISULFID 46 63 BY SIMILARITY.
FT DISULFID 65 74 BY SIMILARITY.
FT DISULFID 82 163 BY SIMILARITY.
FT DISULFID 103 145 BY SIMILARITY.
FT DISULFID 134 158 BY SIMILARITY.
FT DISULFID 168 299 BY SIMILARITY.
FT DISULFID 211 227 BY SIMILARITY.
FT DISULFID 219 288 BY SIMILARITY.
FT DISULFID 313 388 BY SIMILARITY.
FT DISULFID 345 361 BY SIMILARITY.
FT DISULFID 378 406 BY SIMILARITY.
FT CARBOHYD 139 139 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 431 AA; 48221 MW; 699B5E675B162CBF CRC64;
Query Match 39.2%; Score 328.5; DB 1; Length 431;
Best Local Similarity 47.6%; Pred. No. 1.2e-24;
Matches 59; Conservative 16; Mismatches 48; Indels 1; Gaps 1;
QY 9 SNCDCLNGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRGKASDTWVG 68
DB 42 SELRCFNGGTCWAASFSDF-VQCQPKGYTGQCEVDTHATCYKQGVYRGWTSSESG 100
QY 69 RPLCPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDRRPPWCYVGLKPLVOECWV 128
DB 101 AQCIWNSNLLTRTYNGRRSDAITLGLGNHYCRNPDPNNKPCWYKASKFILEFCV 160
QY 129 HDCA 132
DB 161 PVCS 164
RESULT 10
TPA_HUMAN
ID TPA_HUMAN STANDARD; PRT; 562 AA.
AC P00750; Q15103.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
DE (t-PA) (t-plasminogen activator) (Alteplase) (Reteplase).
GN PLAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=83115262; PubMed=6337343;
RA Penica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A., H.L.,
RA Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L.,
RA Goeddel D.V., Collen D.;
RT "Cloning and expression of human tissue-type plasminogen activator
RT cDNA in E. coli.";
RL Nature 301:214-221(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=88262579; PubMed=3133640;
RA Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
RT "Nucleotide sequence of the tissue-type plasminogen activator cDNA

RT from human fetal lung cells.";
RL Nucleic Acids Res. 15:5695-5695(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88054470; PubMed=2824147;
RA Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J.,
RT Hsiung N.;
RA "Expression of human uterine tissue-type plasminogen activator in
RT mouse cells using BPV vectors.";
RL DNA 6:451-472(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=86196143; PubMed=3009482;
RA Friesner Degen S.J., Rajput B., Reich E.;
RT "The human tissue plasminogen activator gene.";
RL J. Biol. Chem. 261:6972-6985(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298137; PubMed=6089198;
RA Ny T., Elgh F., Lund B.;
RT "The structure of the human tissue-type plasminogen activator gene:
RT correlation of intron and exon structures to functional and
RT structural domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284200; PubMed=3090401;
RA Harris T.J., Patel T., Marston F.A., Little S., Ertage J.S.,
RT Opendakker G., Volckaert G., Rembouts W., Billiau A., Somer P.;
RT "Cloning of cDNA coding for human tissue-type plasminogen activator
RT and its expression in Escherichia coli.";
RL Mol. Biol. Med. 3:279-292(1986).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX TISSUE=Umbilical vein;
RA MEDLINE=90192129; PubMed=2107528;
RT Siebert P.D., Fong K.;
RT "Variant tissue-type plasminogen activator (PLAT) cDNA obtained from
RT human endothelial cells.";
RL Nucleic Acids Res. 18:1086-1086(1990).
RN [8]
RP SEQUENCE FROM N.A.
RX TISSUE=Brain;
RA MEDLINE=22388237; PubMed=12477932;
RT Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RT Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,
RT Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RT Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RT Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RT Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RT Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smalilus D.E.,
RT Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 212-361 FROM N.A.
RX MEDLINE=83169656; PubMed=6572897;
RA Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
RT Josephson S.;
RT "Isolation of cDNA sequences coding for a part of human tissue
RT plasminogen activator.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983).
RN [10]

RP SEQUENCE OF 1-36 FROM N.A.
RX MEDLINE=85289338; PubMed=3161893;
RA Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
RT Schleuning W.-D.;
RA "Isolation and characterization of the human tissue-type plasminogen
RT activator structural gene including its 5' flanking region.";
RL J. Biol. Chem. 260:11223-11230(1985).
RN [11]
RP SEQUENCE OF 31-562 FROM N.A.
RX MEDLINE=91291340; PubMed=1368681;
RA Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
RT "Purification and characterization of tissue plasminogen activator
RT secreted by human embryonic lung diploid fibroblasts, IMR-90 cells.";
RL Agric. Biol. Chem. 55:1225-1232(1991).
RN [12]
RP SEQUENCE OF 36-562.
RX TISSUE=Melanoma;
RA MEDLINE=85000468; PubMed=6433976;
RT Pohl G., Kaellstroem M., Bergsdorf N., Wallen P., Joernvall H.;
RT "Tissue plasminogen activator: peptide analyses confirm an indirectly
RT derived amino acid sequence, identify the active site serine residue,
RT establish glycosylation sites, and localize variant differences.";
RL Biochemistry 23:3701-3707(1984).
RN [13]
RP SEQUENCE OF 33-52 AND 311-330.
RX TISSUE=Melanoma;
RA MEDLINE=83209620; PubMed=6682760;
RT Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.;
RT "Purification and characterization of a melanoma cell plasminogen
RT activator.";
RL Eur. J. Biochem. 132:681-686(1983).
RN [14]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=90092112; PubMed=2513186;
RA Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
RT "Carbohydrate structure of recombinant human uterine tissue
RT plasminogen activator expressed in mouse epithelial cells.";
RL Eur. J. Biochem. 186:273-286(1989).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE THR-96.
RX MEDLINE=91159408; PubMed=1900431;
RA Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
RT "Tissue plasminogen activator has an O-linked fucose attached to
RT threonine-61 in the epidermal growth factor domain.";
RL Biochemistry 30:2311-2314(1991).
RN [16]
RP DISULFIDE BONDS IN KRINGLE 2.
RX MEDLINE=91244765; PubMed=1645336;
RA Vlahos C.J., Wilhelm O.G., Hassell T., Jaekunas S.R., Bang N.U.;
RT "Disulfide pairing of the recombinant kringle-2 domain of tissue
RT plasminogen activator produced in Escherichia coli.";
RL J. Biol. Chem. 266:10070-10072(1991).
RN [17]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=95200985; PubMed=9613982;
RA Larba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
RT Bode W.;
RT "The 2.3 Å crystal structure of the catalytic domain of recombinant
RT two-chain human tissue-type plasminogen activator.";
RL J. Mol. Biol. 259:117-135(1996).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=9749126; PubMed=9305622;
RA Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
RT Bode W.;
RT "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
RT crystal structure of single-chain human tPA.";
RL EMBO J. 16:4797-4805(1997).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
RX MEDLINE=92118803; PubMed=1310033;
RA de Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Tulinsky A.,
RT Westbrook M.L., Kossiakof A.A.;

Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Plasma; Kringle; EGF-like domain; Repeat; Signal. PROBABLE.

1 17
FT SIGNAL
FT PROPEP 18 29
FT CHAIN 30 559
FT CHAIN 30 308

TISSUE-TYPE PLASMINOGEN ACTIVATOR.
TISSUE-TYPE PLASMINOGEN ACTIVATOR A

CHAIN.
TISSUE-TYPE PLASMINOGEN ACTIVATOR B

CHAIN.
FIBRONECTIN TYPE-I.

DOMAIN 36 78
DOMAIN 79 117
DOMAIN 124 205
DOMAIN 213 294
DOMAIN 309 559

KRINGLE 1.
KRINGLE 2.
SERINE PROTEASE.
CHARGE RELAY SYSTEM.
CHARGE RELAY SYSTEM.

ACT_SITE 355 355
ACT_SITE 404 404
ACT_SITE 510 510

DISULFID 38 68
DISULFID 66 75
DISULFID 83 94
DISULFID 88 105
DISULFID 107 116
DISULFID 124 205
DISULFID 145 187
DISULFID 176 200
DISULFID 213 294
DISULFID 234 276
DISULFID 265 289
DISULFID 297 428
DISULFID 340 356
DISULFID 348 417
DISULFID 442 516
DISULFID 474 490
DISULFID 506 534
CARBOHYD 149 149
CARBOHYD 481 481
CONFLICT 380 380

SEQUENCE 559 AA; 62903 MW; 7DBD3809C1D1C921 CRC64;

ry Match 38.8%; Score 325; DB 1; Length 559;
st Local Similarity 44.1%; Pred. No. 3.3e-24;
ches 64; Conservative 15; Mismatches 56; Indels 10; Gaps 3;

3 ELHQVP-----SNCDLNGGTGVSNKYFSNIHWCNCPKFGGQHCIDKSKTYENGHHFY 58
74 QCHSVPRVRCSEPCFNGGTCCOALYFSDF-VQCPCDGVGKRCIDITRATCFEGQGIT 132
59 RGRASDTMGRPCLPWNATVLOOTYHAHRSDALQLGLGHNYCRPNRRRPPWCYVQVG 118
133 RGTWSTAENGAEICINNNSALSQKPSARRPNAIKLGLGHNYCRNPDRDVKPVCYVKA 192

119 LKPLVQECVHDCADGKKSPPPEE 143
193 GKYTFEFCSTPAC-----PKGPTED 212

ST 12
TPA_MOUSE STANDARD; PRT; 559 AA.

01-JUL-1989 (Rel. 11, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tissue-type plasminogen activator precursor (EC 3.4.21.68) (TPA)
(t-PA) (t-plasminogen activator).

Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID:10090;
[1]
SEQUENCE FROM N.A.
MEDLINE:88087303; PubMed:2826484;

Rickles R.J., Darrow A.L., Strickland S.;
"Molecular cloning of complementary DNA to mouse tissue plasminogen
activator mRNA and its expression during F9 teratocarcinoma cell
differentiation";
J. Biol. Chem. 263:1563-1569(1988).
[2]
SEQUENCE FROM N.A.
TISSUE-Mammary gland;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen
to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By
controlling plasmin-mediated proteolysis, it plays an important
role in tissue remodeling and degradation, in cell migration and
many other physiological events.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.
-!- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
bond.
-!- SUBCELLULAR LOCATION: Secreted; extracellular.
-!- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
-!- MISCELLANEOUS: Binds to the kringle structure of the fibrin A
chain. Binding to fibrin enhances its catalytic activity.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 2 kringle domains.

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entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

EMBL; J03520; AAA40470.1; -;
EMBL; BC011256; AAH11256.1; -;
PIR; A29941; A29941.
HSP; P00750; 1A5H.
MEROPS; S01.232; -;
MGP; MG1.97610; Plat.
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR006209; EGF-like.
InterPro; IPR000083; Fibronctnl.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 1.
Pfam; PF00039; fnl; 1.
Pfam; PF00051; kringle; 2.

Pfam; PF00089; trypsin; 1.
 PRINTS; PRO0722; CHYMOTRYPSIN.
 PRINTS; PRO0018; KRINGLE.
 ProDom; PD000395; Kringle; 2.
 SMART; SM00181; EGF; 1.
 SMART; SM00058; FNI; 1.
 SMART; SM00130; KR; 2.
 SMART; SM00020; TRYP_SPC; 1.
 PROSITE; PS00022; EGF_1; 1.
 PROSITE; PS01186; EGF_2; 1.
 PROSITE; PS01253; FIBRONECTIN_1; 1.
 PROSITE; PS00026; EGF_3; 1.
 PROSITE; PS00021; KRINGLE_2; 2.
 PROSITE; PS00070; KRINGLE_2; 2.
 PROSITE; PS00240; TRYP_SIN_DOM; 1.
 PROSITE; PS00134; TRYP_SIN_HIS; 1.
 PROSITE; PS00135; TRYP_SIN_SER; 1.
 Plasminogen activator; Hydrolase; Serine protease; Glycoprotein;
 Plasma; Kringle; EGF-like domain; Repeat; Signal.
 SIGNAL 1 17 PROBABLE.
 PROPEP 18 29
 CHAIN 30 559
 CHAIN 30 308
 CHAIN 309 559
 DOMAIN 36 78
 DOMAIN 79 117
 DOMAIN 124 205
 DOMAIN 213 294
 DOMAIN 309 559
 ACT_SITE 355 355
 ACT_SITE 404 404
 ACT_SITE 510 510
 DISULFID 38 68
 DISULFID 66 75
 DISULFID 83 94
 DISULFID 88 105
 DISULFID 107 116
 DISULFID 124 205
 DISULFID 145 187
 DISULFID 176 200
 DISULFID 213 294
 DISULFID 234 276
 DISULFID 265 289
 DISULFID 297 428
 DISULFID 340 356
 DISULFID 348 417
 DISULFID 442 516
 DISULFID 474 490
 DISULFID 506 534
 CARBOHYD 149 149
 CARBOHYD 481 481
 CONFLICT 260 260
 CONFLICT 325 325
 SEQUENCE 559 AA; 63122 MW; 8CEE2BDB94514D9 CRC64;
 Query Match 37.7%; Score 315.5; DB 1; Length 559;
 est Local Similarity 44.5%; Pred. No. 2.8e-23;
 atches 61; Conservative 15; Mismatches 56; Indels 5; Gaps 2;
 3 ELHQVP-----SNCDLNGCTVSNKYFNIHWCNPKFGGCHCIDSIDKTCYEGNGHFY 58
 74 QCHSVPRSCSPRCFNGGTCCQALYFSDP-VCCPDPFGVKRCIDIDTRATCFEEQGIT 132
 59 RGRKASTDTMGRCPLPNWTSATVLQQTVAHRSVALQLGLKKNYCRNPNRRPWCYQVG 118
 133 RGTWSTAESGAECINWSSVLSLKPYNARRPNAIKLGLGNHNYCRNPDRLKPCYVFK 192
 119 LKPLVOECMWHCADGK 135
 193 GKYTFECSTPACPKG 209

RESULT 13

URT1_DESRO STANDARD; PRT; 477 AA.
 ID URT1_DESRO STANDARD; PRT; 477 AA.
 AC P98119; 1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Salivary plasminogen activator alpha 1 precursor (EC 3.4.21.68) (DSPA
 DE alpha-1).
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.
 OX NCBI_TaxID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RT vampire bat Desmodus rotundus: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=9339059; PubMed=1309059;
 RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of Desmodus rotundus (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RC TISSUE=Salivary gland;
 RX MEDLINE=98022741; PubMed=9354616;
 RA Renatus M., Stubbs M.T., Huber R., Bringmann P., Donner P.,
 RA Schleuning W.D., Bode W.;
 RT "Catalytic domain structure of vampire bat plasminogen activator: a
 RT molecular paradigm for proteolysis without activation cleavage.";
 RL Biochemistry 36:13483-13493(1997).
 CC -!- FUNCTION: Probably essential to support the feeding habits of this
 CC exclusively haematophagous animal. Potent thrombolytic agent.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- ENZYME REGULATION: Activity toward plasminogen is stimulated in
 CC the presence of fibrin I.
 CC -!- SUBUNIT: Monomer.
 CC -!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
 CC and the kringle domain apparently mediates fibrin-induced
 CC stimulation of activity.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M63987; AAA31591.1; -;
 CC EMBL; M63986; AAA31592.1; -;
 CC PIR; J50597; J50597.
 CC PDB; 1A51; 23-MAR-99.
 CC MEROPS; S01.232; -;
 CC GlycoSuiteDB; P98119; -;
 CC InterPro; IPR009003; Cys Ser trypsin.
 CC InterPro; IPR006209; EGF_like.

DR InterPro: IPR000083; Fibrinctnl.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Peptidase_s1.
DR InterPro: IPR001314; Peptidase_s1A.
DR Pfam: PF00008; EGF_1.
DR Pfam: PF00039; fnl; 1.
DR Pfam: PF00051; kringle; 1.
DR Pfam: PF00089; crypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00018; KRINGLE.
DR ProDom: PD000395; Kringle; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00058; fnl; 1.
DR SMART: SM00130; KR; 1.
DR SMART: SM00201; Tryp_Spc; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00026; EGF_3; 1.
DR PROSITE: PS01253; FIBRONECTIN_1; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Signal; Multigene family; 3D-structure.
FT SIGNAL 1 36
FT CHAIN 37 477
FT DOMAIN 40 82
FT DOMAIN 83 121
FT DOMAIN 128 209
FT DOMAIN 225 477
FT ACT_SITE 272 272
FT ACT_SITE 321 321
FT ACT_SITE 428 428
FT DISULFID 42 72
FT DISULFID 70 79
FT DISULFID 87 98
FT DISULFID 92 109
FT DISULFID 111 120
FT DISULFID 128 209
FT DISULFID 149 191
FT DISULFID 180 204
FT DISULFID 214 245
FT DISULFID 257 273
FT DISULFID 265 334
FT DISULFID 359 434
FT DISULFID 391 407
FT DISULFID 424 452
FT CARBOHYD 153 153
FT CARBOHYD 398 398
FT TURN 214 215
FT STRAND 223 224
FT TURN 226 227
FT STRAND 230 231
FT HELIX 234 236
FT TURN 238 239
FT STRAND 240 245
FT STRAND 254 263
FT TURN 264 265
FT STRAND 266 269
FT HELIX 271 273
FT TURN 280 282
FT STRAND 284 287
FT TURN 297 298
FT STRAND 300 309
FT TURN 311 312
FT TURN 315 317
FT TURN 319 320
FT STRAND 323 328

FT STRAND 338 338
FT TURN 339 340
FT STRAND 341 341
FT STRAND 345 345
FT TURN 349 350
FT TURN 355 356
FT STRAND 358 363
FT STRAND 366 366
FT STRAND 374 374
FT STRAND 379 385
FT HELIX 388 390
FT TURN 393 398
FT TURN 403 404
FT STRAND 405 409
FT TURN 425 426
FT TURN 428 429
FT STRAND 431 436
FT TURN 437 438
FT STRAND 439 448
FT TURN 455 456
FT STRAND 459 463
FT HELIX 464 467
FT HELIX 468 474
SQ SEQUENCE 477 AA; 53616 MW; AA05FD1739C10B5E CRC64;
Query Match 37.1%; Score 310.5; DB 1; Length 477;
Best Local Similarity 45.5%; Pred. No. 7.2e-23;
Matches 60; Conservative 14; Mismatches 53; Indels 5; Gaps 3;
QY 5 HQVPSN-CD---CLNGGTCVSNKYFSNIHWCNCPKKGGOHCIDKSKTCYEGNGHYRG 60
Db 80 HTVPVNSCEPRCNGGTCQAVYFSD-VCQCPAGTGRKCEVDTRATCYEGGVTYRG 138
QY 61 KASDTTNGRCLPWN SATVLQOTYAHRS DALQGLGKHNCRNPONRRFPWCYVQVGLK 120
Db 139 TWSTAESRVECIINNWSLLTTRTYNGRMPDAFNGLGNHNYCRNPNFGAPKPCVVIKAGK 198
QY 121 PLVQECMVHDC A 132
Db 199 FTSCSCVPVCS 210
RESULT 14
TPA_BOVIN STANDARD; PRT; 566 AA.
AC Q28198;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (tPA)
DE (t-PA) (t-plasminogen activator).
GN PLAT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ravn P., Berglund L., Petersen T.E.;
RT "Cloning and characterization of the bovine plasminogen activators uPA
and tPA";
RL Int. Dairy J. 5:605-617(1995).
CC -!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen
to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By
controlling plasmin-mediated proteolysis, it plays an important
role in tissue remodeling and degradation, in cell migration and
many other physiological events.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.
CC -!- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
bond.

-1- SUBCELLULAR LOCATION: Secreted; extracellular.

-1- PTM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER ARG-314 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.

-1- MISCELLANEOUS: Binds to the kringle structure of the fibrin A chain. Binding to fibrin enhances its catalytic activity.

-1- SIMILARITY: Belongs to peptidase family S1.

-1- SIMILARITY: Contains 1 EGF-like domain.

-1- SIMILARITY: Contains 1 fibronectin type I domain.

-1- SIMILARITY: Contains 2 kringle domains.

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EMBL; X85800; CAA59795.1; --
HSSP; P00750; IRTF.
MEROPS; S01.234; --
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR006209; EGF-like.
InterPro; IPR000083; Fibnctn1.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
Pfam; PF00051; kringle; 2.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 2.
SMART; SM00181; EGF; 1.
SMART; SM00058; FN1; 1.
SMART; SM00130; KR; 2.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00026; EGF_3; 1.
PROSITE; PS01253; FIBRONECTIN_1; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00021; KRINGLE_2; 2.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein; Plasma; Kringle; EGF-like domain; Repeat; Signal.
PROPEP; 22 33
CHAIN; 34 566
CHAIN; 34 314
CHAIN; 315 566
DOMAIN; 40 82
DOMAIN; 83 121
DOMAIN; 128 209
DOMAIN; 219 300
DOMAIN; 315 566
ACT_SITE; 361 381
ACT_SITE; 410 410
ACT_SITE; 517 517
DISULFID; 42 72
DISULFID; 70 98
DISULFID; 87 109
DISULFID; 111 120
DISULFID; 128 209
DISULFID; 149 191

FT DISULFID 180 204 BY SIMILARITY.
FT DISULFID 219 300 BY SIMILARITY.
FT DISULFID 240 282 BY SIMILARITY.
FT DISULFID 271 295 BY SIMILARITY.
FT DISULFID 303 434 INTERCHAIN (BY SIMILARITY).
FT DISULFID 346 362 BY SIMILARITY.
FT DISULFID 354 423 BY SIMILARITY.
FT DISULFID 448 523 BY SIMILARITY.
FT DISULFID 480 496 BY SIMILARITY.
FT DISULFID 513 541 BY SIMILARITY.
FT CARBOHYD 153 153 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 566 AA; 63701 MW; 2E6BEB4E32276C3 CRC64;
Query Match 35.9%; Score 300.5; DB 1; Length 566;
Best Local Similarity 44.0%; Pred. No. 8e-22;
Matches 59; Conservative 16; Mismatches 54; Indels 5; Gaps 3;
QY 3 ELQVPP-SNCD---CLNGGTCTVSNKVFYNIHWCNCPKPGGQHCEDKSKTCYEGNGHFY 58
DB 78 QCHSVPTVRSCEPWCFFNGTCRQALYSSDF-VQCPGEGFMKCEIDATATCYKQGVAY 136
QY 59 RGKASTDTMGRPCLPWNSTVLTQTYHAHRSDALQLGLGKHNYCRNPDRRRPWCYVQVG 118
DB 137 RGTWSTAESGAECANWNSSLAMKPYSGRPNALRLGLGNHNYCRNPDDQSKPWCYVFKA 196
QY 119 LKPLVQECMVHDC A 132
DB 197 GYISEFCSTPACA 210
RESULT 15
FA12_CAVPO STANDARD; PRT; 603 AA.
AC Q04962;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor) (HAF) (Fragment).
GN F12.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-37; 318-332 AND 359-373.
RC TISSUE=Liver;
RX MEDLINE=93003367; PubMed=1390917;
RA Semba U., Yamamoto T., Kunisada T., Shibuya Y., Tanase S.,
RA Kambara T., Okabe H.;
RT "Primary structure of guinea-pig Hageman factor: sequence around the cleavage site differs from the human molecule.";
RL Biochim. Biophys. Acta 1159:113-121(1992).
CC -1- FUNCTION: Factor XII is a serum glycoprotein that participates in the initiation of blood coagulation, fibrinolysis, and the generation of bradykinin and angiotensin.
CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-ile bonds in factor VII to form factor VIIa and factor XI to form factor Xla.
CC -1- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a complex bound to an anionic surface. Prekallikrein is cleaved by factor XII to form kallikrein, which then cleaves factor XII first to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor XIIa activates factor XI to factor Xla.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 1 fibronectin type I domain.
CC -1- SIMILARITY: Contains 1 fibronectin type II domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
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EMBL; X68615; CAA48600.1; --
 DR PIR; S28941; S28941.
 DR HSP; P00763; IDP0.
 DR MEROPS; S01.211; --
 DE InterPro; IPR009003; Cys_Ser_trypsin.
 DE InterPro; IPR000742; EGF_2.
 DE InterPro; IPR001881; EGF_Ca.
 DE InterPro; IPR006209; EGF-like.
 DE InterPro; IPR000083; Fibrinctn.
 DE InterPro; IPR000582; FN_Type_II.
 DE InterPro; IPR006210; EGF.
 DE InterPro; IPR000001; Kringle.
 DE InterPro; IPR001254; Peptidase_S1.
 DE InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00008; EGF_2.
 DR Pfam; PF00039; fn1; 1.
 DR Pfam; PF00040; fn2; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00018; KRINGLE.
 DE ProDom; PD000995; FN_Type_II; 1.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00381; EGF; 2.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00059; FN2; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_SER; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
 DR Hydroxylase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
 FT NON_TER 1
 FT SIGNAL <1 18
 FT CHAIN 19 358
 FT CHAIN 359 603
 FT DOMAIN 46 87
 FT DOMAIN 93 130
 FT DOMAIN 132 172
 FT DOMAIN 173 209
 FT DOMAIN 216 294
 FT DOMAIN 312 342
 FT DOMAIN 359 603
 FT ACT_SITE 398 398
 FT ACT_SITE 447 447
 FT ACT_SITE 551 551
 FT ACT_SITE 97 109
 FT DISULFID 103 118
 FT DISULFID 120 129
 FT DISULFID 134 162
 FT DISULFID 160 169
 FT DISULFID 177 188
 FT DISULFID 182 197
 FT DISULFID 189 208
 FT DISULFID 216 294
 FT DISULFID 237 276
 FT DISULFID 265 289
 FT DISULFID 345 472
 FT DISULFID 383 399

FT DISULFID 391 461 BY SIMILARITY.
 FT DISULFID 422 425 BY SIMILARITY.
 FT DISULFID 488 557 BY SIMILARITY.
 FT DISULFID 520 536 BY SIMILARITY.
 FT DISULFID 547 578 BY SIMILARITY.
 FT CARBOHYD 248 248 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 270 270 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CARBOHYD 419 419 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 603 AA; 66795 MW; 48DC6B946FB9ED59 CRC64;
 Query Match 32.0%; Score 268; DB 1; Length 603;
 Best Local Similarity 38.6%; Pred. No. 1.2e-18;
 Matches 51; Conservative 21; Mismatches 52; Indels 8; Gaps 3;
 QY 13 CLNGCTCVSNKYFSNIHWCNCPKFGQCHCEIDKSKTCYEGNCHFYRGKASTMTMRPCL 72
 DB 182 CLNGCRCL---VEGHLCDPCMGYTGPFCDLDTTASCYEGRGVSRGMARITVSGAKQ 238
 QY 73 PMSATVLQQTFAHRSD-ALQLGLGKHNYCRPNRRRRRRCVQVGLKPLVCECMVHDC 131
 DB 239 RWAS---EATYRMTAEALRRGLGHTFCRPNDRTRWCFVWNGNRLSWEYCDLAQC 294
 QY 132 ADGKKSPSPPEE 143
 DB 295 QYPPQPTATPHD 306
 RESULT 16
 HGFA_HUMAN
 ID HGFA_HUMAN STANDARD; PRT; 655 AA.
 AC Q04756; Q14726;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF
 DE activator) (HGFA).
 GN HGFA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver, and Serum;
 RX MEDLINE=93252878; PubMed=7683665;
 RA Miyazawa K., Shimomura T., Kitamura A., Kondo J., Morimoto Y.,
 RA Kitamura N.;
 RT "Molecular cloning and sequence analysis of the cDNA for a human
 RT serine protease responsible for activation of hepatocyte growth
 RT factor. Structural similarity of the protease precursor to blood
 RT coagulation factor XII.";
 RL J. Biol. Chem. 268:10024-10028(1993).
 RN [2]
 RP SEQUENCE OF 40-655 FROM N.A.
 RA Zhao S., Odell C.;
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Activates hepatocyte growth factor (HGF) by
 CC converting it from a single chain to a heterodimeric form.
 CC -!- SUBUNIT: Dimer of a short chain and a long chain linked by a
 CC disulfide bond.
 CC -!- SUBCELLULAR LOCATION: Secreted as an inactive single-chain
 CC precursor and is then activated to a heterodimeric form.
 CC -!- TISSUE SPECIFICITY: Liver.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 2 EGF-like domains.
 CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC -!- CAUTION: It is uncertain whether Met-1 is the initiator.
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EMBL; D14012; BAA03113.1; -; NOT_ANNOTATED_CDS.
EMBL; 269923; -; NOT_ANNOTATED_CDS.
PIR; A46688; A46688.
HSSP; P00763; IDFO.
MEROPS; S01.228; -; -;
Genew; HGNC:4894; HGFAC.
MIM; 604552; -; -;
GO; GO:0005576; C:extracellular; TAS.
GO; GO:0004252; F:serine-type endopeptidase activity; TAS.
GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF-like.
InterPro; IPR000083; Fibrinctn1.
InterPro; IPR000562; FN_Type_II.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 2.
Pfam; PF00039; fnl; 1.
Pfam; PF00040; fn2; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00013; FNTYPEII.
PRINTS; PR00018; KRINGLE.
ProDom; PD000995; FN_Type_II; 1.
ProDom; PD000395; Kringle; 1.
SMART; SM00181; EGF; 2.
SMART; SM00058; FN1; 1.
SMART; SM00059; FN2; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00022; EGF 1; 2.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS00026; EGF 3; 2.
PROSITE; PS01253; FIBRONECTIN_1; 1.
PROSITE; PS00023; FIBRONECTIN_2; 1.
PROSITE; PS00021; KRINGLE 1; 1.
PROSITE; PS00070; KRINGLE 2; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Hydrolase; Glycoprotein; Plasma; Serine protease; Kringle; Signal;
EGF-like domain; Repeat; Zymogen.
SIGNAL 1 30
PROPEP 31 372
CHAIN 373 407
CLEAVED IN ACTIVE FORM.
HEPATOCYTE GROWTH FACTOR ACTIVATOR SHORT CHAIN
HEPATOCYTE GROWTH FACTOR ACTIVATOR LONG CHAIN
CHAIN 408 655
DOMAIN 108 148
DOMAIN 160 198
DOMAIN 200 240
DOMAIN 241 279
DOMAIN 286 367
DOMAIN 408 655
ACT_SITE 447 447
ACT_SITE 497 497
ACT_SITE 598 598
DISULFID 108 133
DISULFID 122 148
DISULFID 164 175
DISULFID 169 186
DISULFID 188 197
DISULFID 202 230
DISULFID 228 237
FIBRONECTIN TYPE-II.
EGF-LIKE 1.
FIBRONECTIN TYPE-I.
EGF-LIKE 2.
KRINGLE
SERINE PROTEASE.
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.

FT DISULFID 245. 256 BY SIMILARITY.
FT DISULFID 250 267 BY SIMILARITY.
FT DISULFID 269 278 BY SIMILARITY.
FT DISULFID 286 367 BY SIMILARITY.
FT DISULFID 307 349 BY SIMILARITY.
FT DISULFID 338 362 BY SIMILARITY.
FT DISULFID 394 521 INTERCHAIN (BY SIMILARITY).
FT DISULFID 432 448 BY SIMILARITY.
FT DISULFID 440 510 BY SIMILARITY.
FT DISULFID 535 604 BY SIMILARITY.
FT DISULFID 567 583 BY SIMILARITY.
FT DISULFID 594 622 BY SIMILARITY.
FT CARBOHYD 48 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 290 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 468 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 492 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 546 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 644 R -> Q (IN REF. 2).
SQ SEQUENCE 655 AA; 70681 MW; 2CF72F1E1B862ED7 CRC64;
Query Match 31.3%; Score 262; DB 1; Length 655;
Best Local Similarity 36.9%; Pred. No. 5.1e-18;
Matches 58; Conservative 12; Mismatches 57; Indels 30; Gaps 3;
QY 5 HQVPSNCDCLNGGTCVSNKYFSNIHW-----CNCPRKFGQHCIDKSKTCYEGNGH 56
DB 242 HTACLSPCLNGGTC-----HLIVATGTVCACPGAGRLCNIEPDERCFLENGT 292
QY 57 FYRGKASTDMGRPCLPWNATVLTQTYHAHRSDALQLGLGKKNYCRNPDNRPRWCYVQ 116
DB 293 GYRGVASTASGLSCLAWNSDLYQLBHDVSGAAALLGLGPHAYCRNPDNRPRWCYV 352
QY 117 VGLKPLVQECMHDC-----ADGKKPSSP 140
DB 353 KDSALSWEYCRLEACESLIRVQLSPOLLATLPFPASP 389
RESULT 17
HGFA_MOUSE
ID HGFA_MOUSE STANDARD; PRT; 653 AA.
AC QSR038; Q9JKV4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF activator) (HGFA).
GN HGFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Itoh H., Kataoka H., Kono H.;
RT "Mouse hepatocyte growth factor activator.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
MEDLINE=21226753; Pubmed=11032833;
RA van Adelsberg J.S., Sehgal S., Kukes A., Brady C., Barasch J., Yang J., Huan Y.;
RT "Activation of hepatocyte growth factor (HGF) by endogenous HGF activator is required for mesangial kidney morphogenesis in vitro.";
RL J. Biol. Chem. 276:15099-15106(2001).
CC -!- FUNCTION: Activates hepatocyte growth factor (HGF) by converting it from a single chain to a heterodimeric form (By similarity).
CC -!- SUBUNIT: Dimer of a short chain and a long chain linked by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted as an inactive single-chain precursor and is then activated to a heterodimeric form (By similarity).

CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 1 fibronectin type I domain.
CC -1- SIMILARITY: Contains 1 fibronectin type II domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF099017; AF02489.1; -;
CC EMBL; AF224724; AAF34712.1; -;
CC HSP; P00763; IDPO.
CC MEROPS; S01.228; -;
CC MGD; MG1.1859281; Hgfac.
CC InterPro; IPR009003; Cys_ser_trypsin.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR000083; Fibnctni.
CC InterPro; IPR000562; FN_Type_II.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00008; EGF_2.
CC Pfam; PF00039; fn1; 1.
CC Pfam; PF00040; fn2; 1.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00013; PNTYPEII.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000995; FN_Type_II; 1.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00181; EGF_2.
CC SMART; SM00059; FN2; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; TYPD_SPC; 1.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS00026; EGF_3; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 1.
CC PROSITE; PS00023; FIBRONECTIN_2; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS00070; KRINGLE_2; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC Hydrolase; Glycoprotein; Plasma; Serine protease; Kringle; Signal;
KW EGF-like domain; Repeat; Zymogen.
FT SIGNAL 1 29 BY SIMILARITY.
FT PROPEP 30 369 CLEAVED IN ACTIVE FORM (BY SIMILARITY).
FT CHAIN 370 405 HEPATOCYTE GROWTH FACTOR ACTIVATOR SHORT
FT CHAIN
FT CHAIN 406 653 HEPATOCYTE GROWTH FACTOR ACTIVATOR LONG
FT CHAIN
FT DOMAIN 105 145 FIBRONECTIN TYPE-II.
FT DOMAIN 157 195 EGF-LIKE 1.
FT DOMAIN 197 237 FIBRONECTIN TYPE-I.
FT DOMAIN 238 276 EGF-LIKE 2.
FT DOMAIN 283 364 KRINGLE.
FT DOMAIN 406 653 SERINE PROTEASE.
FT ACT_SITE 445 445 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 495 495 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 596 596 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 105 130 BY SIMILARITY.
FT DISULFID 119 145 BY SIMILARITY.
FT DISULFID 161 172 BY SIMILARITY.
FT DISULFID 166 183 BY SIMILARITY.

FT DISULFID 185 194 BY SIMILARITY.
FT DISULFID 199 227 BY SIMILARITY.
FT DISULFID 225 234 BY SIMILARITY.
FT DISULFID 242 253 BY SIMILARITY.
FT DISULFID 247 264 BY SIMILARITY.
FT DISULFID 266 275 BY SIMILARITY.
FT DISULFID 283 364 BY SIMILARITY.
FT DISULFID 304 346 BY SIMILARITY.
FT DISULFID 335 359 INTERCHAIN (BY SIMILARITY).
FT DISULFID 392 519 BY SIMILARITY.
FT DISULFID 430 446 BY SIMILARITY.
FT DISULFID 533 508 BY SIMILARITY.
FT DISULFID 538 602 BY SIMILARITY.
FT DISULFID 565 581 BY SIMILARITY.
FT DISULFID 592 620 BY SIMILARITY.
FT CARBOHYD 39 39 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 63 63 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 466 466 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 544 544 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 164 164 G -> W (IN REF. 2).
SQ SEQUENCE 653 AA; 70567 MW; 88B4B20255DF7FDC CRC64;
Query Match 29.9%; Score 250.5; DB 1; Length 653;
Best Local Similarity 42.0%; Pred. No. 6.6e-17;
Matches 50; Conservative 11; Mismatches 41; Indels 17; Gaps 2;
Qy 5 HQVPSNCDCLNGCTCYSNKYFSNIHW-----CNCPKFGGQHCEIDSKTCYSENGH 56
Db 239 HTACLSFCLNGGTC-----HLIVGTGTSVCTCLGYAGRCNIVTEHCFLNGT 289
Qy 57 FYRGKASTDTMGRFCLPWNSTATVLTQYTHAHRSDALQLGLGKHNCRNPNRRPCYV 115
Db 290 EYRGVASTAASGLSCLAWNSDLLVQELHVDVAVALGLGLPHAYCRNPKDRPCYV 348
RESULT 18
FA12 HUMAN
ID FA12_HUMAN STANDARD; PRT; 615 AA.
AC P00748; P78339;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Consolation factor XII precursor (EC 3.4.21.39) (Hageman factor)
DE (HAP).
GN F12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88007593; PubMed=2888762;
RA Cool D.E., McGilivray R.T.A.;
RT "Characterization of the human blood coagulation factor XII gene.
RT Intron/exon gene organization and analysis of the 5'-flanking
RT region."
RL J. Biol. Chem. 262:13662-13673(1987).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS ALA-207; ASP-545 AND HIS-605.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-615 FROM N.A.
RX MEDLINE=86176794; PubMed=3754331;
RA Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
RA Cortese R.;
RT "cDNA sequence coding for human coagulation factor XII (Hageman).";
RL Nucleic Acids Res. 14:3146-3146(1986).
RN [4]
RP SEQUENCE OF 14-615 FROM N.A.

R MEDLINE=86033830; PubMed=3877053;
R Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.,
R McGallivray R.T.A.,
R "Characterization of human blood coagulation factor XII cDNA.
R Prediction of the primary structure of factor XII and the tertiary
R structure of beta-factor XIIa."
R J. Biol. Chem. 260:13666-13676(1985).
R [5]
R SEQUENCE OF 146-615 FROM N.A.
R MEDLINE=86216049; PubMed=3011063;
R Que B.G., Davie E.W.,
R "Characterization of a cDNA coding for human factor XII (Hageman
R factor)."
R J. Biochemistry 25:1525-1528(1986).
R [6]
R SEQUENCE OF 20-379.
R MEDLINE=85182674; PubMed=3886654;
R McMullen B.A., Fujikawa K.,
R "Amino acid sequence of the heavy chain of human alpha-factor XIIa
R (activated Hageman factor)."
R J. Biol. Chem. 260:5328-5341(1985).
R [7]
R SEQUENCE OF 354-362 AND 373-615.
R MEDLINE=83291041; PubMed=6604055;
R Fujikawa K., McMullen B.A.,
R "Amino acid sequence of human beta-factor XIIa."
R J. Biol. Chem. 258:10924-10933(1983).
R [8]
R SEQUENCE OF 561-615 FROM N.A.
R TISSUE=Blood;
R MEDLINE=96133302; PubMed=8528215;
R Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammle B., Engel W.,
R "The novel acceptor splice site mutation 11396(G->A) in the factor
R XII gene causes a truncated transcript in cross-reacting material
R negative patients."
R Hum. Mol. Genet. 4:1235-1237(1995).
R [9]
R CARBOHYDRATE-LINKAGE SITE THR-109.
R MEDLINE=92184750; PubMed=1544894;
R Harris R.J., Ling V., Spellman M.W.,
R "O-linked fucose is present in the first epidermal growth factor
R domain of factor XII but not protein C."
R J. Biol. Chem. 267:5102-5107(1992).
R [10]
R VARIANT WASHINGTON D.C. SER-590.
R MEDLINE=90046788; PubMed=2510163;
R Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
R Saito H.,
R "Coagulation factor XII (Hageman factor) Washington D.C.: inactive
R factor XIIa results from Cys-571->Ser substitution."
R Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322(1989).
R [11]
R VARIANT LOCARNO PRO-372.
R MEDLINE=94325559; PubMed=8049433;
R Hovenga J.K., Schaller J., Stricker H., Willemin W.A., Furlan M.,
R Laemmle B.,
R "Coagulation factor XII Locarno: the functional defect is caused by
R the amino acid substitution Arg-353->Pro leading to loss of a
R kallikrein cleavage site."
R Blood 84:1173-1181(1994).
R [12]
R VARIANT TENRI CYS-53.
R MEDLINE=99290785; PubMed=10361128;
R Kondo S., Tokunaga F., Kawano S., Oono Y., Kumagai S., Koide T.,
R "Factor XII Tenri, a novel cross-reacting material negative factor XII
R deficiency, occurs through a proteasome-mediated degradation."
R Blood 93:4300-4303(1999).
R C -!- FUNCTION: Factor XII is a serum glycoprotein that participates in
R the initiation of blood coagulation, fibrinolysis, and the
R generation of bradykinin and angiotensin.
R C -!- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
R VII to form factor VIIa and factor XI to form factor XIa.
R C -!- PTM: O- AND N-GLYCOSYLATED.

CC -!- DISEASE: Defects in F12 do not cause any clinical symptoms. The
CC sole effect is that whole-blood clotting time is prolonged.
CC -!- MISCELLANEOUS: Factor XII, prekallikrein, and HWW kininogen form a
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor
CC XIIa activates factor XI to factor Xla.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC -----
CC EMBL; M31315; AAA70225.1; -;
CC EMBL; AP538691; AAM97932.1; -;
CC EMBL; M11723; AA51986.1; -;
CC EMBL; M17466; AAB59490.1; -;
CC EMBL; M17464; AAB59490.1; JOINED.
CC EMBL; M17465; AAB59490.1; JOINED.
CC EMBL; M13147; AAA70224.1; -;
CC EMBL; U71274; AAB51203.1; -;
CC PIR; A29411; KFHU12.
CC HSP; P00763; IDPO.
CC MEROSS; S01.211; -;
CC GENM; HGNC:3530; F12.
CC GEM; 234000; -;
CC GO; GO:0003805; F12 blood coagulation factor XI activity; TAS.
CC GO; GO:0003806; F12 blood coagulation factor XII activity; TAS.
CC GO; GO:0008236; F12 serine-type peptidase activity; TAS.
CC GO; GO:0007596; F12 blood coagulation; TAS.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR000083; Fibrinctnl.
CC InterPro; IPR000562; FN_Type_II.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00008; EGF_2.
CC Pfam; PF00039; fn1; 1.
CC Pfam; PF00040; fn2; 1.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00013; FNTYPEII.
CC PRINTS; PR00016; KRINGLE.
CC ProDom; PD000995; FN_Type_II; 1.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00181; EGF; 2.
CC SMART; SM00058; FN1; 1.
CC SMART; SM00059; FN2; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01186; EGF_2; 1.
CC PROSITE; PS50036; EGF_3; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 1.
CC PROSITE; PS00023; FIBRONECTIN_2; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS00070; KRINGLE_2; 1.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; 1.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
CC KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
CC Hydrolyase; fibrinolysis; Signal; EGF-like domain; Repeat; Zymogen;

Polymorphism; Disease mutation.

FT SIGNAL 1 19 ALPHA-FACTOR XIIA HEAVY CHAIN.

FT CHAIN 20 372 ALPHA-FACTOR XIIA LIGHT CHAIN.

FT CHAIN 373 615 BETA-FACTOR XIIA PART 1.

FT CHAIN 374 615 BETA-FACTOR XIIA PART 2.

FT CHAIN 375 615 FIBRONECTIN TYPE-II.

FT DOMAIN 47 88 EGF-LIKE 1.

FT DOMAIN 94 131 FIBRONECTIN TYPE-I.

FT DOMAIN 133 173 EGF-LIKE 2.

FT DOMAIN 174 210 KRINGLE.

FT DOMAIN 217 295 PRO-RICH.

FT DOMAIN 296 349 SERINE PROTEASE.

FT DOMAIN 373 615 O-LINKED (FUC).

FT CARBOHYD 109 109 O-LINKED (GLCNAC).

FT CARBOHYD 249 249 N-LINKED (POTENTIAL).

FT CARBOHYD 299 299 O-LINKED (POTENTIAL).

FT CARBOHYD 305 305 O-LINKED (POTENTIAL).

FT CARBOHYD 308 308 O-LINKED (POTENTIAL).

FT CARBOHYD 328 328 O-LINKED (POTENTIAL).

FT CARBOHYD 329 329 O-LINKED (POTENTIAL).

Query Match 27.8%; Score 233; DB 1; Length 615;

st Local Similarity 42.3%; Pred. No. 3.1e-15;

ches 44; Conservative 12; Mismatches 40; Indels 8; Gaps 3;

QY 13 CLNGTGVNKFYSNIHWCNCPKFGGQHCETDKSKTCYEGNGHYRGKASTDTNGRPCL 72

Db 183 CLHGGGCLC---VEGRLCHCPVGTGPPCDVDTKASCYDGRGSLYGLARTTSLGAPCQ 239

QY 73 PWSATVLOQTY-HAHRSDALQGLGKGNKNCNPNRRPWCYV 115

Db 240 PWAS-----BATYRVNTAEQARWGLGGHAFCEPNDIRPWCYV 279

RE UT 19

UR DESRO

AC P49150; STANDARD; PRT; 394 AA.

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA gamma).

OS Desmodus rotundus (Vampire bat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;

OC Desmodontinae; Desmodus.

OX NCBI_TaxID=9430;

RN [1]_TaxID=9430;

RP SEQUENCE FROM N.A.

RC TISSUE=Salivary gland;

RX MEDLINE=92039036; PubMed=1937019;

RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,

RA Alagon A., Donner P., Schleuning W.D.;

RT "The plasminogen activator family from the salivary gland of the

RT vampire bat Desmodus rotundus: cloning and expression.";

RL Gene 105:229-237(1991).

RN [2]

RE CHARACTERIZATION.

RX MEDLINE=93393059; PubMed=1309059;

RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,

RA Kraetzschmar J., Haendler B., Langer G., Baidus B., Witt W.,

RA Donner P.;

RT "Plasminogen activators from the saliva of Desmodus rotundus (common

RT vampire bat): unique fibrin specificity.";

RL Ann. N.Y. Acad. Sci. 667:395-403(1992).

CC -!- FUNCTION: Probably essential to support the feeding habits of this

CC exclusively haematophagous animal. Probable potent thrombolytic

CC agent.

CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in

CC plasminogen to form plasmin.

CC -!- SUBUNIT: Monomer.

CC -!- SIMILARITY: Belongs to peptidase family S1.

-!- SIMILARITY: Contains 1 kringle domain.

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CC EMBL; M63990; AAA31595.1; -.

DR PIR; JS0600; JS0600.

DR HSSP; P98119; IASI.

DR MEROPS; S01.239; -.

DR InterPro; IPR009003; Cys Ser trypsin.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR01254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR Pfam; PF00051; Kringle; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00018; KRINGLE.

DR ProDom; PD000395; Kringle; 1.

DR SMART; SM00130; KR, 1.

DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00021; KRINGLE 1; 1.

DR PROSITE; PS00070; KRINGLE 2; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;

KW Kringle; Signal; Multigene family.

FT SIGNAL 1 36 POTENTIAL.

FT CHAIN 37 394 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.

FT DOMAIN 45 126 KRINGLE.

FT DOMAIN 142 394 SERINE PROTEASE.

FT ACT_SITE 189 189 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT ACT_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT DISULFID 45 126 BY SIMILARITY.

FT DISULFID 66 108 BY SIMILARITY.

FT DISULFID 97 121 BY SIMILARITY.

FT DISULFID 131 262 BY SIMILARITY.

FT DISULFID 174 190 BY SIMILARITY.

FT DISULFID 182 251 BY SIMILARITY.

FT DISULFID 276 351 BY SIMILARITY.

FT DISULFID 308 324 BY SIMILARITY.

FT DISULFID 341 369 BY SIMILARITY.

FT CARBOHYD 315 315 N-LINKED (GLCNAC...) (POTENTIAL).

SQ SEQUENCE 394 AA; 44105 MW; 9CCD6F52F3D81PCD CRC64;

Query Match 26.6%; Score 223; DB 1; Length 394;

Best Local Similarity 44.3%; Pred. No. 1.9e-14;

Matches 39; Conservative 13; Mismatches 36; Indels 0; Gaps 0;

QY 45 DKSCTCYEGNGHYRGKASTDTNGRPCLPWSATVLOQTYHAHRSDALQGLGKGNKCN 104

Db 40 DPHATCYKQGVYRGTVGTSTSSGACINWNSLLIRRTYNGRMPEAVKVLGNHNYCRN 99

QY 105 PDNRRPWCYVQGLKPLVQECWHDCA 132

Db 100 PDGASPKWCYVINKARXTSESCSVPVCS 127

RESULT 20

FA12 BOVIN

ID FA12 BOVIN STANDARD; PRT; 593 AA.

AC P98110;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)

DE (HAF) (Fragment).

F12.
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
TISSUE=Liver;
MEDLINE=94242782; PubMed=8186251;
Shibuya Y., Semba U., Okabe H., Kambara T., Yamamoto T.;
"Primary structure of bovine Hageman factor (blood coagulation factor
XII): comparison with human and guinea pig molecules.";
Biochim. Biophys. Acta 1206:63-70 (1994).
[2]
SEQUENCE OF 10-21; 350-364 AND 525-550.
MEDLINE=77182112; PubMed=861210;
Fujikawa K., Walsh A.K., Davie W.E.;
"Isolation and characterization of bovine factor XII (Hageman
factor).";
Biochemistry 16:2270-2278 (1977).
-!- FUNCTION: Factor XII is a serum glycoprotein that participates in
the initiation of blood coagulation, fibrinolysis, and the
generation of bradykinin and angiotensin.
-!- CATALYTIC ACTIVITY: Cleaves selectively Arg-Ile bonds in factor
VII to form factor VIIa and factor XI to form factor Xla.
-!- PTM: O- AND N-Glycosylated (BY SIMILARITY).
-!- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a
complex bound to an anionic surface. Prekallikrein is cleaved by
factor XII to form kallikrein, which then cleaves factor XII first
to alpha-factor Xla and then to beta-factor Xla. Alpha-factor
Xla activates factor XI to factor Xla. Bovine factor XII is
cleaved only to alpha-factor Xla as it lacks the trypsin/
kallikrein cleavage site.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 fibronectin type II domain.
-!- SIMILARITY: Contains 1 kringle domain.

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EMBL; S70164; AB30804.2; -;
PIR; S45281; S45281.
HSP; P00763; IDPO.
MEROPS; S01.211; -;
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR006209; EGF-like.
InterPro; IPR000083; Fibnctnl.
InterPro; IPR00562; FN_Type_II.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 2.
Pfam; PF00039; fn1; 1.
Pfam; PF00040; fn2; 1.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00013; ENTPEPI.
PRINTS; PR00018; KRINGLE.
ProDom; P000995; FN_Type_II; 1.
ProDom; P000395; Kringle; 1.
SMART; SM00181; EGF; 2.
SMART; SM00058; FN1; 1.
SMART; SM00059; FN2; 1.

DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; FALSE NEG.
DR PROSITE; PS00026; EGF_3; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00340; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
KW Hydroxylase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
KW NON_TER 1
FT SIGNAL <1 9
FT CHAIN 10 349
FT CHAIN 350 593
FT DOMAIN 37 78
FT DOMAIN 84 121
FT DOMAIN 123 163
FT DOMAIN 164 200
FT DOMAIN 207 287
FT DOMAIN 297 333
FT DOMAIN 350 593
FT ACT_SITE 389 389
FT ACT_SITE 438 438
FT ACT_SITE 541 541
FT DISULFID 88 100
FT DISULFID 94 109
FT DISULFID 111 120
FT DISULFID 125 133
FT DISULFID 151 160
FT DISULFID 168 179
FT DISULFID 173 188
FT DISULFID 190 199
FT DISULFID 207 287
FT DISULFID 230 289
FT DISULFID 258 282
FT DISULFID 336 463
FT DISULFID 374 390
FT DISULFID 382 452
FT DISULFID 413 416
FT DISULFID 479 547
FT DISULFID 510 526
FT DISULFID 537 588
FT CARBOHYD 99 99
FT CARBOHYD 241 241
FT CARBOHYD 263 263
FT CARBOHYD 410 410
SQ SEQUENCE 593 AA; 65148 MW; 721592BA792BD61F CRC64;

Query Match 25.9%; Score 217; DB 1; Length 593;
Best Local Similarity 35.7%; Pred. No. 1.1e-13;
Matches 46; Conservative 15; Mismatches 58; Indels 10; Gaps 4;

QY 6 QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCVE--GNGHFYRGKAS 63
DB 166 QVCRTPNCLNGSDCLQAE---GHRLCRCAPSPAGRLCDVDLXASCYDDRDGLSYRGWAG 222
QY 64 TDTMGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRNPDRRRPWCYQVGLKPL 122
DB 223 TTLSGAPCQSWAS-----EATYNNVTAEQVLNWLGLGHAFPCRNPDNDTRPWCIFWKGDRLS 278
QY 123 VQECMVHDC 131
DB 279 WNYCRLAPC 287

RESULT 21
RORI DROME
ID RORI DROME STANDARD; PRT; 685 AA.
AC Q24438;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor Ror precursor
DE (EC 2.7.1.112) (dCor).
GN ROR OR CG4926.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Spheroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM 'N.A.' AND TISSUE SPECIFICITY.
RC STRAIN=Canton-S; TISSUE=Larval brain;
RX MEDLINE=93348222; PubMed=8394009;
RA Wilson C., Gohardhan D.C.I., Steiler H.;
RT "Ror", a potential neurotrophic receptor gene, encodes a Drosophila
RT homolog of the vertebrate Ror family of trk-related receptor tyrosine
RT kinases."
RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
RN [2]
RP SEQUENCE FROM 'N.A.'
RC STRAIN=Berkelyev;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Boshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin N.L., Houston K.A., Heiland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Leiby Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klanos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "the genome sequence of Drosophila melanogaster."
RL Science 287:12185-12195(2000).
RN [3]
RP SEQUENCE OF 545-597 FROM 'N.A.'
RX MEDLINE=98401146; PubMed=9731193;
RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT "Sampling the genomic pool of protein tyrosine kinase genes using the
RT polymerase chain reaction with genomic DNA."
RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
CC -1- FUNCTION: Tyrosine-protein kinase receptor that functions during
CC early stages of neuronal development.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
CC system.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
CC subfamily.
CC -1- SIMILARITY: Contains 1 frizzled (Fz) domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
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CC -----
CC EMBL: L20297; AAA28860.1; -;
CC EMBL: AB003628; AAFS2885.1; -;
CC EMBL: AJ002908; CAA05743.1; -;
CC PIR: A48289; A48289.
CC FLYBASE: P11362; 1FGK.
CC GO: GO:0016021; C: integral to membrane; NAS.
CC GO: GO:0004713; P: protein-tyrosine kinase activity; NAS.
CC GO: GO:0007417; P: central nervous system development; IEP.
CC GO: GO:0006468; P: protein amino acid phosphorylation; NAS.
CC InterPro: IPR000024; Fz domain.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR000719; Prot kinase.
CC InterPro: IPR020111; RecepttyrkinII.
CC InterPro: IPR001245; Tyr_kinase.
CC InterPro: IPR008266; Tyr_kinase_AS.
CC Pfam: PF00051; Kringle; 1.
CC Pfam: PF00069; Kkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000395; Kringle; 1.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00130; KR_1.1; 1.
CC SMART: SM00219; TYRK; 1.
CC PROSITE: PS00038; FZ; 1.
CC PROSITE: PS00021; KRINGLE_1; 1.
CC PROSITE: PS00070; KRINGLE_2; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00103; PROTEIN_KINASE_TYR; 1.
CC PROSITE: PS00239; RECEPTOR_TYR_KIN_II; 1.
CC Transerbase: Kinase; Tyrosine-protein kinase; ATP-binding; Receptor;
CC Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
CC Developmental protein.
FT SIGNAL 1 24
FT CHAIN 25 685
FT TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT RECEPTOR ROR (POTENTIAL).
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT FZ.
FT KRINGLE.
FT PROTEIN KINASE.
FT ATP (BY SIMILARITY).
FT ATP (BY SIMILARITY).
FT BY SIMILARITY.
FT PHOSPHORYLATION (AUTO-) (BY
FT SIMILARITY).
FT PHOSPHORYLATION (AUTO-) (BY
FT SIMILARITY).
FT PHOSPHORYLATION (AUTO-) (BY
FT SIMILARITY).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 45 45
FT CARBOHYD 63 63
FT CARBOHYD 129 129
FT CARBOHYD 144 144
FT CARBOHYD 144 144
FT CARBOHYD 250 250

S SEQUENCE 685 AA; 78142 MW; 526162D2D7D5PD7C7 CRC64;
Very Match 20.2%; Score 169; DB 1; Length 685;
Local Similarity 28.8%; Pred. NO. 5.7e-09;
atches 38; Conservative 27; Mismatches 35; Indels 32; Gaps 6;
Q 3 ELHVPSCDCLNGTGVSNKFNHCNCPKXFGGQHCIDKSKTCYEGNGHFYRGKA 62
D 212 DCKLPQKHCLSLGITI-----EVDKTCYWDGSGTYRGVA 249
Q 63 SDTMRGRLPNSAVLQOTVHAHRSDALQGLGKHNYCRNPON-RRRPWCYVOVGLKP 121
D 250 NVSAGKPCLRN-SWLKKEI-----SDPPEL-IGQ-NYCRNPGSVENSPWCFVDSRRR 300
Q 122 LVQECWHDCA 133
D 301 IIECDIPKCA 312
R JLT 22
A HUMAN
I APOA HUMAN STANDARD; PRT; 4548 AA.
A P08519;
D 01-AUG-1988 (Rel. 08, Created)
D 01-AUG-1988 (Rel. 08, Last sequence update)
D 10-OCT-2003 (Rel. 42, Last annotation update)
D Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
C LPA.
O Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
C NCBI TaxID: 9606;
[1]
K K SEQUENCE FROM N.A.
K MEDLINE=8039109; PubMed=3670400;
K McLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
K Fless G.M., Scannu A.M., Lawn R.M.;
K "cdna sequence of human apolipoprotein(a) is homologous to
K plasminogen.";
K Nature 330:132-137(1987).
[2]
K SERINE PROTEASE ACTIVITY.
K MEDLINE=90076123; PubMed=2531657;
K Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Ehnholm C.;
K "lipoprotein(a) binds to fibronectin and has serine proteinase
K activity capable of cleaving it.";
K EMBO J. 8:4035-4040(1989).
[3]
K REVIEW.
K MEDLINE=90049223; PubMed=2530631;
K Utermann G.;
K "The mysteries of lipoprotein(a).";
K Science 246:904-910(1989).
[4]
K CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
K MEDLINE=21303595; PubMed=11294842;
K Garner B., Merry A.H., Royle L., Harvey D.J., Rudd P.M., Thillet J.;
K "Structural elucidation of the N- and O-glycans of human
K apolipoprotein(a): role of o-glycans in conferring protease
K resistance.";
K J. Biol. Chem. 276:22200-22208(2001).
[5]
K X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
K MEDLINE=96217891; PubMed=8642595;
K Nikol V., Locrasso P.V., Boettcher B.R.;
K "Crystal structures of apolipoprotein(a) kringle IV37 free and
K complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
K acid: existence of novel and expected binding modes.";
K J. Mol. Biol. 256:751-761(1996).
[6]
K VARIANT ARG-4193.
K MEDLINE=95002201; PubMed=7918682;
K Scannu A.M., Pfaffinger D., Lee J.C., Hinman J.;

RT "A single point mutation (Trp72-->Arg) in human apo(a) kringle 4-37
RT associated with a lysine binding defect in Lp(a).";
RL Biochim. Biophys. Acta 1227:41-45(1994).
CC -I- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC (Lp(a)). It has serine proteinase activity and is able of
CC autolysis. Inhibits tissue-type plasminogen activator 1.
CC Lp(a) may be a ligand for megalin/Sp 330.
CC -I- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
CC decorin.
CC -I- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
CC structures present in either a mono- or disialylated state. The
CC O-glycans are mostly (80%) represented by the monosialylated core
CC type I structure, NeuNAcGalpha2-3Galbeta1-3GalNAc, with smaller
CC amounts of disialylated and non-sialylated O-glycans also
CC detected.
CC -I- DISEASE: Elevated plasma concentrations of apo(a) and its
CC naturally occurring proteolytic fragments are correlated with
CC atherosclerosis. Homology with plasminogen kringles IV and V is
CC thought to underlie the atherogenicity of the protein, because the
CC fragments are competing with plasminogen for fibrin(ogen) binding.
CC -I- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC leading to the formation of the so called mini-Lp(a). Apo(a)
CC fragments accumulate in atherosclerotic lesions, where they may
CC promote thrombogenesis. O-glycosylation may limit the extent of
CC proteolytic fragmentation.
CC -I- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -I- SIMILARITY: Contains 38 kringle domains.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X06290; CAA29618.1; -;
CC PIR: S00657; S00657.
CC PDB: 1I71; 13-JUN-01.
CC PDB: 1JFN; 28-JUN-02.
CC PDB: 1KIV; 18-MAY-99.
CC PDB: 3KIV; 18-MAY-99.
CC PDB: 4KIV; 18-MAY-99.
CC MEROPS: S01.226; -;
CC Genew, HGNC:5667; LPA.
CC MIM: 152200; -;
CC GO: GO:0004866; F: endopeptidase inhibitor activity; TAS.
CC GO: GO:0008015; P: circulation; TAS.
CC GO: GO:0009405; P: pathogenesis; TAS.
CC InterPro: IPR009003; Cys Ser trypsin.
CC InterPro: IPR000001; Kringle_
CC InterPro: IPR001254; Peptidase_S1.
CC InterPro: IPR001314; Peptidase_S1A.
CC Pfam: PF00051; Kringle; 38.
CC PRINTS: PR00089; trypsin; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC ProDom: PD000395; Kringle; 38.
CC SMART: SW00130; KR; 38.
CC SMART: SW00020; Tryp_Spc; 1.
CC PROSITE: PS00021; KRINGLE_1; 38.
CC PROSITE: PS00070; KRINGLE_2; 38.
CC PROSITE: PS00240; TRYPsin DOM; 1.
CC PROSITE: PS00134; TRYPsin HIS; 1.
CC PROSITE: PS00135; TRYPsin SER; 1.
CC Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein;
CC Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 4548 APOLIPOPROTEIN(A).
FT DOMAIN 20 130 KRINGLE TYPE IV, 1.
FT DOMAIN 131 244 KRINGLE TYPE IV, 2.
FT DOMAIN 245 358 KRINGLE TYPE IV, 3.
FT DOMAIN 359 472 KRINGLE TYPE IV, 4.

FT DOMAIN 473 586 KRINGLE TYPE IV, 5.
FT DOMAIN 587 700 KRINGLE TYPE IV, 6.
FT DOMAIN 701 814 KRINGLE TYPE IV, 7.
FT DOMAIN 815 928 KRINGLE TYPE IV, 8.
FT DOMAIN 929 1042 KRINGLE TYPE IV, 9.
FT DOMAIN 1043 1156 KRINGLE TYPE IV, 10.
FT DOMAIN 1157 1270 KRINGLE TYPE IV, 11.
FT DOMAIN 1271 1384 KRINGLE TYPE IV, 12.
FT DOMAIN 1385 1498 KRINGLE TYPE IV, 13.
FT DOMAIN 1499 1612 KRINGLE TYPE IV, 14.
FT DOMAIN 1613 1726 KRINGLE TYPE IV, 15.
FT DOMAIN 1727 1840 KRINGLE TYPE IV, 16.
FT DOMAIN 1841 1954 KRINGLE TYPE IV, 17.
FT DOMAIN 1955 2068 KRINGLE TYPE IV, 18.
FT DOMAIN 2069 2182 KRINGLE TYPE IV, 19.
FT DOMAIN 2183 2296 KRINGLE TYPE IV, 20.
FT DOMAIN 2297 2410 KRINGLE TYPE IV, 21.
FT DOMAIN 2411 2524 KRINGLE TYPE IV, 22.
FT DOMAIN 2525 2638 KRINGLE TYPE IV, 23.
FT DOMAIN 2639 2752 KRINGLE TYPE IV, 24.
FT DOMAIN 2753 2866 KRINGLE TYPE IV, 25.
FT DOMAIN 2867 2980 KRINGLE TYPE IV, 26.
FT DOMAIN 2981 3094 KRINGLE TYPE IV, 27.
FT DOMAIN 3095 3208 KRINGLE TYPE IV, 28.
FT DOMAIN 3209 3322 KRINGLE TYPE IV, 29.
FT DOMAIN 3323 3436 KRINGLE TYPE IV, 30.
FT DOMAIN 3437 3550 KRINGLE TYPE IV, 31.
FT DOMAIN 3551 3664 KRINGLE TYPE IV, 32.
FT DOMAIN 3665 3778 KRINGLE TYPE IV, 33.
FT DOMAIN 3779 3894 KRINGLE TYPE IV, 34.
FT DOMAIN 3895 3998 KRINGLE TYPE IV, 35.
FT DOMAIN 3999 4112 KRINGLE TYPE IV, 36.
FT DOMAIN 4113 4226 KRINGLE TYPE IV, 37.
FT DOMAIN 4227 4340 KRINGLE TYPE V.
FT ACT_SITE 4341 4454 SERINE PROTEASE.
FT ACT_SITE 4455 4568 CHARGE RELAY SYSTEM.
FT ACT_SITE 4569 4682 CHARGE RELAY SYSTEM.
FT ACT_SITE 4683 4796 CHARGE RELAY SYSTEM.
FT VARIANT 4797 4910 W -> R (LOSS OF LYSINE-SEPHAROSE BINDING).
FT SEQUENCE 4911 5024 /FTIG=VAR 006633.
FT SEQUENCE 5025 5138 4548 AA; 501313 MW; 96921BE96A465C5F CRC64;
FT Query Match 19.4%; Score 162.5; DB 1; Length 4548;
FT Best Local Similarity 33.1%; Pred. No. 1.6e-07;
FT Matches 41; Conservative 12; Mismatches 46; Indels 25; Gaps 7;
QY 27 NIHW--CN---CP-----KKFGQRCCEIDKSKT---CYEGNGHFYRGKASTDTMGR 69
Db 3742 NVREWCNLTQCPVTSSVLATSTAVSECAPEQSPVTQDCYHGDGQSVRGFSFTVTGR 3801
QY 70 PCLPWN SATVLQOYTYHAHSDALQLGLGKHYCRNPNRRRPWCYVQGLKPLV--QECM 127
Db 3802 TCOSWSSMT---PHWHQRTTEYPNGGLTRNCRNPDAEIREWCYT--MDPSVRWEYCN 3855
QY 128 VHDCL131
Db 3856 LTQC13859
RE IT 23
KR RAT
ID KRM1 RAT STANDARD; PRT; 473 AA.
AC Q924S4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (Kringle-containing protein marking the eye
DE and the nose) (Dickkopf receptor).
GN KREMEN1 OR KREMEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura T., Nakamura T.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -i- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
CC to block Wnt/beta-catenin signaling (By similarity)(Potential).
CC -i- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -i- SIMILARITY: Contains 1 CUB domain.
CC -i- SIMILARITY: Contains 1 Kringle domain.
CC -i- SIMILARITY: Contains 1 WSC domain.
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AB065090; BAB62003.1; -.
DR GO: GO:0016021; C-integral to membrane; ISS.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR002889; WSC.
DR Pfam: PF00431; CUB; 1.
DR Pfam: PF00051; kringle; 1.
DR PRINTS: PR001822; WSC; 1.
DR PRINTS: PR00018; KRINGLE.
DR ProDom: PD000395; Kringle; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00130; KR; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
KW Mat signaling pathway; Signal; Transmembrane; Kringle.
FT SIGNAL 1 19
FT CHAIN 20 473 KREMEN PROTEIN 1.
FT DOMAIN 21 392 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 393 413 POTENTIAL.
FT DOMAIN 414 473 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 114 KRINGLE.
FT DOMAIN 120 210 WSC.
FT DOMAIN 214 321 CUB.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 473 AA; 51869 MW; 98510857DF856F08 CRC64;
Query Match 19.2%; Score 161; DB 1; Length 473;
Best Local Similarity 45.1%; Pred. No. 2.3e-08;
Matches 32; Conservative 7; Mismatches 28; Indels 4; Gaps 2;
QY 47 SKTCYEGNGHFYRGKASTDTM--GRCLPWN SATVLQOYTYHAHSDALQLGLGKHYCRN 104
Db 29 SPECFTANGADYRGTSWTALQGGKPLFWE--TFQHPYNTLKYNGEGGLGEHNYCRN 86
QY 105 PDNRRRPWCYV 115
Db 87 PDGDSVSPCYV 97
RESULT 24
APOA MACMU
ID APOA MACMU STANDARD; PRT; 1420 AA.
AC P14417;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apolipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Fragment).

LPA.
Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
Cercopitheinae; Macaca.
NCBI_TaxID=9544;
[1]_Synthesis."
SEQUENCE FROM N.A.
MEDLINE=89174660; PubMed=2925643;
Tomlinson J.E., McLean J.W., Lawn R.M.;
"Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
synthesis."
J. Biol. Chem. 264:5957-5965(1989).
-!- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
(Lp(a)). It has serine proteinase activity and is able of
autocatalysis. Inhibits tissue-type plasminogen activator 1.
Lp(a) may be a ligand for megalin/Gp 330.
-!- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
decorin (By similarity).
-!- PTM: N- and O-glycosylated (By similarity).
-!- DISEASE: Elevated plasma concentrations of apo(a) and its
naturally occurring proteolytic fragments are correlated with
atherosclerosis. Homology with plasminogen kringle IV and V is
thought to underlie the atherogenicity of the protein, because the
fragments are competing with plasminogen for fibrinogen binding.
-!- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
leading to the formation of the so called mini-Lp(a). Apo(a),
fragments accumulate in atherosclerotic lesions, where they may
promote thrombogenesis. O-glycosylation may limit the extent of
proteolytic fragmentation (By similarity).
-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
-!- SIMILARITY: Contains at least 10 kringle domains.
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EMBL; J04635; AAA36933.1; -
PIR; A32869; A32869.
HSSP; P00747; 2PK4.
MEROPS; S01.226; -
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR000001; Kringle_
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00051; kringle; 11.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 10.
SMART; SM00130; KR; 10.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00021; KRINGLE_1; 10.
PROSITE; PS00070; KRINGLE_2; 10.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; FALSE NEG.
PROSITE; PS00135; TRYPSIN_SER; FALSE NEG.
Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein;
Kringle; Repeat; Atherosclerosis.
NON_TER 1
DOMAIN 1
DOMAIN 2
DOMAIN 3
DOMAIN 4
DOMAIN 5
DOMAIN 6
DOMAIN 7
DOMAIN 8
DOMAIN 9
KRINGLE 1.
KRINGLE 2.
KRINGLE 3.
KRINGLE 4.
KRINGLE 5.
KRINGLE 6.
KRINGLE 7.
KRINGLE 8.
KRINGLE 9.

FT DOMAIN 1067 1145 KRINGLE 10.
FT DOMAIN 1191 1420 SERINE PROTEASE.
SQ SEQUENCE 1420 AA; 158367 MW; BE102949E03C5BOE CRC64;
Query Match 19.2%; Score 161; DB 1; Length 1420;
Best Local Similarity 40.9%; Pred. No. 7e-08;
Matches 36; Conservative 9; Mismatches 31; Indels 12; Gaps 4;
QY 50 CYEGNGHYRGRKASTDTMGPRCLPWNASATVLO--QTYHAHRSDALQQLGLGKKNYCNPN 107
Db 1068 CYHGNGQSYRGTFTVTGRTQSSMTFPHQKTPENHPNDLTM-----NYCENPDA 1122
QY 108 RRPWCYVQVGLKPLVQE--CMVHDCAD 133
Db 1123 DTGPWCFT---MDPSVREYCNLTRCS 1147
RESULT 25
PLMN MACMU STANDARD; PRT; 810 AA.
ID PLMN MACMU
AC P12545;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89174660; PubMed=2925643;
RA Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of
RT synthesis."
RL J. Biol. Chem. 264:5957-5965(1989).
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including
embryonic development, tissue remodeling, tumor invasion, and
inflammation; in ovulation it weakens the walls of the Graafian
follicle. It activates the urokinase-type plasminogen activator,
collagenases and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
Willebrand factor.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
products.
CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Activated with catalytic amounts of streptokinase.
CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clot.
CC -!- MISCELLANEOUS: In the presence of the inhibitor, the activation
CC involves only cleavage after Arg-580, resulting in 2 chains held
CC together by 2 disulfide bonds. Without the inhibitor, the
CC activation involves also removal of the activation peptide.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 5 kringle domains.
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EMBL; J04697; AAA36901.1; -
PIR; B32869; B30848.
HSSP; P00747; 1PMK.
MEROPS; S01.233; -.

DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_s1.
DR InterPro; IPR001314; Peptidase_s1A.
DR InterPro; IPR003966; Peptidase_s1A_pr.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 810 PLASMINOGEN.
FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
FT DOMAIN 103 181 KRINGLE 1.
FT DOMAIN 184 282 KRINGLE 2.
FT DOMAIN 275 352 KRINGLE 3.
FT DOMAIN 377 454 KRINGLE 4.
FT DOMAIN 481 560 KRINGLE 5.
FT DOMAIN 581 810 SERINE PROTEASE.
FT ACT_SITE 622 622 CHARGE RELAY SYSTEM.
FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
FT BINDING 134 134 FIBRIN.
FT BINDING 136 136 FIBRIN.
FT DISULFID 49 73 BY SIMILARITY.
FT DISULFID 53 61 BY SIMILARITY.
FT DISULFID 103 181 BY SIMILARITY.
FT DISULFID 124 164 BY SIMILARITY.
FT DISULFID 152 176 BY SIMILARITY.
FT DISULFID 185 262 BY SIMILARITY.
FT DISULFID 188 316 BY SIMILARITY.
FT DISULFID 206 245 BY SIMILARITY.
FT DISULFID 234 257 BY SIMILARITY.
FT DISULFID 275 352 BY SIMILARITY.
FT DISULFID 296 335 BY SIMILARITY.
FT DISULFID 324 347 BY SIMILARITY.
FT DISULFID 377 454 BY SIMILARITY.
FT DISULFID 398 437 BY SIMILARITY.
FT DISULFID 426 449 BY SIMILARITY.
FT DISULFID 481 560 BY SIMILARITY.
FT DISULFID 502 543 BY SIMILARITY.
FT DISULFID 531 555 BY SIMILARITY.
FT DISULFID 567 685 BY SIMILARITY.
FT DISULFID 577 685 BY SIMILARITY.
FT DISULFID 607 623 BY SIMILARITY.
FT DISULFID 699 766 BY SIMILARITY.
FT DISULFID 729 745 BY SIMILARITY.
FT DISULFID 756 784 BY SIMILARITY.
FT CARBOHYD 365 365 O-LINKED (GALNAc...) (BY SIMILARITY).
SQ SEQUENCE 810 AA; 90255 MW; A75B1C51A1A0F24A CRC64;

Query Match 19.1%; Score 159.5; DB 1; Length 810;
Best Local Similarity 31.4%; Pred. No. 5.6e-08;
Matches 49; Conservative 12; Mismatches 66; Indels 29; Gaps 7;
QY 10 NCDCLNGGTCVKNKYPNSIHWCNCPKKGQ-----HCEIDKSKTCVEGNH 56
DB 428 NPDADKGPWCFTTDPVRWEYCNLKCKSGTGVAAAPPVQLPDAETPSEEDCMFGNGK 487
QY 57 FYEGKASTDTMGRCPLPMSATVLTQYHAHR-----SDALQLGLGHNYCRNPD-NRRRP 111
DB 488 GYRGKATTTVTGTCQENAA-----QEPHSHRIFFTNPRAGLEK-NYCRNPDGDVGCP 541
QY 112 WCYVQVGLKPLVQECMVHDC-----DGKXPSSPPEE 143
DB 542 WCYT-TNPRKLFYCDVPQCAASSFDCGKQVEPKK 576
RESULT 26
KRM1_XENLA
ID KRM1_XENLA STANDARD; PRT; 452 AA.
AC Q30Y90;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (Kringle-containing protein marking the eye
DE and the nose) (Dickkopf receptor).
GN KREME1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura T.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for dickkopf protein. Cooperates with Dickkopf
CC to block Wnt/beta-catenin signaling (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 1 CUB domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -!- SIMILARITY: Contains 1 WSC domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; AB070851; BAB64294.1; -.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR002889; WSC.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF01822; WSC; 1.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00321; WSC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Wnt signaling pathway; Glycoprotein; Kringle;
KW Transmembrane; Signal
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 452 KREME1 PROTEIN 1.
FT DOMAIN 23 369 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 370 390 POTENTIAL.

F DOMAIN 391 452 CYTOPLASMIC (POTENTIAL).
F DOMAIN 29 112 KRINGLE.
F DOMAIN 118 208 WSC.
F DOMAIN 212 319 CUB.
F CARBOHYD 43 43 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 328 328 N-LINKED (GLCNAC. . .) (POTENTIAL).
F CARBOHYD 344 344 N-LINKED (GLCNAC. . .) (POTENTIAL).
S SEQUENCE 452 AA; 50188 MW; ED24BCD1AP4564E2 CRC64;

Query Match 19.0%; Score 159; DB 1; Length 452;
Best Local Similarity 40.8%; Pred. No. 3.5e-08;
Matches 31; Conservative 9; Mismatches 32; Indels 4; Gaps 2;

Q 42 CEIDSKTCYEGNGHYFGKASTDTM--GRCLPWSATVLQOQTYHAHRSDALQGLGKH 99
D 22 CSDSFHSECYTVNGADYRGTSQNTSLDGGKPCLFWNE--TFQHPYNTLKYNGEGGLGEH 79

Q 100 NYCRRPDRRRPWCYV 115
D 80 NYCRRPDRRRPWCYV 95

R JLT 27
K MOUSE STANDARD; PRT; 473 AA.
I KRM_MOUSE STANDARD; PRT; 473 AA.
A Q99N43; 28-FEB-2003 (Rel. 41, Created)
D 28-FEB-2003 (Rel. 41, Last sequence update)
D 10-OCT-2003 (Rel. 42, Last annotation update)
D Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
D KREMN1 OR KREMEN.
C Mus musculus (Mouse).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
C NCBI_TaxID=10090;
K [1]
K SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
R TISSUE=Brain, and Kidney;
R MEDLINE=21167372; PubMed=11267660;
K Nakamura T.; Aoki S.; Kitajima K.; Takahashi T.; Matsumoto K.;
R Nakamura T.;
R "Molecular cloning and characterization of Kremen, a novel
Kringle-containing transmembrane protein.";
R Biochim. Biophys. Acta 1518:63-72(2001).
C -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
to block Wnt/beta-catenin signaling (By similarity).
C -!- SUBCELLULAR LOCATION: Type I membrane protein (potential).
C -!- TISSUE SPECIFICITY: In the adult, widely expressed with high
levels in heart, lung, kidney, skeletal muscle and testis.
C -!- DEVELOPMENTAL STAGE: In the embryo, expression is first detected
on day 9 and increases up to day 18. Lower levels are found in
adult. At 9.5 dpc, expression is localised to the apical
ectodermal ridge (AER) of the developing fore- and hindlimb buds,
the telencephalon and the first brachial arch. At 10.5 dpc,
expression is also observed in the myotome and in sensory tissues
such as the nasal pit and optic vesicle.
C -!- SIMILARITY: Contains 1 CUB domain.
C -!- SIMILARITY: Contains 1 Kringle domain.
C -!- SIMILARITY: Contains 1 WSC domain.

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or send an email to license@isb-sib.ch).

DR EMBL; AB059617; BAB40968.1; -.
DR HSP; P00747; ICEA.
DR MGD; MGI:1933988; Kremen.
DR GO; GO:0016021; C:Integral to membrane; NAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR002889; WSC.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF01822; WSC; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
KW Wnt signaling pathway; Signal; Transmembrane; Kringle.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 473 KREMEN PROTEIN 1.
FT DOMAIN 21 392 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 393 413 POTENTIAL.
FT DOMAIN 414 473 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 114 KRINGLE.
FT DOMAIN 120 210 WSC.
FT DOMAIN 214 321 CUB.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 473 AA; 51716 MW; 586827788BE3FDD1 CRC64;

Query Match 19.0%; Score 159; DB 1; Length 473;
Best Local Similarity 45.8%; Pred. No. 3.7e-08;
Matches 31; Conservative 7; Mismatches 26; Indels 4; Gaps 2;

Qy 50 CYEGNGHYFGKASTDTM--GRCLPWSATVLQOQTYHAHRSDALQGLGKHNCNPON 107
Db 32 CFTANGADYRGTSQNTSLDGGKPCLFWNE--TFQHPYNTLKYNGEGGLGEHNCNPDG 89

Qy 108 RRRPWCYV 115
Db 90 DVSPWCYV 97

RESULT 28
PLMN BOVIN
ID PLMN_BOVIN STANDARD; PRT; 812 AA.
AC P06868; Q28162;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Berglund L.; Andersen M.D.; Petersen T.E.;
RT "Cloning and characterization of the bovine plasminogen cDNA.";
RL Int. Dairy J. 5:593-603(1995).
RN [2]
RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=85203906; PubMed=3845532;
RA Schaller J.; Moser P.W.; Danneberger-Muller G.A.K.; Rosselet S.J.;
RA Kampfer U.; Rickli E.E.;
RT "Complete amino acid sequence of bovine plasminogen. Comparison with

human plasminogen.";
[3] Eur. J. Biochem. 149:267-278(1985).
[3] SEQUENCE OF 706-812 FROM N.A.
RX MEDLINE-85023311; PubMed-6148961;
RA Malinowski D.P.; Sadler J.E.; Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
RL human and bovine plasminogen."
RL Biochemistry 23:4243-4250(1984).
[4]
RX CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE-88185329; PubMed-3356193;
RA Marti T., Schaller J., Rickli E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vlieghart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns."
RL Eur. J. Biochem. 173:57-63(1988).
CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion,
CC and inflammation; in ovulation it weakens the walls of the
CC Graafian follicle. It activates the urokinase-type plasminogen
CC activator, collagenases and several complement zymogens, such
CC as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin,
CC laminin and von Willebrand factor.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen
CC activators, both plasminogen and its activator being bound to
CC fibrin. Cannot be activated with streptokinase.
CC -1- PTM: N-LINKED GLYCANS CONTAIN N-ACETYLACTOSAMINE AND SIALIC ACID.
CC O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS
CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
CC -1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
CC immediately after dissociation from the clot.
CC -1- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -1- SIMILARITY: Contains 5 kringle domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcements>
CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; X79402; CAA65939.1; --
CC EMBL; K02935; AAA30714.1; --
CC PIR; S45046; PLBO.
CC HSP; P00747; 2PK4.
CC MEROPS; S01.233; --
CC GlycoSuiteDB; P06868; --
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR003014; PAN.
CC InterPro; IPR003609; Pan_app.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC InterPro; IPR003966; Peptidase_S1A_pr.
CC Pfam; PF00051; Kringle; 5.
CC Pfam; PF00024; PAN; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC PRINTS; PR01505; PROTHROMBIN.
CC ProDom; PD000395; Kringle; 5.
CC SMART; SM00130; KR; 5.
CC SMART; SM00473; PAN AP; 1.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00021; KRINGLE_1; 5.
CC PROSITE; PS00070; KRINGLE_2; 5.

DR PROSITE; PS0240; TRYPSIN DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
KW Signal.
FT SIGNAL 1 26
FT CHAIN 27 812 PLASMINOGEN.
FT CHAIN 27 583 PLASMIN HEAVY CHAIN A.
FT CHAIN 584 812 PLASMIN LIGHT CHAIN B.
FT DOMAIN 110 188 KRINGLE 1.
FT DOMAIN 192 269 KRINGLE 2.
FT DOMAIN 282 359 KRINGLE 3.
FT DOMAIN 384 461 KRINGLE 4.
FT DOMAIN 485 564 KRINGLE 5.
FT DOMAIN 584 812 SERINE PROTEASE.
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .).
FT CARBOHYD 365 365 O-LINKED (GALNAc. . .).
FT ACT_SITE 624 624 /FTID-CAR 000015.
FT ACT_SITE 667 667 /FTID-CAR 000015.
FT ACT_SITE 762 762 CHARGE RELAY SYSTEM.
FT CONFLICT 335 335 CHARGE RELAY SYSTEM.
FT CONFLICT 516 516 N -> D (IN REF. 2).
FT CONFLICT 555 555 Q -> H (IN REF. 2).
FT CONFLICT 744 744 P -> L (IN REF. 2).
FT CONFLICT 744 744 T -> R (IN REF. 3).
SQ SEQUENCE 812 AA; 91216 MW; 38A6A691E220946 CRC64;
Query Match 19.0%; Score 159; DB 1; Length 812;
Best Local Similarity 28.0%; Pred. No. 6.3e-08;
Matches 49; Conservative 15; Mismatches 55; Indels 56; Gaps 11;
QY 5 HQVPSNCDCLN-----GGTCVSNKYPNSIHW--CNCPKKFGSQHCEIDSKT 49
Db 315 NRTPEPCKNLEENYCRNPNNGEKAFCWYTTN--SEVRWEYCTIPS-----CESSPLST 366
QY 50 -----CYEGNGHFYRGKASTDMGRPLCPMNSATVLOQTYHAH---RS 89
Db 367 ERMDVPVPPQTPVPODCYHGNGOSYRGTSSTITGCKQSWSS-----MTPRHLKTP 421
QY 90 DALQLGLGKKNYCNPNRRRPNWYQVGLKPLV--QECMVHDCADGKK--PSSP 140
Db 422 NYFNAGL-TWNYCRNPADKSPWCYT--TDPVRWEFCNLKCKSETPEQVPAAP 472
RESULT 29
ID_ROR1 HUMAN STANDARD; PRT; 937 AA.
AC Q01973; Q92776;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor ROR1 precursor
DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1).
GN ROR1 OR NTRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=93100347; PubMed=1334494;
RA Masiakowski P., Carroll R.D.;
RT "A novel family of cell surface receptors with tyrosine kinase-like
RT domain."
RL J. Biol. Chem. 267:26181-26190(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=97030043; PubMed=8875995;
RA Reddy U.R., Phatak S., Pleasure D.;
RT "Human neural tissues express a truncated Ror1 receptor tyrosine
RT kinase, lacking both extracellular and transmembrane domains."

Oncogene 13:1555-1559(1996).

-!- FUNCTION: Tyrosine-protein kinase receptor whose role is not yet clear.

-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-!- SUBCELLULAR LOCATION: Type I membrane protein.

-!- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms=2;

Name=Long;

isoId=Q01973-1; Sequence=Displayed;

Name=Short; Synonym=T-ROR1;

isoId=Q01973-2; Sequence=VSP_005008;

-!- TISSUE SPECIFICITY: Expressed strongly in human heart, lung, and kidney, but weakly in the CNS. The short isoform is strongly expressed in fetal and adult CNS and in a variety of human cancers, including those originating from CNS or PNS neuroectoderm.

-!- DEVELOPMENTAL STAGE: Expressed at high levels during early embryonic development. The expression levels drop strongly around day 16 and there are only very low levels in adult tissues.

-!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR subfamily.

-!- SIMILARITY: Contains 1 frizzled (FZ) domain.

-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

-!- SIMILARITY: Contains 1 kringle domain.

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EMBL; M97675; AAC60275.1; -

EMBL; U38894; AAC50714.1; -

PIR; A45082; A45082.

HSP; P00747; ICRA.

Genew; HGNC:10256; ROR1.

MIM; 602335; -

GO; GO:0005737; Cytoplasm; TAS.

GO; GO:0005887; C: integral to plasma membrane; TAS.

GO; GO:0004714; F: transmembrane receptor protein tyrosine kin. . . ; TAS.

GO; GO:0007169; P: transmembrane receptor protein tyrosine kin. . . ; TAS.

InterPro; IPR000024; Fz domain.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_c2.

InterPro; IPR000001; Kringle.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR001345; Tyr_kinase.

InterPro; IPR008266; Tyr_kinase_AS.

Pfam; PF01392; Fz; 1.

Pfam; PF00047; ig; 1.

Pfam; PF00051; kringle; 1.

Pfam; PF00691; pkinase; 1.

PRINTS; PR00018; KRINGLE.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000395; Kringle; 1.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00408; IgC2; 1.

SMART; SM00130; KR; 1.

SMART; SM00219; Tyrc; 1.

PROSITE; PS00038; FZ; 1.

PROSITE; PS00835; IG_LIKE; 1.

PROSITE; PS00021; KRINGLE; 1.

PROSITE; PS00070; KRINGLE_2; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

Transferase; Tyrosine-protein kinase; ATP-binding; Receptor; Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation; Immunoglobulin domain; Alternative splicing.

SIGNAL 1 29 POTENTIAL.

FT	CHAIN	30	937	TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT	RECEPTOR ROR1			
FT	EXTRACELLULAR			
FT	POTENTIAL			
FT	CYTOPLASMIC			
FT	IG-LIKE C2-TYPE			
FT	FZ			
FT	KRINGLE			
FT	PROTEIN KINASE			
FT	SER/THR-RICH			
FT	PRO-RICH			
FT	SER/THR-RICH			
FT	ATP (BY SIMILARITY)			
FT	ATP (BY SIMILARITY)			
FT	ACT SITE			
FT	BY SIMILARITY			
FT	PHOSPHORYLATION (AUTO-)			
FT	BY SIMILARITY			
FT	N-LINKED (GLCNAC)			
FT	N-LINKED (GLCNAC)			
FT	N-LINKED (GLCNAC)			
FT	N-LINKED (GLCNAC)			
FT	N-LINKED (GLCNAC)			
FT	Missing (in isoform Short)			
FT	FTId=VSP_005008			
FT	SEQUENCE	937 AA; 104312 MW; 0D0694DBF29F4773 CRC64;		
FT	Query Match	18.9%; Score 158.5; DB 1; Length 937;		
FT	Best Local Similarity	29.7%; Pred. No. 8.1e-08;		
FT	Matches	43; Conservative 14; Mismatches 51; Indels 37; Gaps 7;		
QY	2 NELHQP	-----SNCDCLNGTGVSNKYFS-----NIHWNC-----PKKFGGOH 41		
Db	236 DEISSVFKPRDLCDCEILENVLCQTEYIFARSNPMLMRKLPNCEDLPQESPEAN 295			
QY	42 C-----EIDSKTYCEGNGHYRKGASTDTWGRPCLPWNSATVLTQTHAHSDAL 92			
Db	296 CIRIGIPMADPINKHKNKYNSTGVDYRGTSVTKSGRQCPWNS-----QYPTHHTFTAL 350			
QY	93 QLG--LGKKNYCNPNRER-PWCY 114			
Db	351 RPPELNGHSYCRNPGNKEAPWCP 375			
RESULT 30				
ROR1_MOUSE	STANDARD; PRT; 937 AA.			
ID_ROR1_MOUSE				
AC	Q92L39;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Tyrosine-protein kinase transmembrane receptor ROR1 precursor			
DE	(EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1)			
DE	(mROR1)			
GN	ROR1 OR NTRKX1			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99248426; PubMed=102311392;			
RA	Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J.,			
RA	Hatta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.;			
RT	"Spatio-temporally regulated expression of receptor tyrosine kinases,			
RT	mRor1, mRor2, during mouse development: implications in development			
RT	and function of the nervous system."			
RL	Genes Cells 4:41-56(1999).			
CC	-!- FUNCTION: Tyrosine-protein kinase receptor whose role is not yet			
CC	clear.			
CC	-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC	tyrosine phosphate.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR			
CC	subfamily.			

"Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that forms the linkage between the plasmin chains.";
 Eur. J. Biochem. 58:539-547(1975).
 [9]
 SEQUENCE OF 581-810.
 MEDLINE=77225245; PubMed=142009;
 Kiman B.;
 "Primary structure of the B-chain of human plasmin.";
 Eur. J. Biochem. 76:129-137(1977).
 [10]
 ACTIVE SITE.
 MEDLINE=73149248; PubMed=4694729;
 Robbins K.C., Bernabe P., Arzadon L., Summaria L.;
 "The primary structure of human plasminogen. II. The histidine loop of human plasmin: light (B) chain active center histidine sequence.";
 J. Biol. Chem. 248:1631-1633(1973).
 [11]
 ACTIVE SITE.
 MEDLINE=69234739; PubMed=4240117;
 Groskopf W.R.; Summaria L., Robbins K.C.;
 "Studies on the active center of human plasmin. Partial amino acid sequence of a peptide containing the active center serine residue.";
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 Trexler M., Vali Z., Pathy L.;
 "Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen. Arginine 70 and aspartic acid 56 are essential for binding of ligand by kringle 4.";
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 MEDLINE=85054794; PubMed=6094526;
 Vali Z., Pathy L.;
 "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin affinity of the kringle 1 domain.";
 J. Biol. Chem. 259:13690-13694(1984).
 [14]
 PHOSPHORYLATION SITE SER-597.
 MEDLINE=97345939; PubMed=9201958;
 Wang H., Proxok M., Bretthauer R.K., Castellino F.J.;
 "Serine-578 is a major phosphorylation locus in human plasma plasminogen.";
 Biochemistry 36:8100-8106(1997).
 [15]
 CARBOHYDRATE-LINKAGE SITES.
 MEDLINE=88185329; PubMed=3356193;
 Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P., Gerwig G.J., van Halbeek H., Vliegthart J.F.;
 "The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns.";
 Eur. J. Biochem. 173:57-63(1988).
 [16]
 CARBOHYDRATE-LINKAGE SITE SER-268.
 MEDLINE=97207306; PubMed=9054441;
 Pirle-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J., Pizzo S.V.;
 "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of human plasminogen 2.";
 J. Biol. Chem. 272:7408-7411(1997).
 [17]
 CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
 MEDLINE=95042728; PubMed=7525077;
 O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A., Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 "Angiostatin: a novel angiogenesis inhibitor that mediates the suppression of metastases by a Lewis lung carcinoma.";
 Cell 79:315-328(1994).
 [18]
 CHARACTERIZATION OF ANGIOSTATIN.
 MEDLINE=97238710; PubMed=9102221;

RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
 RA Lapcevic R., Nacy C.A.;
 RT "A recombinant human angiotensin protein inhibits experimental primary
 RT and metastatic cancer.";
 RL Cancer Res. 57:1329-1334(1997).
 RN [19]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
 RX MEDLINE=92031502; PubMed=1657148;
 RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
 RT "Crystal and molecular structure of human plasminogen kringle 4
 RT refined at 1.9-A resolution.";
 RL Biochemistry 30:10576-10588(1991).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
 RX MEDLINE=92031503; PubMed=1657149;
 RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
 RT "The refined structure of the epsilon-aminocaproic acid complex of
 RT human plasminogen kringle 4.";
 RL Biochemistry 30:10589-10594(1991).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
 RA Stec B., Yamano A., Whitlow M., Teeter M.M.;
 RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
 RT A possible structural role of disordered residues.";
 RL Acta Crystallogr. D 53:169-178(1997).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
 RX MEDLINE=96180681; PubMed=8611560;
 RA Mathews I.I., Vanderhoff-Hanaver P., Castellino F.J., Tulinsky A.;
 RT "Crystal structures of the recombinant kringle 1 domain of human
 RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
 RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
 RL Biochemistry 35:2567-2576(1996).
 RN [23]
 RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
 RX MEDLINE=98198034; PubMed=9521645;
 RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
 RA Castellino F.J.;
 RT "Structure and ligand binding determinants of the recombinant kringle
 RT 5 domain of human plasminogen.";
 RL Biochemistry 37:3258-3271(1998).
 RN [24]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237157; PubMed=8181475;
 RA Rejante M.R., Llinas M.;
 RT "1H-NMR assignments and secondary structure of human plasminogen
 RT kringle 1.";
 RL Eur. J. Biochem. 221:927-937(1994).
 RN [25]
 RP STRUCTURE BY NMR OF 96-184.
 RX MEDLINE=94237158; PubMed=8181476;
 RA Rejante M.R., Llinas M.;
 RT "Solution structure of the epsilon-aminohexanoic acid complex of
 RT human plasminogen kringle 1.";
 RL Eur. J. Biochem. 221:939-949(1994).
 RN [26]
 RP STRUCTURE BY NMR OF 183-354.
 RX MEDLINE=96194156; PubMed=8652577;
 RA Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
 RA Rickli E.E.;
 RT "Recombinant gene expression and 1H NMR characteristics of the
 RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
 RT of plasminogen kringle domains.";
 RL Biochemistry 35:2357-2364(1996).
 RN [27]
 RP STRUCTURE BY NMR OF 374-461.
 RX MEDLINE=90219023; PubMed=2157850;

Query Match 18.7%; Score 156.5; DB 1; Length 810;
 Best Local Similarity 28.5%; Pred. No. 1.1e-07;
 Matches 49; Conservative 22; Mismatches 52; Indels 49; Gaps 12;

Oy 5 HQVPSNCDLNGTGVSNKYFSN-----IHWNCNP-KKFGQHCEI---DKS----- 47

308 NRTPEFPCKK-----LDENYCRNPDGKRAPWCHTTSQVRYEYCKIPSCDSSPVSTEQIA 363
48 -----KTCYGNHGFVRGKASTMTGRPCLPWNSATVLOQTTHAHR---SDALQ 93
364 PTAPPETLPVQDCYRGDSQVAGTSTTTGKKQCSWSS-----MTRHOKTPTENYFN 418
94 LGIGKKNYCRNPNRRPNCYQVQGLKPLV--QECNVHDCADGKPS--SPP 141
419 AGL-TNYCENPDADGKPCFT---TDPVRYEYCNLKKS-GTASVAVPP 465

RE [T 32
KX HUMAN
ID KRM1 HUMAN STANDARD; PRT; 475 AA.
AC Q96MJB; Q96V70; Q9UGS5; Q9UGU1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (kringle-containing protein marking the eye
and the nose) (Dickkopf receptor).
GN KREMN1 OR KREMN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RF SEQUENCE FROM N.A. (ISOFORM 1).
RA Nakamura T., Nakamura T.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RF SEQUENCE FROM N.A. (ISOFORM 2).
RA Tashiro H., Yamazaki M., Watanabe K., Kunagai A., Itakura S.,
RA Otsukumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahara K., Masuho Y., Negai K.,
RA Isogai T.;
RT NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RF SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Begguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson B.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcott R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,
RA McLaren J.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spraggon L., Stewart C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shinkai A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hua A., Kerton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,

Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K., Nelson J.,
Korf I., Bekefi J.A., Hillier L.W., Mardis E., Waterston R.,
Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
Budarf M.L., Mcdermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
Peyraud M., Kedia D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
CC -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
to block Wnt/beta-catenin signaling (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96MJB-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96MJB-2; Sequence=VSP_003900;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Contains 1 CUB domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -!- SIMILARITY: Contains 1 WSC domain.
CC -----
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or send an email to license@isb-sib.ch).

DR EMBL; AB059618; BAB40369.1; -;
DR EMBL; AK056425; BAB71180.1; -;
DR EMBL; Z95116; CAB62952.1; -;
DR EMBL; AL021393; CAB62959.1; -;
DR Gene; HGNC:17550; KREMN1.
DR GO; GO:0016021; C:integral to membrane; ISS.
DR GO; GO:0005624; C:membrane fraction; TAS.
DR GO; GO:0007154; P:cell communication; TAS.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000003; Kringle.
DR InterPro; IPR002889; WSC.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF01822; WSC; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
KW Wnt signaling pathway; Signal; Transmembrane; Kringle;
KW Alternative splicing;
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 475 KREMN PROTEIN 1.
FT DOMAIN 21 394 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 395 415 POTENTIAL.
FT DOMAIN 416 475 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 116 KRINGLE.
FT DOMAIN 121 202 WSC.
FT DOMAIN 216 323 CUB.
FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).

10-OCT-2003 (Rel. 42, Last sequence update)
 15-MAR-2004 (Rel. 43, Last annotation update)
 Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
 PLG.
 CC Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID:10090;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINE:91184812; PubMed:2081600;
 CC Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
 CC "Characterization of the cDNA coding for mouse plasminogen and
 CC localization of the gene to mouse chromosome 17";
 CC Genomics 8:49-61(1990).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=129/Sv;
 CC Brathwaite M.; Waeltz P., Qian Y., Dudekula D., Schlessinger D.,
 CC Nagaraja R.;
 CC "Genomic sequence analysis in the mouse t-complex region.";
 CC Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC [3]
 CC SEQUENCE FROM N.A.
 CC TISSUE=Liver;
 CC MEDLINE:22388257; PubMed:12477932;
 CC Strausberg K.L., Feigold E.A., Grouse L.H., Derge J.G.,
 CC Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 CC Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 CC Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 CC Diachenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,
 CC Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 CC Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 CC Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 CC Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 CC Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 CC Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 CC Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 CC Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 CC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 CC Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 CC Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 CC "Generation and initial analysis of more than 15,000 full-length human
 CC and mouse cDNA sequences";
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC [4]
 CC SEQUENCE OF 1-16 FROM N.A.
 CC STRAIN=129/SvJ; TISSUE=Liver;
 CC PubMed:12149246;
 CC Farmer R.J., Miles L.A.;
 CC "Localization of regulatory elements mediating constitutive and
 CC cytokine-stimulated plasminogen gene expression";
 CC J. Biol. Chem. 277:38579-38588(2002).
 CC [5]
 CC CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
 CC MEDLINE:95042728; PubMed:7525077;
 CC O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
 CC Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 CC "Angiostatin: a novel angiogenesis inhibitor that mediates the
 CC suppression of metastases by a Lewis lung carcinoma";
 CC Cell 79:315-328(1994).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammatory development. In ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -!- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks
 CC neovascularization and growth of experimental primary and

metastatic tumors in vivo.
 -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 higher selectivity than trypsin. Converts fibrin into soluble
 products.
 -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 activators, both plasminogen and its activator being bound to
 fibrin. Cannot be activated with streptokinase.
 -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 immediately after dissociation from the clot.
 -!- MISCELLANEOUS: In the presence of the inhibitor, the activation
 involves only cleavage after Arg-581, resulting in 2 chains held
 together by 2 disulfide bonds. Without the inhibitor, the
 activation involves also removal of the activation peptide.
 -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 -!- SIMILARITY: Contains 5 kringle domains.

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 EMBL; J04766; AA50168.1; -
 EMBL; AF481053; AM22156.1; -
 EMBL; BC014773; AAH14773.1; -
 EMBL; BC057186; AAH5186.1; -
 EMBL; AY134430; AAH15805.1; -
 PIR; A38514; PLMS.
 HSP; P00747; IPMK.
 MEROPS; S01.233; -
 MGD; MGI:197620; Plg.
 DR GO; GO:0016506; Fibrinolysis activator activity; IDA.
 DR GO; GO:0006915; Apoptosis; IDA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pr.
 DR Pfam; PF00051; kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; Tryp SPC; 1.
 DR PROSITE; PS00021; KRINGLE 1; 5.
 DR PROSITE; PS00070; KRINGLE 2; 5.
 DR PROSITE; PS02400; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT SIGNAL
 FT CHAIN 1 19 PLASMINOGEN.
 FT CHAIN 20 812 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 97 ACTIVATION PEPTIDE.
 FT CHAIN 98 581 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 98 7436 ANGIOSTATIN.
 FT CHAIN 582 812 PLASMIN LIGHT CHAIN B.
 FT CHAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 582 812 SERINE PROTEASE.

ACT SITE 624 624 CHARGE RELAY SYSTEM (BY SIMILARITY).
 ACT SITE 667 667 CHARGE RELAY SYSTEM (BY SIMILARITY).
 ACT SITE 762 762 CHARGE RELAY SYSTEM (BY SIMILARITY).
 DISULFID 49 61 BY SIMILARITY.
 DISULFID 103 181 BY SIMILARITY.
 DISULFID 124 164 BY SIMILARITY.
 DISULFID 152 176 BY SIMILARITY.
 DISULFID 188 316 BY SIMILARITY.
 DISULFID 206 245 BY SIMILARITY.
 DISULFID 234 257 BY SIMILARITY.
 DISULFID 275 352 BY SIMILARITY.
 DISULFID 296 335 BY SIMILARITY.
 DISULFID 334 347 BY SIMILARITY.
 DISULFID 377 454 BY SIMILARITY.
 DISULFID 398 437 BY SIMILARITY.
 DISULFID 426 449 BY SIMILARITY.
 DISULFID 481 560 BY SIMILARITY.
 DISULFID 502 543 BY SIMILARITY.
 DISULFID 531 555 BY SIMILARITY.
 DISULFID 568 657 INTERCHAIN (BY SIMILARITY).
 DISULFID 578 586 INTERCHAIN (BY SIMILARITY).
 DISULFID 609 625 BY SIMILARITY.
 DISULFID 701 768 BY SIMILARITY.
 DISULFID 731 747 BY SIMILARITY.
 DISULFID 758 786 BY SIMILARITY.
 CONFLICT 235 235 R -> H (IN REF. 1).
 CONFLICT 525 525 S -> D (IN REF. 1).
 CONFLICT 649 649 S -> L (IN REF. 1).
 SEQUENCE 812 AA; 90781 MW; 24173260B6A2FFD2 CRC64;
 Very Match 18.5%; Score 155; DB 1; Length 812;
 est Local Similarity 30.1%; Pred. No. 1.5e-07;
 atches 40; Conservative 12; Mismatches 55; Indels 26; Gaps 7;
 Q 30 WC--NCPKFGQHCHEIDKSKT-----CYENGHGFYRGKASTDTMGRPCLPWNSA 77
 D 244 WCFTIDPTK-RWEYCDIPRCTPPPPPTQYCLKGRGNYKTVSVTSGKTQRMWS-- 300
 Q 78 TVLQQTTHARSDALQLGLG--KHNYCRNPDNRPPWVQGLKPLVQECWHDGADGK 135
 D 301 ----EOTPHRHNTFNPCKNLEENYCRNPDGETAPWCYT-TDSQLRWEYCEIFSCSSA 356
 Q 136 KP-----SSPPEE 143
 D 357 SPDQSDSSVPPEE 369
 R JLT 35
 F VERIEU STANDARD; PRT; 810 AA.
 I Q29485;
 A 01-NOV-1997 (Rel. 35, Created)
 D 01-NOV-1997 (Rel. 35, Last sequence update)
 D 28-FEB-2003 (Rel. 41, Last annotation update)
 D Plasminogen precursor (EC 3.4.21.7).
 G PLG.
 O Brinaceus europaeus (Western European hedgehog).
 O Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 O Mammalia; Eutheria; Insectivora; Brinaceidae; Brinaceinae; Brinaceus.
 O NCBI_TaxID=9345;
 R [1]
 R SEQUENCE FROM N.A.
 R TISSUE=Liver;
 R MEDLINE=96025977; PubMed=7592597;
 R Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
 R Byrne C.D., Fong K.J., Meer K., Pathy L.;
 R "The recurring evolution of lipoprotein(a). Insights from cloning of
 R hedgehog apolipoprotein(a).";
 R J. Biol. Chem. 270:24004-24009(1995).
 R [2]
 R REVISIONS.

Lawn R.M.;
 Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RL FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -/- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -/- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -/- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -/- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 CC -/- SIMILARITY: Contains 5 kringle domains.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U33171; AAC48717.1; -.
 CC PIR; I46260; I46260.
 CC HSP; P00747; IPMK.
 CC MROPS; S01.233.
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR003014; PAN.
 CC InterPro; IPR003609; Pan app.
 CC InterPro; IPR001254; Peptidase S1.
 CC InterPro; IPR001314; Peptidase_S1A.
 CC InterPro; IPR003966; Peptidase_S1A_pr.
 CC Pfam; PF00051; Kringle; 5.
 CC Pfam; PF00024; PAN; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC PRINTS; PR01505; PROTHROMBIN.
 CC PRODOM; PD000395; Kringle; 5.
 CC SMART; SMC0130; KR; 5.
 CC SMART; SMC0473; PAN AP; 1.
 CC SMART; SMC0020; TRYP_SPC; 1.
 CC PROSITE; PS00021; KRINGLE_1; 5.
 CC PROSITE; PS00070; KRINGLE_2; 5.
 CC PROSITE; PS00240; TRYPsin_DOM; 1.
 CC PROSITE; PS00134; TRYPsin_HIS; 1.
 CC PROSITE; PS00135; TRYPsin_SER; 1.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
 KW Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 810 PLASMINOGEN.
 FT CHAIN 20 582 PLASMIN HEAVY CHAIN A (BY SIMILARITY).
 FT CHAIN 583 810 PLASMIN LIGHT CHAIN B (BY SIMILARITY).
 FT DOMAIN 103 181 SERINE PROTEASE.
 FT DOMAIN 185 262 KRINGLE 1.
 FT DOMAIN 275 352 KRINGLE 2.
 FT DOMAIN 379 456 KRINGLE 3.
 FT DOMAIN 482 561 KRINGLE 4.
 FT DOMAIN 622 665 KRINGLE 5.
 FT ACT_SITE 665 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT CARBOHYD 339 339 N-LINKED (GLCNAC... (POTENTIAL).
 SQ SEQUENCE 810 AA; 90902 MW; 8E75780946017A16 CRC64;

Query Match 18.3%; Score 153.5; DB 1; Length 810;
 Best Local Similarity 27.3%; Pred. No. 2.1e-07;
 Matches 39; Conservative 12; Mismatches 47; Indels 45; Gaps 6;

QY 6 QVPSNCCILN-----GTCVSNKYFSNIHW--CNCPPKFGGQHCEIDKSKT- 49
 Db 309 RTPENPCXNLDENYCRNPDGPAPWCFITN--SSVRWEFCIKP-----DCVSSASETE 360
 QY 50 -----CYEGNGHFYRCKASTDTMGRPCLPWNASATVLQTYHAHRSDA 91
 Db 361 HSDAPVIVPEPTFPVQECYQNGQYRGTSTTTTGKCKQCPWMSRPHRHSKTPENYPD 420

QY 92 LQGLGKXNYCRNPDNRFPWCY 114
 Db 421 ADLTM--NYCRNPDGKGPWCY 440

RE UT 36
 FLN RAT
 ID PLMN RAT STANDARD; PRT; 169 AA.
 AC Q01177;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PLG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.J., Makker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
 RL J. Biol. Chem. 266:10825-10829 (1991).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 CC -!- SIMILARITY: Contains 5 kringle domains.

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 or send an email to license@isb-sib.ch).

EMBL; MG2832; AAA41884.1; -;
 PIR; A40522; A40522.
 HSSP; P00747; IPMK.
 MEROPS; S01.233; -;
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR003966; Peptidase_S1A_pr.

DR Pfam; PF00051; kringle_2.
 DR PRINTS; PRO0016; KRINGLE.
 DR PRINTS; PRO1505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS00070; KRINGLE 2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Repeat.
 FT NON TER 1
 FT DOMAIN <1 10 KRINGLE 3 (BY SIMILARITY).
 FT DOMAIN 34 112 KRINGLE 4 (BY SIMILARITY).
 FT DOMAIN 139 >169 KRINGLE 5 (BY SIMILARITY).
 FT DISULFID 34 112 BY SIMILARITY.
 FT DISULFID 55 95 BY SIMILARITY.
 FT DISULFID 83 107 BY SIMILARITY.
 FT NON TER 169 169
 SQ SEQUENCE 169 AA; 77A54214C49D010C CRC64;

Query Match 18.2%; Score 152.5; DB 1; Length 169;
 Best Local Similarity 30.2%; Pred. No. 5.6e-08;
 Matches 42; Conservative 18; Mismatches 32; Indels 47; Gaps 9;

QY 40 QHCEI-----DKS-----KTCYEGNGHFYRCKASTDTMGRPCLPWNASAT 78
 Db 3 EYCEIPSCGSSVPDQSDSVLPETQPVVQECYQNGKSYRGTSTTTGKCKQSW--- 58
 QY 79 VLQQTVAHESDALQL--GLGKXNYCRNPDN--RRPWCYQVGLKPLV--QECMVHDC 132
 Db 59 -VSMTPHSHSKTIPANFPDGL-EMNYCRNPDNDQGPWCFT---TDPVSRWEYCNLRCS 113

QY 133 D-----GKFPSSP 140
 Db 114 ETGGGVAESAIVPQVPSAP 132

RESULT 37
 HGFL HUMAN STANDARD; PRT; 711 AA.
 AC P26927; Q13350; Q14870;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hepatocyte growth factor-like protein precursor (Macrophage
 DE stimulatory protein) (MSP) (Macrophage stimulating protein).
 GN MST1 OR HGFL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=92002016; PubMed=1655021;
 RA Han S., Stuart L.A., Priezenner Degen S.J.;
 RT "Characterization of the DNP152 locus on human chromosome 3:
 RT identification of a gene coding for four kringle domains with
 RT homology to hepatocyte growth factor.";
 RN Biochemistry 30:9768-9780 (1991).
 RC TISSUE=Liver;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;
 RT "Cloning, sequencing, and expression of human macrophage stimulating
 RT protein (MSP, MST1) confirms MSP as a member of the family of kringle
 RL J. Biol. Chem. 268:15461-15468 (1993).
 CC -!- FUNCTION: Probably has no proteolytic activity, since crucial AA
 CC characteristic of serine proteases catalytic sites are not

FT	CARBOHYD	296	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	615	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARIANT	13	Y -> C.
FT	VARIANT	212	C -> F. /FTid=VAR_006631.
FT	VARIANT	676	E -> K (in dbSNP:7798). /FTid=VAR_006632.
FT	VARIANT	676	E -> K (in dbSNP:7798). /FTid=VAR_014569.
FT	CONFLICT	623	L -> F (IN REF. 2).
FT	SEQUENCE	711 AA;	80379 MW; 596ED21F180290EA CRC64;
SO			

Query Match
Best Local Similarity 17.9%; Score 150; DB 1; Length 711;
Matches 34; Conservative 20; Mismatches 46; Indels 26; Gaps 6;

QY	30	WC-NCEKFGGHCIDK-----SKTCYEGNHFRCKASTDTMGPRCPWPNS	76
Db	250	WCYTTDFQIERFCDFRCGSAQPRQEAATVSCFRKGEGYRGTAATTAGVPCQRWDA	309
QY	77	ATVLCQTYHAHRSDALQLGLG--KHNYCRNPNNRRPWCYVQVGLKPLVQEC---NVHDC	131
Db	310	----QIPHOHRTPEKYACKDLRENFENPDGSEAPCFT--LRFGRFAAFYQIRRC	361
QY	132	ADGKXP	137
Db	362	TDVVRP	367

RESULT 38
KRM2 HUMAN STANDARD; PRT: 462 AA.

ID	KRM2 HUMAN	Q8N2J4; Q8NCW1; Q96GL8; Q9ETP9;
AC	Q8N2J4; Q8NCW1; Q96GL8; Q9ETP9;	
DT	10-OCT-2003 (Rel. 42, Created)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Kremen protein 2 precursor (Kringler-containing protein marking the eye and the nose) (Dickkopf receptor 2).	
DE	KREMEN2 OR KRM2.	
OS	homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_Taxid=9606;	
RI	[1]	
RT	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.	
RT	Tanaka S., Sugimachi K.;	
RT	"Human Kremen2 and Wnt signaling.";	
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.	
RL	[2]	
RP	SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).	
RP	TISSUE=Ovarian carcinoma;	
RC	Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,	
RA	Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,	
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,	
RA	Masuhara Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,	
RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;	
RT	"NEO human cDNA sequencing project.";	
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.	
RL	[3]	
RP	SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).	
RP	TISSUE=Brain, and Uterus;	
RC	MEDLINE=22388257; PubMed=12477932;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diachenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udwin T.B., Tothylky S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Faber J., Helton E., Kettner M., Madan, A., Botstein D., Scheraga	

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.S., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
 to block Wnt/beta-catenin signaling. Forms a ternary complex with
 Dkk1 and LRP6 and induces rapid endocytosis and removal of the Wnt
 receptor LRP6 from the plasma membrane (by similarity).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q8NCW0-1; Sequence=Displayed;
 CC Name=2; Synonyms=Kremen2a;
 CC IsoId=Q8NCW0-2; Sequence=VSP_050509, VSP_050510;
 CC Name=3; Synonyms=Kremen2b;
 CC IsoId=Q8NCW0-3; Sequence=VSP_050511, VSP_050512;
 CC Name=4; Synonyms=Kremen2c;
 CC IsoId=Q8NCW0-4; Sequence=VSP_050513, VSP_050514;
 CC -!- SIMILARITY: Contains 1 CUB domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC -!- SIMILARITY: Contains 1 WSC domain.

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 or send an email to license@isb-sib.ch).

DR EMBL; AB086405; BAC00872.1; -
 DR EMBL; AB086355; BAC00823.1; -
 DR EMBL; AB086356; BAC00824.1; -
 DR EMBL; AB086357; BAC00825.1; -
 DR EMBL; AK027669; BAB55281.1; -
 DR EMBL; AK075033; BAC11365.1; -
 DR EMBL; BC003533; AAH03533.1; -
 DR EMBL; BC009383; AAH03983.1; -
 DR HSSP; P00750.1; PK2.
 DR Genew; HGNC:18797; KREMEN2.
 DR InterPro; IPR000859; CUB.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR002889; WSC.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00511; kringle; 1.
 DR Pfam; PF01822; WSC; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00321; WSC; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS0070; KRINGLE 2; 1.
 KW Wnt signaling pathway; Glycoprotein; Kringle; Signal; Transmembrane;
 KW Alternative splicing;
 FT SIGNAL 1 25
 FT CHAIN 26 42
 FT DOMAIN 26 42 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 365 387
 FT DOMAIN 388 462 POTENTIAL.
 FT DOMAIN 35 119 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 121 215 KRINGLE.
 FT DOMAIN 219 326 WSC.
 FT DOMAIN 219 326 CUB.
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 394 424 SCILAPKGGPPALGASRPRRWAVVYQOPR -> CGALGQ
 FT GRADRWGAGAPENRANKELLGS (in isoform
 2).
 FT /FTId=VSP_050509.
 FT Missing (in isoform 2).
 FT /FTId=VSP_050510.
 FT ARVFTVAVSVLLILLGLLRPLRRRSCILAPGKGGPALG
 FT ASRGPRRSWAVV -> GAVCWLRKGRWGLPGAGGAG
 FT LOGTNSPEGWPCPAPGTPRLRVLPATGL (in
 isoform 3).
 FT /FTId=VSP_050511.
 FT Missing (in isoform 3).
 FT /FTId=VSP_050512.
 FT ARVFTVAVSVLLILLGLLRPLRRRSCILAP -> GEAG
 FT ARDGSRSRPLAPILTAACVCPQGSRR (in isoform
 4).
 FT /FTId=VSP_050513.
 FT Missing (in isoform 4).
 FT /FTId=VSP_050514.
 FT Missing (in Ref. 2; BAC11365).
 FT CONFLICT 164 202 A -> D (in Ref. 2; BAC11365).
 FT CONFLICT 285 285 A -> D (in Ref. 2; BAC11365).
 SQ SEQUENCE 462 AA; 48849 MW; CE33015917A9AA68 CRC64;
 Query Match 17.7%; Score 148.5; DB 1; Length 462;
 Best Local Similarity 42.0%; Pred. No. 3.7e-07;
 Matches 29; Conservative 9; Mismatches 26; Indels 5; Gaps 2;
 Qy 50 CYEGNGHFYRG---KASTDTMGRCPLPMSATVLOQTYHAHRSALQLGLGHKHYCRNPD 106
 Db 36 CFQVNGADYRGHGNRGRGAGRCPLFWQTOQ--QHSYSSADPHGRWGLGHAHFCRNP 93
 Qy 107 NRPRPWCYV 115
 Db 94 GDVQPCYV 102
 RESULT 39
 PLMN CANFA
 ID PLMN CANFA STANDARD; PRT; 333 AA.
 AC P80039;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PLG.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Plasma;
 RX MEDLINE=90175323; PubMed=2626424;
 RA Schaller J., Straub C., Kaempfer U., Rickli B.E.;
 RI "Complete amino acid sequence of canine miniplasminogen.";
 RL Protein Seq. Data Anal. 2:445-450(1989).
 CC -!- FUNCTION: Plasmn dissolves the fibrin of blood clots and acts as
 a proteolytic factor in a variety of other processes including
 embryonic development, tissue remodeling, tumor invasion, and
 inflammation; in ovulation it weakens the walls of the Graafian
 follicle. It activates the urokinase-type plasminogen activator,
 collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 Willebrand factor.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 products.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 activators, both plasminogen and its activator being bound to
 fibrin. Activated with urokinase and high concentrations of
 streptokinase.
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.

C -1- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 C -1- SIMILARITY: Contains at least 1 kringle domain.
 C HSP, P00747; SHPG.
 D MEROPS; S01.233; -.
 D InterPro; IPR009003; Cys Ser_1trypsin.
 D InterPro; IPR000001; Kringle.
 D InterPro; IPR001254; Peptidase S1.
 D InterPro; IPR001314; Peptidase_S1A.
 D InterPro; IPR003966; Peptidase_S1A_pr.
 D Pfam; PF00051; kringle; 1.
 D Pfam; PF00089; trypsin; 1.
 D PRINTS; PR00722; CHYNOTRYPIN.
 D PRINTS; PR00018; KRINGLE.
 D PRINTS; PR01505; PROTHROMBIN.
 D ProDom; PD000395; Kringle; 1.
 D SMART; SM00130; KR; 1.
 D SMART; SM00026; Tryp_SPc; 1.
 D PROSITE; PS00021; KRINGLE_1; 1.
 D PROSITE; PS00070; KRINGLE_2; 1.
 D PROSITE; PS00240; TRYPsin_DOM; 1.
 D PROSITE; PS00134; TRYPsin_HIS; 1.
 D PROSITE; PS00135; TRYPsin_SER; 1.
 K Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 K Tissue remodeling; blood coagulation; Kringle; Zymogen.
 F NON_TER 1
 F CHAIN 1
 F CHAIN 103
 F CHAIN 104
 F DOMAIN 4
 F DOMAIN 104
 F DISULFID 4
 F DISULFID 25
 F DISULFID 34
 F DISULFID 90
 F DISULFID 100
 F DISULFID 130
 F DISULFID 222
 F DISULFID 252
 F DISULFID 252
 F DISULFID 252
 F ACT_SITE 145
 F ACT_SITE 145
 F ACT_SITE 188
 F ACT_SITE 283
 F SITE 152
 F SITE 186
 F SITE 264
 F SITE 264
 F SITE 277
 F SITE 277
 F SEQUENCE 333 AA; 36678 MW; C8C0271B6C6AC8D4 CRC64;
 Very Match 17.7%; Score 148; DB 1; Length 333;
 est Local Similarity 38.8%; Pred. No. 3e-07;
 atches 40; Conservative 7; Mismatches 40; Indels 16; Gaps 6;
 Q 50 CYEGNGHYFGKASTDTWGRPCLPWNSATVLOQTHAHR----SDALQGLGKKNYCRNP 105
 D 4 CMFGNGKGYRGKATVNGIPQEWAA-----QEPHRSIFTPETNPQAGLEK-NYCRNP 57
 Q 106 D-NRRPRWCYOVGLKPLVQECMWDCA----DGKKPSPPPE 143
 D 58 DGDVNGPWCYT-MNQRKLFYDCVPCQVSTSFDCGKQVPEPK 99
 R JLT 40
 R 2 HUMAN
 I 1 HUMAN
 I 2 HUMAN
 A Q01974; Q9HAY7; Q9HB61;
 D 16-OCT-2001 (Rel. 40, Created)
 D 16-OCT-2001 (Rel. 40, Last sequence update)
 D 15-MAR-2004 (Rel. 43, Last annotation update)
 D Tyrosine-protein kinase transmembrane receptor ROR2 precursor
 D (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).
 G ROR2 OR NTRK2.
 C Homo sapiens (Human).
 C Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93100347; PubMed=1334494;
 RA Maslakowski P., Carroll R.D.;
 RT "A novel family of cell surface receptors with tyrosine kinase-like domain.";
 RL J. Biol. Chem. 267:26181-26190(1992).
 RN [2]
 RP SEQUENCE OF 34-943 FROM N.A., AND VARIANT ILE-819.
 RX MEDLINE=20164326; PubMed=10700182;
 RA Oldridge M., Fortuna A.M., Maringa M., Propping P., Mansour S.,
 RA Pollitt C., DeChiara T.M., Kimble R.B., Valenzuela D.M.,
 RA Yancopoulos G.D., Wilkie A.O.M.;
 RT "Dominant mutations in ROR2, encoding an orphan receptor tyrosine kinase, cause brachydactyly type B.";
 RL Nat. Genet. 24:275-278(2000).
 RN [3]
 RP SEQUENCE OF 34-574 FROM N.A., AND VARIANT THR-245.
 RX MEDLINE=20442029; PubMed=10986040;
 RA Schwabe G.C., Tinschert S., Buschow C., Meinecke P., Wolff G.,
 RA Gillespie-Kaebach G., Oldridge M., Wilkie A.O.M., Koemec R.,
 RA Mundlos S.;
 RT "Distinct mutations in the receptor tyrosine kinase gene ROR2 cause brachydactyly type B.";
 RL Am. J. Hum. Genet. 67:822-831(2000).
 RN [4]
 RP VARIANTS RRS CYS-184; TRP-189; TRP-366 AND LYS-620.
 RX MEDLINE=20392394; PubMed=10932186;
 RA Azal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,
 RA Teres-Ferreira E., Teyssiez B., Murday V.A., Patton M.A.,
 RA Wilkie A.O.M., Jeffery S.;
 RT "Recessive Robinow syndrome, allelic to dominant brachydactyly type B, is caused by mutation of ROR2.";
 RL Nat. Genet. 25:419-422(2000).
 RN [5]
 RP VARIANT RRS TYR-182
 RX MEDLINE=20392385; PubMed=10932187;
 RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
 RA Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;
 RL Nat. Genet. 26:383-383(2000).
 CC -1- FUNCTION: Tyrosine-protein kinase receptor which may be involved in the early formation of the chondrocytes. It seems to be required for cartilage and growth plate development.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DEVELOPMENTAL STAGE: Expressed at high levels during early embryonic development. The expression levels drop strongly around day 16 and there are only very low levels in adult tissues.
 CC -1- DISEASE: Defects in ROR2 are a cause of brachydactyly type B1 (BDB1) [MIM:113000]. BDB1 is an autosomal dominant skeletal disorder characterized by hypoplasia/aplasia of distal phalanges and nails. In BDB1 the middle phalanges are short but in addition the terminal phalanges are rudimentary or absent. Both fingers and toes are affected. The thumbs and big toes are usually deformed.
 CC -1- DISEASE: Defects in ROR2 are a cause of recessive Robinow syndrome (RRS) [MIM:268110]. RRS is an autosomal disorder characterized by skeletal dysplasia with generalized limb bone shortening, segmental defects of the spine, brachydactyly and a dysmorphic facial appearance.
 CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR subfamily.
 CC -1- SIMILARITY: Contains 1 frizzled (FZ) domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC CC -1- SIMILARITY: Contains 1 kringle domain.
 CC CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
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 CC CC or send an email to license@isb-sib.ch).
 CC CC -----
 CC DR EMBL; N97639; AAG60276.1; -
 CC DR EMBL; AF294796; AAG01184.2; JOINED.
 CC DR EMBL; AF254747; AAG01184.2; JOINED.
 CC DR EMBL; AF254748; AAG01184.2; JOINED.
 CC DR EMBL; AF254749; AAG01184.2; JOINED.
 CC DR EMBL; AF254750; AAG01184.2; JOINED.
 CC DR EMBL; AF254751; AAG01184.2; JOINED.
 CC DR EMBL; AF254752; AAG01184.2; JOINED.
 CC DR EMBL; AF254753; AAG01184.2; JOINED.
 CC DR EMBL; AF279762; AAG33132.1; -
 CC DR EMBL; AF279755; AAG33132.1; JOINED.
 CC DR EMBL; AF279756; AAG33132.1; JOINED.
 CC DR EMBL; AF279757; AAG33132.1; JOINED.
 CC DR EMBL; AF279758; AAG33132.1; JOINED.
 CC DR EMBL; AF279759; AAG33132.1; JOINED.
 CC DR EMBL; AF279760; AAG33132.1; JOINED.
 CC DR EMBL; AF279761; AAG33132.1; JOINED.
 CC DR PIR; B45082; B45082.
 CC DR HSP; P00747; 1KRN.
 CC DR Genew; HGNC:10257; ROR2.
 CC DR MIM; 602337; -
 CC DR MIM; 113000; -
 CC DR MIM; 268310; -
 CC DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. .; TAS.
 CC DR GO; GO:0007275; F:development; TAS.
 CC DR GO; GO:0007165; P:signal transduction; TAS.
 CC DR InterPro; IPR000024; Fz-domain.
 CC DR InterPro; IPR007110; Ig-like.
 CC DR InterPro; IPR003598; Ig_c2.
 CC DR InterPro; IPR000001; Kringle.
 CC DR InterPro; IPR000719; Prot_kinase.
 CC DR InterPro; IPR01245; Tyr_kinase.
 CC DR InterPro; IPR008266; Tyr_kinase_AS.
 CC DR Pfam; PF01392; Fz; 1.
 CC DR Pfam; PF000470; Ig; 1.
 CC DR Pfam; PF000514; kringle; 1.
 CC DR Pfam; PF00069; pkinase; 1.
 CC DR PRINTS; PR00018; KRINGLE.
 CC DR PRINTS; PR00109; TYRKINASE.
 CC DR ProDom; PD000395; Kringle; 1.
 CC DR ProDom; PD000001; Prot_kinase; 1.
 CC DR SMART; SM00408; IGc2; 1.
 CC DR SMART; SM00130; KG; 1.
 CC DR SMART; SM00219; TyrKc; 1.
 CC DR PROSITE; PS00038; FZ; 1.
 CC DR PROSITE; PS00835; IG LIKE; 1.
 CC DR PROSITE; PS00021; KRINGLE 1; 1.
 CC DR PROSITE; PS00070; KRINGLE 2; 1.
 CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR Transferrase; Tyrosine-protein kinase; ATP-binding; Receptor;
 CC DR Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
 CC DR Immunoglobulin domain; Developmental protein; Polymorphism;
 CC DR Disease mutation.
 CC DR SIGNAL 1 33 POTENTIAL,
 CC DR CHAIN 34 943 TYROSINE-PROTEIN KINASE TRANSMEMBRANE
 CC DR RECEPTOR ROR2.
 CC DR DOMAIN 34 403 EXTRACELLULAR (POTENTIAL).
 CC DR TRANSMEM 404 424 POTENTIAL.
 CC DR DOMAIN 425 943 CYTOPLASMIC (POTENTIAL).
 CC DR DOMAIN 55 145 IG-LIKE C2-TYPE.

FT DOMAIN 169 303 FZ.
 FT DOMAIN 316 394 KRINGLE.
 FT DOMAIN 473 746 PROTEIN KINASE.
 FT DOMAIN 753 782 SER/THR-RICH.
 FT DOMAIN 784 857 PRO-RICH.
 FT DOMAIN 859 882 SER/THR-RICH.
 FT NP BIND 479 487 ATP (BY SIMILARITY).
 FT BINDING 507 507 ATP (BY SIMILARITY).
 FT ACT_SITE 615 615 BY SIMILARITY.
 FT MOD_RES 646 646 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT DISULFID 83 135 BY SIMILARITY.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 318 318 C -> Y (in RES).
 FT VARIANT 182 182 /FTID=VAR_010911.
 FT VARIANT 184 184 R -> C (in RES).
 FT VARIANT 189 189 /FTID=VAR_010768.
 FT VARIANT 245 245 /FTID=VAR_010769.
 FT VARIANT 366 366 A -> T.
 FT VARIANT 620 620 R -> W (in RES).
 FT VARIANT 620 620 /FTID=VAR_010770.
 FT VARIANT 819 819 N -> K (in RES).
 FT VARIANT 819 819 /FTID=VAR_010771.
 FT VARIANT 819 819 V -> I.
 FT SEQUENCE 943 AA; 104726 MW; DBAC1E4622B5ECA0 CRC64;
 Query Match 17.7%; Score 148; DB 1; Length 943;
 Best Local Similarity 34.3%; Pred. No. 8.5e-07;
 Matches 37; Conservative 12; Mismatches 41; Indels 18; Gaps 6;
 Qy 32 NC-----PKKFGQHCIEDKSKTCEGNGHFYRGKASTDTMGRPCLPWNSTVLQQTYYH 85
 Db 299 NCMRIGIPAEPLGRYH-----QCNGSGMDYRGFTASTTKSGHQCPW--ALQHPHSHH 349
 Qy 86 AHRSDALQLGLGKHNCRPNDRR--PWCYVQVGLKPLVQECWHDCA 132
 Db 350 LSSTDPELG-GGHAYCRNPGQMEGWCFTQ-NKVMELCDVPSCS 395
 RESULT 41
 ROR2 MOUSE
 ID "ROR2_MOUSE STANDARD; PRT; 944 AA.
 AC Q9Z138;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor
 DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2)
 DE (mROR2).
 GN ROR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99248426; PubMed=10231392;
 RA Oishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J.,
 RA Hata T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.,
 RT "Spatio-temporally regulated expression of receptor tyrosine kinases,
 RT mRor1, mRor2, during mouse development: implications in development
 RT and function of the nervous system.";
 RL Genes Cells 4:41-56(1999).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=20164325; PubMed=10700181;
 RA DeChiara T.M., Kimble R.B., Poueymiro W.T., Rojas J., Masiakowski P.,
 RA Valenzuela D.M., Vancopoulos G.D.;
 RT "Ror2, encoding a receptor-like tyrosine kinase, is required for

cartilage and growth plate development." ;

Rat. Genet. 24:271-274 (2000).

-I- FUNCTION: Tyrosine-protein kinase receptor which may be involved in the early formation of the chondrocytes. It seems to be required for cartilage and growth plate development.

-I- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR subfamily.

-I- SIMILARITY: Contains 1 frizzled (FZ) domain.

-I- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

-I- SIMILARITY: Contains 1 kringle domain.

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ENBL; AB010384; BAA75481.1; ;

HSPG; P00747; SHPG.

MGD; MGI:1347521; Ror2.

GO; GO:0001501; P:skeletal development; IMP.

InterPro; IPR000024; Pz_domain.

InterPro; IPR007110; Ig-like.

InterPro; IPR003598; Ig_C2.

InterPro; IPR000001; Kringle.

InterPro; IPR000719; Prot_kinase.

InterPro; IPR001245; Tyr_kinase.

InterPro; IPR008266; Tyr_kinase_AS.

Pfam; PF01392; Fz; 1.

Pfam; PF00047; Ig; 1.

Pfam; PF00051; kringle; 1.

Pfam; PF00069; pkinase; 1.

PRINTS; PR00018; KRINGLE.

PRINTS; PR00109; TYRKINASE.

ProDom; PD000395; Kringle; 1.

ProDom; PD000001; Prot_kinase; 1.

SMART; SM00408; IGC2; 1.

SMART; SM00130; KR; 1.

SMART; SM00219; TYRK; 1.

PROSITE; PS50038; FZ; 1.

PROSITE; PS50835; IG LIKE; 1.

PROSITE; PS00021; KRINGLE 1; 1.

PROSITE; PS50070; KRINGLE 2; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

K0 Transferrase; Tyrosine-protein kinase; ATP-binding; Receptor;

K0 Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;

K0 Immunoglobulin domain; Developmental protein.

K SIGNAL 1 33

F CHAIN 34 944

DOMAIN 34 403

TRANSMEM 404 424

DOMAIN 425 944

DOMAIN 55 145

DOMAIN 169 303

DOMAIN 316 394

DOMAIN 473 746

DOMAIN 753 782

DOMAIN 784 857

DOMAIN 859 882

NP BIND 479 487

BLIND 507 507

ACT SITE 615 615

MOD_RES 646 646

DISULFID 83 135

CARBOHYD 70 170

EXTRACELLULAR (POTENTIAL) .

POTENTIAL.

CYTOPLASMIC (POTENTIAL) .

IG-LIKE C2-TYPE.

FZ.

KRINGLE.

PROTEIN KINASE.

SER/THR-RICH.

PRO-RICH.

SER/THR-RICH.

ATP (BY SIMILARITY) .

ATP (BY SIMILARITY) .

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY) .

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL) .

DR InterPro: IPR001314; Peptidase S1A.
 DR InterPro: IPR003966; Peptidase S1A_pr.
 DR Pfam: PF00051; Kringle; 4.
 DR Pfam: PF00024; PAN; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00018; KRINGLE.
 DR PRINTS: PR01505; PROTHROMBIN.
 DR ProDom: PD000395; Kringle; 4.
 DR SMART: SM00130; KR; 4.
 DR SMART: SM00473; PAN_Ap; 1.
 DR SMART: SM00020; TRYD_SPC; 1.
 DR PROSITE: PS00021; KRINGLE 1; 4.
 DR PROSITE: PS00070; KRINGLE 2; 4.
 DR PROSITE: PS0240; TRYPSIN_DOM; 1.
 DR Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 716
 FT DOMAIN 19 109 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.
 FT DOMAIN 110 186 PAP.
 FT DOMAIN 111 186 KRINGLE 1.
 FT DOMAIN 191 268 KRINGLE 2.
 FT DOMAIN 292 370 KRINGLE 3.
 FT DOMAIN 373 457 KRINGLE 4.
 FT DOMAIN 483 716 SERINE PROTEASE-LIKE.
 FT DISULFID 56 78 BY SIMILARITY.
 FT DISULFID 60 66 BY SIMILARITY.
 FT DISULFID 110 186 BY SIMILARITY.
 FT DISULFID 131 169 BY SIMILARITY.
 FT DISULFID 157 181 BY SIMILARITY.
 FT DISULFID 191 268 BY SIMILARITY.
 FT DISULFID 194 333 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 212 251 BY SIMILARITY.
 FT DISULFID 240 263 BY SIMILARITY.
 FT DISULFID 292 370 BY SIMILARITY.
 FT DISULFID 313 352 BY SIMILARITY.
 FT DISULFID 341 364 BY SIMILARITY.
 FT DISULFID 379 457 BY SIMILARITY.
 FT DISULFID 400 440 BY SIMILARITY.
 FT DISULFID 428 452 BY SIMILARITY.
 FT DISULFID 477 593 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 512 528 BY SIMILARITY.
 FT DISULFID 607 672 BY SIMILARITY.
 FT DISULFID 637 651 BY SIMILARITY.
 FT DISULFID 662 690 BY SIMILARITY.
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 19 19 P -> Q (IN GENOMIC SEQUENCE).
 SQ SEQUENCE 716 AA; 80588 MW; BBCE02EF85213ACC CRC64;
 Query Match 17.6%; Score 147.5; DB 1; Length 716;
 Best Local Similarity 36.5%; Pred. No. 7.3e-07;
 Matches 38; Conservative 11; Mismatches 34; Indels 21; Gaps 7;
 QY 50 CYEGNGHFYRGKASTDITMGRPCLPNSATVLOQTYHAHR-----SDALQLGLGKHNYCRN 104
 DB 379 CYHSGEQYRGVSKTRGVQCHWSSET-----PHKQPTPTSAQAGL-EANFCRN 430
 QY 105 PD-NRRPWCYVQVGLKP--LYQECWHDCAKCKPS--SPPEE 143
 DB 431 PGDSHGHPWCYT---LDPDILFDYCALORCDDDPSPSLDPPDQ 471
 RE UT 43
 KR MOUSE
 ID KRM2 MOUSE STANDARD; PRT; 461 AA.
 AC Q8K157;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kremen protein 2 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor 2).

GN KREMEN2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RC STRAIN=CS7BL/60;
 RX MEDLINE=22045977; PubMed=12050670;
 RA Mac B., Wu W., Davidson G., Marhold J., Li M., Mechler B.M.,
 RA Delius H., Hoppe D., Stannek P., Walter C., Glinka A., Niehrs C.;
 RT "Kremen proteins are Dickkopf receptors that regulate Wnt/beta-catenin
 signalling";
 EL Nature 417:664-667(2002).
 CC -!- FUNCTION: Receptor for dickkopf protein. Cooperates with Dickkopf
 CC to block Wnt/beta-catenin signaling. Forms a ternary complex with
 CC Dkk1 and LRP6 and induces rapid endocytosis and removal of the Wnt
 CC receptor LRP6 from the plasma membrane.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -!- SIMILARITY: Contains 1 CUB domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC -!- SIMILARITY: Contains 1 WSC domain.
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 DR EMBL; AJ457192; CAD29805.1; -.
 DR MGD; MGI:1920266; Kremen2.
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR002889; WSC.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00051; Kringle; 1.
 DR Pfam: PF01822; WSC; 1.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00321; WSC; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS00021; KRINGLE 1; 1.
 DR PROSITE: PS00070; KRINGLE 2; 1.
 KW Wnt signaling pathway; Glycoprotein; Kringle; Signal; Transmembrane.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 461 KREMEN PROTEIN 2.
 FT DOMAIN 25 363 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 364 366 POTENTIAL.
 FT DOMAIN 387 461 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 118 KRINGLE.
 FT DOMAIN 120 214 WSC.
 FT DOMAIN 218 325 CUB.
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 243 243 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 461 AA; 49170 MW; 6D58C4A2858E09DA CRC64;
 Query Match 17.5%; Score 146.5; DB 1; Length 461;
 Best Local Similarity 42.0%; Pred. No. 5.8e-07;
 Matches 29; Conservative 8; Mismatches 27; Indels 5; Gaps 2;
 QY 50 CYEGNGHFYRGK---ASTDTMGRPCLPNSATVLOQTYHAHRSDALQLGLGKHNYCRNP 106
 DB 35 CFQVNGADYRGHONYTGPGRGACRCLFWDQIQ--QHSYSSASDPQGRWGLGAGHFCRNP 92
 QY 107 NRRRPWCYV 115
 DB 93 GDVQPCYV 101

DR	ENBL;	D90330;	BAA14348.1;	JOINED.
DR	ENBL;	D90331;	BAA14348.1;	JOINED.
DR	ENBL;	D90332;	BAA14348.1;	JOINED.
DR	ENBL;	D90333;	BAA14348.1;	JOINED.
DR	ENBL;	M29145;	AAA52650.1;	-
DR	ENBL;	M60718;	AAB26648.1;	-
DR	ENBL;	X16323;	CAR34237.1;	-
DR	ENBL;	M73239;	AAA64239.1;	-
DR	ENBL;	M73240;	AAA64297.1;	-
DR	ENBL;	AY246560;	AAO61091.1;	--
DR	ENBL;	AC004960;	AAC71655.1;	--
DR	ENBL;	M75983;	AAG53460.1;	-
DR	ENBL;	M75972;	AAG53460.1;	JOINED.
DR	ENBL;	M75973;	AAG53460.1;	JOINED.
DR	ENBL;	M75974;	AAG53460.1;	JOINED.
DR	ENBL;	M75975;	AAG53460.1;	JOINED.
DR	ENBL;	M75976;	AAG53460.1;	JOINED.
DR	ENBL;	M75977;	AAG53460.1;	JOINED.
DR	ENBL;	M75978;	AAG53460.1;	JOINED.
DR	ENBL;	M75979;	AAG53460.1;	JOINED.
DR	ENBL;	M75980;	AAG53460.1;	JOINED.
DR	ENBL;	M75981;	AAG53460.1;	JOINED.
DR	ENBL;	M75982;	AAG53460.1;	JOINED.
DR	PIR;	JH0579;	JH0579.	
DR	PDB;	2HGf;	24-JUN-98.	
DR	PDB;	1BHT;	18-NOV-98.	
DR	PDB;	1NK1;	29-DEC-99.	
DR	MEROPS;	SOL.976;	--	
DR	GlycoSuiteDB;	P14210;	--	
DR	Genew;	HGNC:4893;	HGF.	
DR	MIM;	142409;	--	
DR	GO;	GO:0008083;	P.growth factor activity; NAS.	
DR	GO;	GO:0007067;	P.mitosis; NAS.	
DR	InterPro;	IPT009003;	Cys_Ser_trypsin.	
DR	InterPro;	IPT000001;	Kringie.	
DR	InterPro;	IPT003014;	PAN.	
DR	InterPro;	IPT003609;	Pan app.	
DR	InterPro;	IPT001254;	Peptidase S1.	
DR	InterPro;	IPT001314;	Peptidase_S1A.	
DR	Pfam;	PF00051;	kringle; 4.	
DR	Pfam;	PF00024;	PAN; 1.	
DR	Pfam;	PF00089;	trypsin; 1.	
DR	PRINTS;	PR00722;	CHYMOTRYPSIN.	
DR	PRINTS;	PR00018;	KRINGLE.	
DR	ProDom;	PD000395;	Kringie; 4.	
DR	SMART;	SM00130;	KR; 4.	
DR	SMART;	SM00473;	PAN AP; 1.	
DR	SMART;	SM00020;	TTPA_SPC; 1.	
DR	PROSITE;	PS00021;	KRINGLE_1; 4.	
DR	PROSITE;	PS00070;	KRINGLE_2; 4.	
DR	PROSITE;	PS0340;	TRYPSIN_DOM; 1.	
DR	KW	Growth factor; Kringie; Glycoprotein; Serine protease homolog; Repeat;		
DR	KW	Signal; 3D-structure; Polymorphism; Pyrrolidone carboxylic acid.		
FT	SIGNAL	1	31	
FT	CHAIN	32	434	
FT	CHAIN	435	728	
FT	MOD_RES	32	32	
FT	DOMAIN	32	127	
(Try Match 17.3%; Score 144.5; DB 1; Length 728;				
Local Similarity 29.6%; Pred. No. 1.4e-06;				
Matches 45; Conservative 13; Mismatches 69; Indels 25; Gaps 10;				
QY	2	NELHQVSPNCDCL--LNGTGVSNKYFNHW-----NCKPKFGG--HCEIDKSKTYCYE 52		
Db	335	HEHDMTPEFKKDLRENYC-RNPDGSESPWCFTDPNIRAVGCSIPNCDMSHGQDCYR 393		
QY	53	GNGHFYRGKASDTDMGRCLPWNSATVLQQTYYAH---RSDALQLGLGKHNYCRNP-DNR 108		
Db	394	GNKNYMGNLSTRLSLTSMDKN---MEDLHHFWEPDASKU----NENYCRNPDDDA 447		
QY	109	RPPWCIVQGLKLPLV--QECMVHDCADGKKPS 138		

[illegible]

DISULFID 75 85 BY SIMILARITY.
 PT DISULFID 488 607 INTERCHAIN (BY SIMILARITY).
 PT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 656 656 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 728 AA; 82905 MW; 3E0BF1F96ADCEDF CRC64;
 Query Match 17.0%; Score 142; DB 1; Length 728;
 Best Local Similarity 26.8%; Pred. No. 2,5e-06;
 Matches 45; Conservative 11; Mismatches 62; Indels 38; Gaps 11;
 QY 5 HQV-FSNDC--LNGGTCVNKYNFNIHWC-----NCPKFGQGHCEIDKSK 48
 DB 338 HDITENFKDLRENYC-RNPDGAEPCWFTDPNIRVGYSQIPK-----CDVSSGQ 390
 QY 49 TCVEGNHGYRCKASTDTMGRCLPNSATVLQOYHAH---RSDALQLGLGKNYCRNP 105
 DB 391 DCYRGNKYNMGLSKTRSGLTCSWDRN---MEDLHRHIFWEPDASKL---TKNYCRNP 444
 QY 106 -DNRERPWCYQVGLKPLV--OECMVHDCADGKPS 138
 DB 445 DDDAGHPWCYTG---NPLVPWDYCPISRCGGDTTPT 477
 RE PETMA
 ID PLMN PETMA STANDARD; PRT; 325 AA.
 AC P33574;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragments).
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE
 RA Affolter M., Schaller J., Rickli E.E.;
 RT Isolation, characterization and partial amino acid sequence of
 RL lamprey plasminogen.;
 RL Protein Seq. Data Anal. 5:207-211(1993).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion,
 CC and inflammation.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 CC -!- SIMILARITY: Contains at least 2 kringle domains.
 DR PIR; S33879; S33879.
 DR HSP; P00747; SHPG.
 DR MEROPS; S01.233;
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE 1; 2.
 DR PROSITE; PS00070; KRINGLE 2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE; PS00135; TRYPSIN_SSR; PARTIAL.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
 FT NON_CONS 15 16
 FT NON_CONS 34 35
 FT NON_CONS 44 45
 FT NON_CONS 76 77

PT NON_CONS 111 112
 PT NON_CONS 138 139
 PT NON_CONS 158 159
 FT NON_CONS 178 179
 PT NON_CONS 216 217
 PT NON_CONS 236 237
 PT NON_CONS 267 268
 FT NON_CONS 282 283
 FT NON_CONS 295 296
 FT NON_CONS 307 308
 FT NON_CONS 315 316
 FT NON_TER 325 325
 SQ SEQUENCE 325 AA; 35194 MW; 1B5F0B539AC6ED3C CRC64;
 Query Match 16.2%; Score 136; DB 1; Length 325;
 Best Local Similarity 30.7%; Pred. No. 4,3e-06;
 Matches 31; Conservative 7; Mismatches 41; Indels 22; Gaps 3;
 QY 34 PKFGQGHCEIDKSKTCYEGNGHFGYRKGASTDTMGRCLPNSATVLQOYHAHSDALQ 93
 DB 71 POSFAG-----LTACVKGTEGVRGTAALTVSGKACQAWASQT-----PDVYS 115
 QY 94 LGLGKNYCRNPDRRPPWCYQVGLKPLVQECMVHDCADG 134
 DB 116 CQGLVSNYCRNPDGKLPWCYT-----TEYCNVPSCTGG 149
 RESULT 48
 THRE MOUSE
 ID THRE MOUSE STANDARD; PRT; 618 AA.
 AC P19221;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 DE F2 OR CP2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Liver;
 RX MEDLINE=9102551; PubMed=222810;
 RA Frieren Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
 RA Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
 RT "Characterization of the cDNA coding for mouse prothrombin and
 RT localization of the gene on mouse chromosome 2.";
 RL DNA Cell Biol. 9:487-498(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Suetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schurch A., Schein J.E., Jones S.D.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[3] SEQUENCE OF 384-618 FROM N.A.
TISSUE=Liver;
MEDLINE=92212913; PubMed=1557383;
Banfield D.K., Macgillivray R.R.;
"Partial characterization of vertebrate prothrombin cDNAs:
amplification and sequence analysis of the B chain of thrombin from
nine different species.";
Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783(1992).
C -!- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
converts fibrinogen to fibrin and activates factors V, VII, VIII,
XIII, and, in complex with thrombomodulin, protein C.
C -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
fibrinogen to fibrin and releases fibrinopeptide A and B.
C -!- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
OF PROTHROMBIN TO THROMBIN.
C -!- MISCELLANEOUS: Prothrombin is activated on the surface of a
phospholipid membrane that binds the amino end of prothrombin and
factors Va and Xa in Ca-dependent interactions; factor Xa removes
the activation peptide and cleaves the remaining part into light
and heavy chains. The activation process starts slowly because
factor V itself has to be activated by the initial, small amounts
of thrombin.
C -!- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
fragment (fragment 1) of the prothrombin, prior to its activation
by factor Xa.
C -!- SIMILARITY: Belongs to peptidase family S1.
C -!- SIMILARITY: Contains 2 kringle domains.
C
C This SWISS-PROT entry is copyright. It is produced through a collaboration
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the European Bioinformatics Institute. There are no restrictions on its
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or send an email to license@sib-sib.ch).
C
C EMBL: X52308; CAA36548.1; -
C EMBL: BC013662; AAH13662.1; -
C EMBL: M81394; AAA40435.1; -
C PIR: A35827; A35827.
C HSP: P00734; I87X.
C MEROPS: S01.217; -
C InterPro: IPR009003; Cys_Ser_trypsin.
C InterPro: IPR002383; GLA_blood.
C InterPro: IPR000001; Kringle.
C InterPro: IPR001254; Peptidase_S1.
C InterPro: IPR001314; Peptidase_S1A.
C InterPro: IPR003966; Peptidase_S1A_pr.
C InterPro: IPR000294; VitK_dep_GLA.
C Pfam: PF00594; gla; 1.
C Pfam: PF00051; kringle; 2.
C Pfam: PF00089; trypsin; 1.
C PRINTS: P00722; CHYMOTRYPSIN.
C PRINTS: P00001; GLABLOOD.
C PRINTS: P00018; KRINGLE.
C PRINTS: P01505; PROTHROMBIN.
C ProDom: PD000395; Kringle; 2.
C SMART: SM00069; GLA; 1.
C SMART: SM00130; KR; 2.
C SMART: SM00020; TRYPSIN; 1.
C PROSITE: PS00011; GLI_CARBOXYLATION; 1.
C PROSITE: PS00021; KRINGLE_1; 2.
C PROSITE: PS00070; KRINGLE_2; 2.
C PROSITE: PS00240; TRYPSIN_DOM; 1.
C PROSITE: PS00134; TRYPSIN_HIS; 1.
C PROSITE: PS00135; TRYPSIN_SER; 1.
C Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;

KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolyase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 618 PROTHROMBIN
FT PEPTIDE 44 200 ACTIVATION PEPTIDE (FRAGMENT 1).
FT PEPTIDE 321 324 ACTIVATION PEPTIDE (FRAGMENT 2).
FT CHAIN 305 360 THROMBIN LIGHT CHAIN (A).
FT CHAIN 361 618 THROMBIN HEAVY CHAIN (B).
FT DOMAIN 109 187 KRINGLE 1.
FT DOMAIN 215 292 KRINGLE 2.
FT DOMAIN 361 618 SERINE PROTEASE.
FT SITE 200 201 CLEAVAGE (BY THROMBIN).
FT SITE 324 325 CLEAVAGE (BY FACTOR XA).
FT SITE 360 361 CLEAVAGE (BY FACTOR XA).
FT ACT_SITE 403 403 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 459 459 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 565 565 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT MOD_RES 50 50 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 51 51 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 58 58 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 60 60 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 63 63 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 64 64 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 69 69 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 70 70 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 73 73 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 76 76 GAMMA-CARBOXYGLUTAMIC ACID.
FT DISULFID 61 66 BY SIMILARITY.
FT DISULFID 91 104 BY SIMILARITY.
FT DISULFID 109 187 BY SIMILARITY.
FT DISULFID 130 170 BY SIMILARITY.
FT DISULFID 158 182 BY SIMILARITY.
FT DISULFID 215 293 BY SIMILARITY.
FT DISULFID 236 276 BY SIMILARITY.
FT DISULFID 264 288 BY SIMILARITY.
FT DISULFID 333 479 INTERCHAIN (BY SIMILARITY).
FT DISULFID 388 404 BY SIMILARITY.
FT DISULFID 533 547 BY SIMILARITY.
FT DISULFID 561 591 BY SIMILARITY.
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. .).
FT CARBOHYD 413 413 N-LINKED (GLCNAC. .).
FT CARBOHYD 553 553 N-LINKED (GLCNAC. .).
SQ SEQUENCE 618 AA; 70268 MW; B89F719AAPD601E0 CRC64;
Query Match 15.0%; Score 125.5; DB 1; Length 618;
Best Local Similarity 31.8%; Pred. No. 8.6e-05;
Matches 27; Conservative 13; Mismatches 40; Indels 5; Gaps 3;
Qy 50 CYEGNGHFYRGKASTDTMGPCPLPWSATVLTQTYHAHRSALQLGLGKHNYCRNPD-NR 108
Db 215 CLTGERGLYQGNLAVTTLGSPCLPWSLPAKTLISKYQDFPEVKL---VENFCRNFWDDE 271
Qy 109 RRPWCYVQGLKPLVQECMVHDCAD 133
Db 272 EGAWCYV-AGQPGDFEYCNLYCEE 295
RESULT 49
ID PLMN_SHEEP STANDARD; PRT; 343 AA.
AC P61286;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragment).
GN PLG.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;

RP SEQUENCE.
 RA MEDLINE=93149995; PubMed=1492092;
 RT Schaller J., Straub C., Kampfer U., Rickli E.B.;
 RL "Complete amino acid sequence of ovine miniplasminogen.";
 CC Protein Seq. Data Anal. 5:21-25(1992).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 CC -!- SIMILARITY: Contains at least 2 kringle domains.
 DR FIR; B61545.
 DR HSP; P00747; SHPG.
 DR MEROPS; S01.233; -.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pr.
 DR Pfam; P00051; kringle; 1.
 DR Pfam; P00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PSS0070; KRINGLE 2; 1.
 DR PROSITE; PSS0240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 DR Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
 FT NON_TER 1
 FT DOMAIN <1 140 HEAVY CHAIN A.
 FT DOMAIN 141 >343 LIGHT CHAIN A.
 FT DOMAIN <1 17 KRINGLE 4.
 FT DOMAIN 41 120 KRINGLE 5.
 FT DOMAIN 114 341 SERINE PROTEASE.
 FT ACT_SITE 181 181 CHARGE RELAY SYSTEM.
 FT ACT_SITE 224 224 CHARGE RELAY SYSTEM.
 FT ACT_SITE 319 319 CHARGE RELAY SYSTEM.
 FT NON_TER 343 343
 SQ SEQUENCE 343 AA; 37662 MW; 8DFEBA92D596EE0 CRC64;
 Local Match 14.9%; Score 124.5; DB 1; Length 343;
 Local Similarity 35.3%; Pred. No. 5.9e-05;
 Cons 36; Conservative 8; Mismatches 43; Indels 15; Gaps 6;
 50 CYEGNGHYFGKASTDTMGKPCLPWNSATVLQTYHAH----RSDALQLGLGKHYCRNP 105
 15 CMLGIGKGYGKATTVAGVPQEWAA----QEPHGHGIFTPETNPRAGLEK-NYCRNP 68
 106 D-NRRPWCYVGLPLVQECMVHCA----DGKPPSSPPE 143
 69 GDGVNGWCYV-TNPKRLFDYCDIPQCESSFGCGKPKVFPKX 109
 JT 50

THRB HUMAN
 ID THRB_HUMAN STANDARD; PRT; 622 AA.
 AC P00734;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
 GN F2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88077877; PubMed=28257773;
 RA Degen S.J.F., Davie E.W.;
 RT "Nucleotide sequence of the gene for human prothrombin.";
 RL Biochemistry 26:6165-6177(1987).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT MET-165.
 RX Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Ozuna M., Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 8-622 FROM N.A.
 RX MEDLINE=83231469; PubMed=6305407;
 RA Degen S.J.F., McGillivray R.T.A., Davie E.W.;
 RT "Characterization of the complementary deoxyribonucleic acid and gene
 RL Biochemistry 22:2087-2097(1983).
 RN [4]
 RP SEQUENCE OF 44-314.
 RX MEDLINE=77193964; PubMed=266717;
 RA Walz D.A., Hewett-Emmett D., Seegers W.H.;
 RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
 RN [5]
 RP SEQUENCE OF 315-622.
 RX MEDLINE=77207112; PubMed=873923;
 RA Buckowski R.J., Ellison J., Downing M.R., Mann K.G.;
 RT "Primary structure of human prothrombin 2 and alpha-thrombin.";
 RL J. Biol. Chem. 252:4942-4957(1977).
 RN [6]
 RP PROCESSING.
 RX MEDLINE=87008532; PubMed=3759958;
 RA Rabiet M.J., Blashill A., Furie B., Furie B.C.;
 RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
 RL J. Biol. Chem. 261:13210-13215(1986).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=90059942; PubMed=2583108;
 RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
 RT "The refined 1.9 A crystal structure of human alpha-thrombin:
 RT interaction with D-Phe-Pro-Arg chloromethylketone and significance of
 RT the Tyr-Pro-Pro-Trp insertion segment.";
 RL EMBO J. 8:3467-3475(1989).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=90327074; PubMed=2374926;
 RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
 RA Roitsch C., Fenton J.W. II;
 RT "The structure of a complex of recombinant hirudin and human alpha-
 RT thrombin.";
 RL Science 249:277-280(1990).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94350942; PubMed=8071320;
 RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;
 RT "Crystallographic structure of human gamma-thrombin.";
 RL J. Biol. Chem. 269:22000-22006(1994).
 RN [10]

R R X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
R MEDLINE=97357286; PubMed=9214615;
R van de Locht A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
R Esmen C.T., Stubbs M.T.;
R "The thrombin E192Q-BPTI complex reveals gross structural
R rearrangements: Implications for the interaction with antithrombin
R and thrombomodulin.";
R EMBO J. 16:2977-2984(1997).
R [11]
R X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
R MEDLINE=99162521; PubMed=10051558;
R Quinto E.R., Caccia S., Rose T., Fueterer K., Waksman G., di Cera E.;
R "Unexpected crucial role of residue 225 in serine proteases.";
R Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).
R [12]
R VARIANT DYSPROTHROMBINEMIA CYS-314.
R MEDLINE=87033739; PubMed=3771562;
R Rabiet M.-J., Furlie B.C., Furlie B.;
R "Molecular defect of prothrombin Barcelona. Substitution of cysteine
R for arginine at residue 273.";
R J. Biol. Chem. 261:15045-15048(1986).
R [13]
R VARIANT DYSPROTHROMBINEMIA ALA-509.
R MEDLINE=95313001; PubMed=7792730;
R Degen S.J.F., McDowell S.A., Sparks L.M., Scharrer I.;
R "Prothrombin: Frankfurt: a dysfunctional prothrombin characterized by
R substitution of Glu-466 by Ala.";
R Thromb. Haemost. 73:203-209(1995).
R [14]
R VARIANTS DYSPROTHROMBINEMIA THR-380 AND HIS-431.
R MEDLINE=93043342; PubMed=1421398;
R Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,
R Yamaguchi K.;
R "Prothrombin-Himi: a compound heterozygote for two dysfunctional
R prothrombin molecules (Met-337-->Thr and Arg-388-->His).";
R Blood 80:2275-2280(1992).
R [15]
R VARIANT DYSPROTHROMBINEMIA HIS-314.
R MEDLINE=95169898; PubMed=7865694;
R James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
R "Prothrombin: Padua I: incomplete activation due to an amino acid
R substitution at a factor Xa cleavage site.";
R Blood Coagul. Fibrinolysis 5:841-844(1994).
R [16]
R VARIANT DYSPROTHROMBINEMIA CYS-425.
R MEDLINE=89207504; PubMed=3242619;
R Henriksen R.A., Mann K.G.;
R "Identification of the primary structural defect in the dyschrobin
R thrombin Quick I: substitution of cysteine for arginine-382.";
R Biochemistry 27:9160-9165(1988).
R [17]
R VARIANT DYSPROTHROMBINEMIA VAL-601.
R MEDLINE=89247398; PubMed=2719946;
R Henriksen R.A., Mann K.G.;
R "Substitution of valine for glycine-558 in the congenital dyschrobin
R thrombin Quick II alters primary substrate specificity.";
R Biochemistry 28:2078-2082(1989).
R [18]
R VARIANT DYSPROTHROMBINEMIA ALA-509.
R MEDLINE=92378975; PubMed=1354985;
R Miyata T., Aruga R., Umayama H., Bezeaud A., Guillin M.-C.,
R Iwanaga S.;
R "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
R reduces the fibrinogen clotting activity and the esterase activity.";
R Biochemistry 31:7457-7462(1992).
R [19]
R VARIANT DYSPROTHROMBINEMIA TRP-461.
R MEDLINE=87185407; PubMed=3567158;
R Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
R Iwanaga S.;
R "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
R that impairs the fibrinogen clotting activity of derived thrombin
R Tokushima.";

RL Biochemistry 26:1117-1122(1987).
RN [20]
RX VARIANT DYSPROTHROMBINEMIA TRP-461.
RP MEDLINE=87101511; PubMed=3801571;
RA Inomoto T., Shirakami A., Kawauchi S., Shigeiyo T., Saito S.,
RA Miyoshi K., Morita T., Iwanaga S.;
RT "Prothrombin Tokushima: characterization of dysfunctional thrombin
RT derived from a variant of human prothrombin.";
RL Blood 69:565-569(1987).
RN [21]
RP VARIANT DYSPROTHROMBINEMIA TRP-461.
RX MEDLINE=92256895; PubMed=1349838;
RA Iwahana H., Yoshimoto K., Shigeiyo T., Shirakami A., Saito S.,
RA Itakura M.;
RT "Detection of a single base substitution of the gene for prothrombin
RT Tokushima. The application of PCR-SSCP for the genetic and molecular
RT analysis of dysprothrombinemia.";
RL Int. J. Hematol. 55:93-100(1992).
RN [22]
RP VARIANT DYSPROTHROMBINEMIA LYS-200.
RX MEDLINE=83204687; PubMed=6405779;
RA Board P.C., Shaw D.C.;
RT "Determination of the amino acid substitution in human prothrombin
RT type 3 (157 Glu leads to Lys) and the localization of a third
RT thrombin cleavage site.";
RL Bx. J. Haematol. 54:245-254(1983).
RN [23]
RP VARIANTS MET-165 AND THR-386.
RX MEDLINE=9318093; PubMed=10391209;
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes.";
RL Nat. Genet. 22:231-238(1999).
RN [24]
RP ERRATUM.
RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373(1999).
CC -1- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XIII, and, in complex with thrombomodulin, protein C.
CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME, THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS.
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE, THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION

Query Match 14.8%; Score 124; DB 1; Length 622;
Best Local Similarity 38.8%; Pred. No. 0.00012;
Matches 26; Conservative 8; Mismatches 29; Indels 4; Gaps 2;
Qy 50 CYSNGHGFYRGKASTDTMGPCPLPWNASATVLTQTYHAHSDALQGLGKHGNCND-NR 108
Db 213 CVPDRGQYGRGLAVTTHTGLPLCLAWASQAQKALSKHDFNSAVQL---VENFCRNPDGDE 269
Qy 109 RRPWCYV 115
Db 270 EGVWCYV 276

Search completed: May 25, 2004, 14:53:56
Job time : 6.51446 secs

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rotein - protein search, using sw model

on: May 25, 2004, 14:44:05 ; Search time 23.6871 Seconds
(without alignments)
1904.795 Million cell updates/sec

e: US-09-880-503-8

ect score: 837

ence: 1 SNELHQVPSNCDLNGTGV.....QECMVHDCADGKPPSPPEE 143

ing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 1017041 seqs, 315518202 residues

il number of hits satisfying chosen parameters: 1017041

imum DB seq length: 0

imum DB seq length: 2000000000

rocessing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

ase :

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	778	93.0	154 4 Q96SE8	Q96SE8 homo sapien
2	627	74.9	433 6 Q8MI10	Q8MI10 oryctolagus
3	627	74.9	433 6 Q8MHY7	Q8MHY7 oryctolagus
4	576	68.8	157 6 Q9TVA8	Q9TVA8 bos taurus
5	569	68.0	231 11 Q8C6L2	Q8C6L2 mus musculus
6	337.5	40.3	214 6 Q9X170	Q9X170 oryctolagus
7	328.5	39.2	291 4 Q7Z7N2	Q7Z7N2 homo sapien
8	328.5	39.2	562 4 Q86YK8	Q86YK8 homo sapien
9	322.5	38.5	516 4 Q9BU99	Q9BU99 homo sapien
10	311.5	37.2	562 6 Q8SQ23	Q8SQ23 sus scrofa
11	301.5	36.0	564 6 Q8MK51	Q8MK51 oryctolagus
12	265	31.7	517 11 Q8K0D2	Q8K0D2 mus musculus
13	263.5	31.5	560 4 Q14520	Q14520 homo sapien
14	258	30.8	616 6 Q97507	Q97507 sus scrofa
15	255.5	30.5	540 13 Q800Y7	Q800Y7 meleagris g
16	250.5	29.9	653 11 Q8VCS4	Q8VCS4 mus musculus

17	250	29.9	597	11	Q35727	Q35727 mus musculus
18	250	29.9	609	11	Q80VC5	Q80VC5 mus musculus
19	233	27.8	395	4	Q8ZM1	Q8ZM1 homo sapien
20	233	27.8	615	4	Q8IZZ5	Q8IZZ5 homo sapien
21	218.5	26.1	90	4	Q8NG20	Q8NG20 homo sapien
22	197.5	23.6	202	13	Q90675	Q90675 gallus gall
23	174	20.8	421	13	Q8AXX3	Q8AXX3 xenopus lae
24	174	20.8	947	13	Q8AXY6	Q8AXY6 gallus gall
25	166	19.8	263	13	Q7SXB3	Q7SXB3 brachydanio
26	166	19.8	716	13	Q91691	Q91691 xenopus lae
27	165.5	19.8	359	6	Q8WML1	Q8WML1 canis fami
28	165.5	19.8	812	11	Q9ROW3	Q9ROW3 rattus norv
29	158.5	18.9	393	4	Q8BRB6	Q8BRB6 homo sapien
30	158.5	18.9	937	11	Q8BNP9	Q8BNP9 mus musculus
31	158.5	18.9	937	11	Q8BG10	Q8BG10 mus musculus
32	158	18.9	454	6	Q46506	Q46506 papio hamad
33	157	18.8	113	4	Q9UIR5	Q9UIR5 homo sapien
34	156.5	18.7	759	11	Q7TP84	Q7TP84 rattus norv
35	156.5	18.7	810	4	Q5146	Q5146 homo sapien
36	154	18.4	801	11	Q8KQ08	Q8KQ08 mus musculus
37	154	18.4	806	6	Q18783	Q18783 macropus eu
38	154	18.4	944	11	Q8C3W2	Q8C3W2 mus musculus
39	154	18.4	944	11	Q8BGP6	Q8BGP6 mus musculus
40	153	18.3	113	4	Q9UIR7	Q9UIR7 homo sapien
41	152.5	18.2	717	13	Q700C6	Q700C6 xenopus lae
42	152	18.2	567	4	Q3208	Q3208 homo sapien
43	152	18.2	648	4	Q9H1V4	Q9H1V4 homo sapien
44	150.5	18.0	930	13	Q8AV69	Q8AV69 xenopus lae
45	149.5	17.9	709	13	Q7ZTN9	Q7ZTN9 xenopus lae
46	148	17.7	105	4	Q9UIR8	Q9UIR8 homo sapien
47	148	17.7	704	13	Q90865	Q90865 gallus gall
48	147.5	17.6	716	11	Q91XG8	Q91XG8 mus musculus
49	147	17.6	113	4	Q9UIR6	Q9UIR6 homo sapien
50	147	17.6	2869	6	Q28398	Q28398 erinaceus e
51	146.5	17.5	709	13	Q902N6	Q902N6 brachydanio
52	146.5	17.5	902	5	Q17576	Q17576 caenorhabdi
53	146.5	17.5	928	5	Q9BLV1	Q9BLV1 caenorhabdi
54	145.5	17.4	313	13	Q9PU78	Q9PU78 crocodylus
55	145.5	17.4	716	11	Q70521	Q70521 rattus norv
56	145	17.3	726	13	Q90978	Q90978 gallus gall
57	142.5	17.0	213	11	Q81123	Q81123 mus musculus
58	142.5	17.0	264	11	Q81122	Q81122 mus musculus
59	142.5	17.0	264	11	Q7TMJ8	Q7TMJ8 mus musculus
60	142	17.0	215	13	Q42341	Q42341 gallus gall
61	142	17.0	728	6	Q9BH09	Q9BH09 felis silve
62	142	17.0	728	11	Q8C9G5	Q8C9G5 mus musculus
63	142	17.0	730	6	Q867B7	Q867B7 canis fami
64	142	17.0	948	5	Q911Y6	Q911Y6 ephydatia f
65	141	16.8	710	13	Q91402	Q91402 xenopus, he
66	140	16.7	132	4	Q16609	Q16609 homo sapien
67	138	16.5	1145	5	Q9BKL8	Q9BKL8 aplysia cal
68	137	16.4	334	6	Q46507	Q46507 papio hamad
69	135.5	16.2	553	13	Q7Z292	Q7Z292 brachydanio
70	135	16.1	429	13	Q8AVD0	Q8AVD0 brachydanio
71	134	16.0	211	11	Q55027	Q55027 mus musculus
72	133.5	15.9	145	6	Q28911	Q28911 macaca fasc
73	131.5	15.7	234	4	Q86YW2	Q86YW2 homo sapien
74	131.5	15.7	263	4	Q00318	Q00318 homo sapien
75	131.5	15.7	263	4	Q8NCJ9	Q8NCJ9 homo sapien

ALIGNMENTS

RESULT 1
Q96SE8
ID Q96SE8 PRELIMINARY; PRT; 154 AA.
AC Q96SE8
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Urokinase-type plasminogen activator amino-terminal fragment.
GN ATF.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu J., Bai X., Ruan C.;
RT "Cloning and expression of the amino-terminal fragment of human
RT urokinase-type plasminogen activator."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bai X., Fu J., Wang W., Xi X., Ruan C.;
RT "Overexpression of the amino-terminal fragment of human urokinase-type
RT plasminogen activator in breast cancer cells results in decreased
RT tumor invasion, growth and angiogenesis."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL: AY029537; AAK38734.1; -
DR GO: GO:0016301; F-kinase activity; IEA.
DR InterPro: IPR006209; EGF-like.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1A.
DR Pfam: PF00051; kringle; 1.
DR PRINTS: PR00018; KRINGLE.
DR PRODOM: PD000395; kringle; 1.
DR SMART: SM00130; KR; 1.
DR PROSITE: PS00022; EGF_1; 1.
DR PROSITE: PS00021; KRINGLE_1; 1.
DR PROSITE: PS00070; KRINGLE_2; 1.
DR PROSITE: PS00240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR PIRSF: PIRSF001144; Uro_kinase; 1.
KW Glycoprotein; Kinase; Kringle.
SQ SEQUENCE 154 AA; 17305 MW; A3CCF2PCFF505572 CRC64;

Query Match 93.0%; Score 778; DB 4; Length 154;
Best Local Similarity 99.3%; Pred. No. 1.4e-75;
Matches 133; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNELHQPNCCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCVEGNGHFRG 60
DB 21 SNELHQPNCCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCVEGNGHFRG 80

QY 61 KASTDTMGRCPLPWSATVLOQTHAHSRSDALQLGLGKHNYCRNPNRRPWCYVQGLK 120
DB 81 KASTDTMGRCPLPWSATVLOQTHAHSRSDALQLGLGKHNYCRNPNRRPWCYVQGLK 140

QY 121 PLVQECMVHDCADG 134
DB 141 LLVQECMVHDCADG 154

RESULT 2
Q8MHY7 PRELIMINARY; PRT; 433 AA.
AC Q8MHY7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Urokinase-type plasminogen activator.
GN PLAU.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann R.,
RA Dichek D.A.;
RT "Increased expression of urokinase during atherosclerotic lesion
RT development causes arterial constriction and lumen loss, and
RT accelerates lesion growth."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10665-10670(2002).

-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
EMBL: AY122285; AAM83187.1; -
GO: GO:0004263; F-kinase activity; IEA.
GO: GO:0016301; F-kinase activity; IEA.
GO: GO:0008233; F-kinase activity; IEA.
GO: GO:0004295; F-kinase activity; IEA.
GO: GO:0006508; P-kinase activity; IEA.
InterPro: IPR009003; Cys Ser trypsin.
InterPro: IPR006209; EGF-like.
InterPro: IPR000001; Kringle.
InterPro: IPR001254; Peptidase_S1.
InterPro: IPR001314; Peptidase_S1A.
Pfam: PF00051; kringle; 1.
PRINTS: PR00018; KRINGLE.
PRODOM: PD000395; kringle; 1.
SMART: SM00130; KR; 1.
PROSITE: PS00022; EGF_1; 1.
PROSITE: PS00021; KRINGLE_1; 1.
PROSITE: PS00070; KRINGLE_2; 1.
PROSITE: PS00240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; 1.
PROSITE: PS00135; TRYPSIN_SER; 1.
PIRSF: PIRSF001144; Uro_kinase; 1.
KW Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SQ SEQUENCE 433 AA; 48375 MW; 65E64F36415549B0 CRC64;

Query Match 74.9%; Score 627; DB 6; Length 433;
Best Local Similarity 76.2%; Pred. No. 6.8e-59;
Matches 109; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

QY 1 SNELHQV--PSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCVEGNGHFRG 58
DB 21 SNELHQVSDASNGCLNGGTCVTVKYFSNIHWCNCPKFGQHCIDKSKTCVEGNGHFRG 80

QY 59 RGASTDTMGRCPLPWSATVLOQTHAHSRSDALQLGLGKHNYCRNPNRRPWCYVQVG 118
DB 81 RGASTDTMGRCPLPWSATVLOQTHAHSRSDALQLGLGKHNYCRNPNRRPWCYVQVG 140

QY 119 LKPLVQECMVHDCADGCKPSSPP 141
DB 141 LKPLVQECMVHDCADGCKPSSPP 163

RESULT 3
Q8MHY7 PRELIMINARY; PRT; 433 AA.
AC Q8MHY7
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Urokinase-type plasminogen activator.
GN UROKINASE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugiki M., Yoshida E., Anai K., Maruyama M.;
RA Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yano W., Watanabe M.;
RT "Oryctolagus cuniculus urokinase-type plasminogen activator, mRNA,
RT complete cds."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

D EMBL; AY029517; AAK40239.1; --
D EMBL; AB087224; BAC02685.1; --
D GO; GO:0004263; F:chymotrypsin activity; IEA.
D GO; GO:0016301; F:kinase activity; IEA.
D GO; GO:0008233; F:peptidase activity; IEA.
D GO; GO:0004295; F:trypsin activity; IEA.
D GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
D InterPro; IPR009003; Cys_Ser_trypsin.
D InterPro; IPR006209; EGF_like.
D InterPro; IPR000001; Kringle.
D InterPro; IPR001254; Peptidase S1.
D InterPro; IPR001314; Peptidase S1A.
D InterPro; IPR008293; Pept_S1A_UPA.
D Pfam; PF00051; kringle; 1.
D Pfam; PF00089; trypsin; 1.
D PRINTS; PRO06209; EGF_like.
D PRINTS; PRO00001; Kringle.
D PRINTS; PRO0018; KRINGLE.
D PRINTS; PRO00395; Kringle; 1.
D SMART; SM00130; KR; 1.
D SMART; SM00020; Tryp_SPC; 1.
D PROSITE; PS00022; EGF_1; 1.
D PROSITE; PS00021; KRINGLE_1; 1.
D PROSITE; PS00070; KRINGLE_2; 1.
D PROSITE; PS00240; TRYPSIN_DOM; 1.
D PROSITE; PS00134; TRYPSIN_HIS; 1.
D PROSITE; PS00135; TRYPSIN_SER; 1.
D PIRSF; PIRSF001144; Urk_P1asm_act; 1.
D Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
D SEQUENCE 433 AA; 48444 MW; 6D35A371010A6EE CRC64;

Query Match 74.9%; Score 627; DB 6; Length 433;
Best Local Similarity 76.2%; Pred. No. 6.8e-59;
Matches 109; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

Q 1 SNEHGV--PNCDCGLNGTGVSNKYFNSIHWCNCPKFGGQHCEDKSKTCYEGNGHFY 58
D 21 SHELHGVSDASNGCLNGTGVYKYFNSIWRNCNPKFKQGEHCEDTLTKCYEGDGHYS 80

Q 59 RGKASTDTWGRPLPNSATVLOQTYHAHRSDALQLGLGKHYCRNPDNRRPWCYVQVVG 118
D 81 RGKANTDMDRCLAWNSANVLTXTYHAHRPDALQLGLGKHYCRNPDNRRPWCYVQVVG 140

Q 119 LKPLVQECWHDCAQKPSPP 141
D 141 LKQLIOECKVHDCSSGKKPALUP 163

R LT 4
Q /AS
I Q9TVAS PRELIMINARY; PRT; 157 AA.
A Q9TVAS;
D 01-MAY-2000 (TREMELrel. 13, Created)
D 01-MAY-2000 (TREMELrel. 13, Last sequence update)
D 01-JUN-2003 (TREMELrel. 24, Last annotation update)
D Urokinase plasminogen activator (Fragment).
O Bos taurus (Bovine)
O Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
O Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
O Bovidae; Bovinae; Bos.
O NCBI_TaxID=9913;
R [1]
R SEQUENCE FROM N.A.
R TISSUE-Skeletal muscle;
R MEDLINE=21071388; PubMed=11204721;
R Balcerzak D., Quereguesser L., Dixon W.T., Baracos V.E.;
R "Coordinate expression of matrix-degrading proteinases and their
R activators and inhibitors in bovine skeletal muscle.";
R J. Anim. Sci. 79:94-107(2001).
C -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
D EMBL; AF144761; AAD30301.1; --
D HSP; P00749; IUXK.
D GO; GO:0016301; F:kinase activity; IEA.
D InterPro; IPR006209; EGF_like.

DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Glycoprotein; Kinase; Kringle.
FT NON_TER 1
FT NON_TER 157 157
SQ SEQUENCE 157 AA; 17858 MW; A768D6C72C1FBFB7 CRC64;

Query Match 58.8%; Score 576; DB 6; Length 157;
Best Local Similarity 74.8%; Pred. No. 6.7e-54;
Matches 98; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 13 CLNGGTCVSNKYFNSIHWCNCPKFGGQHCEDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
DB 1 CLNGGKCVTYKYFNSIQRCSCKPKQGEHCEDTSKTCYQGNHGSYRGKANEDLSGRPCL 60

QY 73 PWSATVLOQTYHAHRSDALQLGLGKHYCRNPDNRRPWCYVQVGLKPLVQECWHDCA 132
DB 61 AWDSPTVLLKMYHAHRSDAQLGLGKHYCRNPDNRRPWCYVQVGLKPLVQECWHDCA 120

QY 133 DGKKPSSPPEE 143
DB 121 VKSPSSPREK 131

RESULT 5
Q8C6L2 PRELIMINARY; PRT; 231 AA.
ID Q8C6L2;
AC Q8C6L2;
DT 01-MAR-2003 (TREMELrel. 23, Created)
DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Plasminogen activator (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary;
RX MEDLINE=22954683; PubMed=12466851;
RA The RIKEN Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK054349; BAC35743.1; --
DR PIR; PT0534; PT0534.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
FT NON_TER 231 231
SQ SEQUENCE 231 AA; 25510 MW; 25B9980A682737F2 CRC64;

Query Match 58.0%; Score 569; DB 11; Length 231;
Best Local Similarity 70.4%; Pred. No. 5.7e-53;
Matches 95; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

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QY 9 SNCDLNGTGVSNKYFNSHNCNCPKFGQHQHCEIDSKTCYEGNGHGYRGKASTDTMG 68
DB 30 SNGCQNGGVSVYKYFNSHNCNCPKFGQHQHCEIDSKTCYEGNGHGYRGKASTDTMG 89
QY 69 RCLPWNATVLOQTTHAHSRDLQGLGKHNCRNPNRRPWCYVQVGLKPLVQECMV 128
DB 90 RCLAWNAVQLQPNHAPDAISLGLGKHNCRNPNQKRPWCYVQVGLRQFVQECMV 149
QY 129 HCDAGKGFSSPPEE 143
DB 150 HDCSLSKFSSSDVQ 164

RE .T 6
QY 0 Q9XT70 PRELIMINARY; PRT; 214 AA.
AC Q9XT70;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Urokinase-type plasminogen activator (Fragment).
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Yin J., Idell S.;
RT Partial mRNA of rabbit uPA.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF097647; AAD39351.1; -.
DR HSSP; P00749; LEJN.
DR MEROPS; S01.231; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KB; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR GlycoProtein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
FT NON_TER 214 214
SQ SEQUENCE 214 AA; 24314 MW; 69975C41C32B0D7E CRC64;

Query Match
Best Local Similarity 40.3%; Score 337.5; DB 6; Length 214;
Matches 59; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 67 MGRPCLPWNATVLOQTTHAHSRDLQGLGKHNCRNPNRRPWCYVQVGLKPLVQEC 126
DB 1 MDRPCLAWNSANVLTTHAHRPDLQGLGKHNCRNPNRRPWCYVQVGLKPLVQEC 60

QY 127 MVHDCADGKFPSSPP 141
DB 61 KVHD-SSGKKPALPP 74

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RESULT 7
QY 727N2 PRELIMINARY; PRT; 291 AA.
ID QY727N2;
AC QY727N2;
DT 01-OCT-2003 (TEMBLrel. 25, Created)
DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Plasminogen activator, tissue type isoform 2.
GN PLAI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA Ahearne M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
RA Nickerson D.A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291060; AAP34246.1; -.
SQ SEQUENCE 291 AA; 32191 MW; 874E38C52F50E1D CRC64;

Query Match
Best Local Similarity 39.2%; Score 328.5; DB 4; Length 291;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

QY 3 ELHQVP-SNCD---CLNGGTCVSNKYFNSHNCNCPKFGQHQHCEIDSKTCYEGNGHGY 58
DB 77 QCHSVPVKSCSEPRFCNGGTCQALYFSDP-VQCPEGFAGKCEIDTRATCYEDQGISY 135
QY 59 RGKASTDTMRPCLPWNATVLOQTTHAHSRDLQGLGKHNCRNPNRRPWCYVQVGL 118
DB 136 RGTWSTAESGAECTNWNSSALAKPYSGRRPDAIRLGLGHNHNYCRNPNDRSKPWCYV 195
QY 119 LKPLVQECVHDCADG 134
DB 196 GKYSSSEFCSTPACSEG 211

RESULT 8
QY 86YK8 PRELIMINARY; PRT; 562 AA.
ID Q86YK8;
AC Q86YK8;
DT 01-JUN-2003 (TEMBLrel. 24, Created)
DT 01-JUN-2003 (TEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Tissue plasminogen activator.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RA Liu Y., Xu L., Zeng Y., He X.;
RT "cDNA of tissue plasminogen activator.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY221101; AA034406.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.

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DR PROSITE; PS000395; Kringle_1; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
KW Serine protease.
SQ SEQUENCE 516 AA; 57370 MW; BAB31901FDC96800 CRC64;

Query Match 38.5%; Score 322.5; DB 4; Length 516;
Best Local Similarity 44.4%; Pred. No. 3.7e-26;
Matches 64; Conservative 13; Mismatches 56; Indels 11; Gaps 2;

QY 1 SNEHL-----QVPSNCDCLNGGTCVSNKYFNIHWCNCPKFGGHCIDKSKTCYEGNGHGFY 58
DB 23 SGEIHFRRFGARSGYQGCSEPRFCNGTCCQALYFSDF-VQCPGEGFAGKCCIDTRATC 81
QY 51 YEGNGHGFYRGKASDTWGRPCLPWNSTVLTQYTHAHRSDALGLGKHNKNCNPNRR 110
DB 82 YEDQGISYRGVWSTAESGAECTWNSSALAQKPYSGRRPDAIRLGLGNHNYCNPRDSK 141
QY 111 PWCYVQGLKPLVQECMVHDCADG 134
DB 142 PWCYVFKAGYSSEFCSTPACSEG 165

RESULT 10
Q8SQ23 PRELIMINARY; PRT; 562 AA.
AC Q8SQ23;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2003 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T-plasminogen activator.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Enamel organ;
RA Ding Y., Xue J., Bartlett J.D.;
RT T-plasminogen activator in tooth tissues.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DR EMBL; AF364605; AAM00297.1; -;
DR HSSP; P00761; 1ANI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000883; Fibrinctn.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00039; fnl; 1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; K-kringle; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.

ProDom; PD000395; Kringle; 2.
SMART; SM00058; FN1; 1.
SMART; SM00130; KR; 2.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01253; FIBRONECTIN_1; 1.
PROSITE; PS00021; KRINGLE_1; 2.
PROSITE; PS00070; KRINGLE_2; 2.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
SEQUENCE 562 AA; 62902 MW; 837D98392F6EDD1F CRC64;

Query Match 39.2%; Score 328.5; DB 4; Length 562;
Best Local Similarity 46.3%; Pred. No. 9.3e-27;
Matches 63; Conservative 14; Mismatches 55; Indels 5; Gaps 3;

Q 3 ELHQP-SNCD---CLNGGTCVSNKYFNIHWCNCPKFGGHCIDKSKTCYEGNGHGFY 58
D 77 QCHSVFVKSCSPRCFNGTCCQALYFSDF-VQCPGEGFAGKCCIDTRATCYEDQGISY 135
Q 59 RGKASDTWGRPCLPWNSTVLTQYTHAHRSDALGLGKHNKNCNPNRRRPWCYVQVG 118
D 136 RGTWSTAESGAECTWNSSALAQKPYSGRRPDAIRLGLGNHNYCNPRDSKPCWCVYFKA 195
Q 119 LKPLVQECMVHDCADG 134
D 196 GKYSSEFCSTPACSEG 211

Q8BU99 PRELIMINARY; PRT; 516 AA.
AC Q8BU99;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2003 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to plasminogen activator, tissue.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
C -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DR EMBL; BC002795; AAB02795.1; -;
DR HSSP; P00750; 1A5H.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.


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Query Match          31.7%; Score 265; DB 11; Length 517;
Best Local Similarity 41.1%; Pred. No. 5.4e-20;
atches 53; Conservative 19; Mismatches 51; Indels 6; Gaps 4;

C 13 CLNGGTCVSNKYFSNIHWCNCPKKGQHCCEIDKSKTCYEGNGHYPYRGKASTDTMGRPCL 72
D 116 CQGGVCSRHRRSRF--TCACPDQVKGKCEIGPD--DCYVGDSYGRGKSVKTNQNPCL 173
C 73 PWSNATVLOQTYHAHRSDALQLGLGKHNYCRPNRRRWCVQVGLKPLVQE--CMVHDC 131
D 174 YNNSHLLLOETYNMFEDAEITHGIEHFCRNPDGDHRCWPCFKVNSKYKWEYCDVTVC 233
C 132 ADGKDPSP 140
D 234 ---PVPDTP 239

F ULT 13
C 520 PRELIMINARY; PRT; 560 AA.
I Q14520; O00663;
A 01-NOV-1996 (Tremblrel. 01, Created)
D 01-NOV-1996 (Tremblrel. 01, Last sequence update)
E 01-OCT-2003 (Tremblrel. 25, Last annotation update)
C HGF activator like protein (Hyaluronan binding protein 2).
C Homo sapiens (Human)
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
C NCBI_TaxID=9606;
F (1)
C SEQUENCE FROM N.A.
K Kitamura N.;
F Submitted (MAR-1995) to the EMBL/GenBank/DBSJ databases.
F (2)
C SEQUENCE FROM N.A.
F MEDLINE=96425001; PubMed=8827452;
F Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
F Tomita M.;
F "Purification and characterization of a novel hyaluronan-binding
F protein (PHEP) from human plasma: it has three EGF, a kringle and a
F serine protease domain, similar to hepatocyte growth factor
F activator.";
F J. Biochem. 119:1157-1165(1996).
F (3)
C SEQUENCE FROM N.A.
F TISSUE=Colon; and Kidney;
F Strausberg R.;
F Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
C -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
C -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
D EMBL; D49742; BAA08576.1; -.
D EMBL; S83182; AAB46909.1; -.
D EMBL; BC031412; AAH31412.1; -.
D FIR; JC4795; J04795.
D HSP; P00763; IDPO.
D MEROPS; S01.033; -.
D Genew; HGNC:4798; HABP2.
D GO; GO:0005615; C:extracellular space; TAS.
D GO; GO:0005539; F:glycosaminoglycan binding; TAS.
D GO; GO:0007155; P:cell adhesion; TAS.
D InterPro; IPR009003; Cys_Ser_trypsin.
D InterPro; IPR006209; EGF-like.
D InterPro; IPR000001; Kringle.
D InterPro; IPR001254; Peptidase_S1.
D InterPro; IPR001314; Peptidase_S1A.
D Pfam; PF00008; EGF; 3.
D Pfam; PF00051; kringle; 1.
D Pfam; PF00089; trypsin; 1.
D PRINTS; PR00722; CHYMOTRYPSIN.
D PRINTS; PR00018; KRINGLE.
D ProDom; PD000395; Kringle; 1.
D PROSITE; PS00022; EGF 1; 3.
D PROSITE; PS01186; EGF_2; 2.

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DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
KW Serine protease.
SQ SEQUENCE 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;

Query Match          31.5%; Score 263.5; DB 4; Length 560;
Best Local Similarity 41.0%; Pred. No. 8.6e-20;
Matches 55; Conservative 18; Mismatches 56; Indels 5; Gaps 4;

QY 13 CLNGGTCVSNKYFSNIHWCNCPKKGQHCCEIDKSKTCYEGNGHYPYRGKASTDTMGRPCL 72
DB 159 CQGGATCSRHKRSKF--TCACPDQVKGKCEIG--SDCYVGDSYGRGKNRTVNGHACL 216
QY 73 PWSNATVLOQTYHAHRSDALQLGLGKHNYCRPNRRRWCVQVGLKPLVQE--CMVHDC 131
DB 217 YNNSHLLLOETYNMFEDAEITHGIEHFCRNPDADKPCFKIKVTNDKYKWEYCDVSAC 276
QY 132 A--DGKPPSPPEE 143
DB 277 SAQDVAYPESPTPE 290

RESULT 14
O97507 PRELIMINARY; PRT; 616 AA.
ID O97507;
AC O97507;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE FXII.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Takahashi T., Kihara T.;
RT "Porcine liver factor XII.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBSJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AB022426; BAA37148.1; -.
DR HSP; P00763; IDPO.
DR MEROPS; S01.211; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibinctnl.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00013; FNYPEII.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; FN_Type_II; 1.
DR ProDom; PD000395; Kringle; 1.

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DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TYP SPC; 1.
DR PROSITE; PS00022; EGF 1; 2.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS01253; FIBRONECTIN 1; 1.
DR PROSITE; PS00023; FIBRONECTIN 2; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
KW Serine protease.
SQ SEQUENCE 616 AA; 68012 MW; 4CSFE3D71EBBD1A9 CRC64;

Query Match 30.8%; Score 258; DB 6; Length 616;
Best Local Similarity 39.0%; Pred. No. 3,7e-19;
Matches 57; Conservative 15; Mismatches 58; Indels 16; Gaps 5;

QY 6 QVPSNCDCLNGTCTVSNKYFSNIHWCNCPKPGGQHCIDKSKTYEGNGHFGKASTD 65
DB 176 QVCSNPNCLNGSGCLQTE---GRLRCRPTGYAGRLCDVLRKERCYSRGLSYRGMAQT 232
QY 66 TWGRPLPWSATVLQQTQY-HAHRSDALQLGKHNCRNPNRRPKCYQVGLKPLVQ 124
DB 233 LSGACQCPWAS-----EATVNTATQALNWGLGDHAFRCNPNDRTPRCFCVWRGDLSWQ 288

QY 125 ECVHDCAD--GKXP-----SSPPE 142
DB 289 YCLARCAPIGEAPPILPTQSPSE 314

RE 15
Q8 Q800Y7 PRELIMINARY; PRT; 540 AA.
AC Q800Y7;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hepatocyte growth factor activator (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22122796; PubMed=12128063;
RA Holmberg D.R., Becker A.E., Thurston R.J., Rice C.D.;
RT "Expression of a hepatocyte growth-factor activator protein in turkey
RL (Meleagris gallopavo) deferent duct epithelial cells.";
RL Comp. Biochem. Physiol. 132:769-777(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Holmberg D.R., Becker A.E., Thurston R.J., Rice C.D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY216598; AAO46038.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR DF; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser_trypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1a.
PFam; PF00008; EGF; 2.

DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TYP SPC; 1.
DR PROSITE; PS00022; EGF 1; 2.
DR PROSITE; PS01186; EGF 2; 1.
DR PROSITE; PS01253; FIBRONECTIN 1; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS00070; KRINGLE 2; 1.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
FT NON_TER 1 540
FT NON_TER 540 540
SQ SEQUENCE 540 AA; 61159 MW; 0B83B4A89C0B577F CRC64;

Query Match 30.5%; Score 255.5; DB 13; Length 540;
Best Local Similarity 38.3%; Pred. No. 6e-19;
Matches 51; Conservative 17; Mismatches 54; Indels 11; Gaps 3;

QY 13 CLNGTCTC-----VSNKYFSNIHWCNCPKPGGQHCIDKSKTYEGNGHFGKASTDTMG 68
DB 143 CMNGGCKMIASGKTV-----CDCKGPFVGVKYNIVPNHHCYRGNGTEYRGTAKTITISG 197
QY 69 RPLCPNWSATVLQQTQY-HAHRSDALQLGKHNCRNPNRRPKCYQVGLKPLVQECMV 128
DB 198 HSLCPNWSLLYRELHVDVSERKAVQLGLGPFYCRNPNDRPDEKFCWYIMKDNLSWEYCN 257
QY 129 HDCADGKPSPP 141
DB 258 TSCASRER--RPP 268

RESULT 16
Q8VCS4 PRELIMINARY; PRT; 653 AA.
ID Q8VCS4;
AC Q8VCS4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; BC019376; AAR19376.1; -.
DR HSP; P00761; LAN1.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:trypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser_trypsin.
DR InterPro; IPR000742; EGF 2.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.

D: InterPro; IPR001314; Peptidase_S1A.
D: Pfam; PF00008; EGF; 2.
D: Pfam; PF00039; fn1; 1.
D: Pfam; PF00040; fn2; 1.
D: Pfam; PF00051; kringle; 1.
D: Pfam; PF00089; trypsin; 1.
D: PRINTS; PR00722; CHYMOTRYPSIN.
D: PRINTS; PR00013; FNTYPEII.
D: PRINTS; PR00018; KRINGLE.
D: ProDom; PD000995; FN Type II; 1.
D: ProDom; PD000395; Kringle; 1.
D: SMART; SM00181; EGF; 2.
D: SMART; SM00059; FN2; 1.
D: SMART; SM00130; KR; 1.
D: SMART; SM00020; Tryp_Spc; 1.
D: PROSITE; PS00022; EGF_1; 2.
D: PROSITE; PS01186; EGF_2; 1.
D: PROSITE; PS01253; FIBRONECTIN_1; 1.
D: PROSITE; PS00023; FIBRONECTIN_2; 1.
D: PROSITE; PS00021; KRINGLE_1; 1.
D: PROSITE; PS00070; KRINGLE_2; 1.
D: PROSITE; PS00240; TRYPSIN_DOM; 1.
D: PROSITE; PS00134; TRYPSIN_HIS; 1.
D: PROSITE; PS00135; TRYPSIN_SER; 1.
K: Hypothetical protein; EGF-like domain; Glycoprotein; Hydrolase;
K: Kringle; Protease; Serine protease.
S: SEQUENCE 653 AA; 70553 MW; F18D90174ED6FDD CRC64;

Query Match 29.9%; Score 250.5; DB 11; Length 653;
Best Local Similarity 42.0%; Pred. No. 2.5e-18;
atches 50; Conservative 11; Mismatches 41; Indels 17; Gaps 2;

Q: 5 HQVENCCLNGGTCVSNKYFSNTHW-----CNCPKFGGQHCIDKSKTCYEGNGH 56
D: 239 HTACUSSFLNGGTC-----HLVGTGTSVCTPLGAGRCNIVPTEHFLNGT 289

Q: 57 FYRGKASTDTWGRPLCPWNSATVLQOYHAHRSALQLGLGKHNYCRPNRRPWCYV 115
D: 290 EYRGVASTAAGSLCLAWSNLLYQELHVDGVAALVLLGLGPHAYCRNPKDERPCYV 348

R: ILT 17
Q: 27 O35727 PRELIMINARY; PRT; 597 AA.
A: O35727;
D: 01-JAN-1998 (Tremblrel. 05, Created)
D: 01-JAN-1998 (Tremblrel. 05, Last sequence update)
D: 01-OCT-2003 (Tremblrel. 25, Last annotation update)
D: Factor XII.
G: F12.
O: Mus musculus (Mouse).
O: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
O: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
O: NCBI_TaxID=10090;
R: [1]
R: SEQUENCE FROM N.A.
R: TISSUE=Liver.
R: Submitter M., Schwager S., Engel W.;
R: Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
C: -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
C: -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
D: EMBL; X9571; CAA67891.1; -.
D: HSP; P00760; 1AQ7.
D: MEROPS; S01.211; -.
D: MGD; MG1:1891012; F12.
D: GO; GO:0005576; C:extracellular; IEA.
D: GO; GO:0004263; F:chymotrypsin activity; IEA.
D: GO; GO:0008233; F:peptidase activity; IEA.
D: GO; GO:0004295; F:trypsin activity; IEA.
D: GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
D: InterPro; IPR00003; Cys_Ser_trypsin.
D: InterPro; IPR006209; EGF-like.
D: InterPro; IPR000083; Fibrinectn.

D: InterPro; IPR000562; FN Type II.
D: InterPro; IPR006210; IEGF.
D: InterPro; IPR000001; Kringle.
D: InterPro; IPR001254; Peptidase_S1.
D: InterPro; IPR001314; Peptidase_S1A.
D: Pfam; PF00008; EGF; 2.
D: Pfam; PF00039; fn1; 1.
D: Pfam; PF00040; fn2; 1.
D: Pfam; PF00051; kringle; 1.
D: Pfam; PF00089; trypsin; 1.
D: PRINTS; PR00722; CHYMOTRYPSIN.
D: PRINTS; PR00013; FNTYPEII.
D: PRINTS; PR00018; KRINGLE.
D: ProDom; PD000995; FN Type II; 1.
D: ProDom; PD000395; Kringle; 1.
D: SMART; SM00181; EGF; 2.
D: SMART; SM00058; FN1; 1.
D: SMART; SM00059; FN2; 1.
D: SMART; SM00130; KR; 1.
D: SMART; SM00020; Tryp_Spc; 1.
D: PROSITE; PS00022; EGF_1; 2.
D: PROSITE; PS01186; EGF_2; 1.
D: PROSITE; PS01253; FIBRONECTIN_1; 1.
D: PROSITE; PS00023; FIBRONECTIN_2; 1.
D: PROSITE; PS00021; KRINGLE_1; 1.
D: PROSITE; PS00070; KRINGLE_2; 1.
D: PROSITE; PS00240; TRYPSIN_DOM; 1.
D: PROSITE; PS00134; TRYPSIN_HIS; 1.
D: PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
KW Serine protease.
SQ SEQUENCE 597 AA; 65638 MW; F3AC07C37D0C0FBA CRC64;

Query Match 29.9%; Score 250; DB 11; Length 597;
Best Local Similarity 36.6%; Pred. No. 2.6e-18;
Matches 52; Conservative 16; Mismatches 54; Indels 20; Gaps 4;

QY 13 CLNGGCVSNKYFSNTHWNCNPKFGGQHCIDKSKTCYEGNGHFGYRGKASTDTWGRPCL 72
DB 183 CLNGGSCL---LVEDHPLCRCPGTGYGFCDDLWATCYEGRLSYRGAGTQSGAPCQ 239

QY 73 PWSATVLQOYTHAHSALQLGLGKHNYCRPNRRPWCYVQVGLKPLVQECMVHDC 131
DB 240 RW----TVEATYRNMTKEQALSWGLGHAFRCNPNDTRPWCFCVWSGDRLSWDYQGLEQC 295

QY 132 -----ADGKKPSSPP 141
DB 296 QPTFPAPLVVPESQESPSQAP 317

RESULT 18
ID Q80YCS PRELIMINARY; PRT; 609 AA.
AC Q80YCS;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to coagulation factor XII (Hageman factor) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Liver;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049867; AAH49867.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro: IPR009003; Cys_Ser_trypsin.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR000083; Fibrinctnl.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR006210; IEGF.
 DR InterPro: IPR000001; Kringle.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00008; EGF_2.
 DR Pfam: PF00039; fn1; 1.
 DR Pfam: PF00400; fn2; 1.
 DR Pfam: PF00051; kringle; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00013; FN_Type_II.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000995; FN_Type_II; 1.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00179; EGF_Ca; 2.
 DR SMART: SM00058; FN1; 1.
 DR SMART: SM00059; FN2; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS00022; EGF_1; 2.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01253; FIBRONECTIN_1; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS00070; KRINGLE_2; 1.
 DR PROSITE: PS02400; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 FT NON_TER
 SQ SEQUENCE 509 AA; 66783 MW; DF97D4DB2369B6D2 CRC64;

Query Match 29.9%; Score 250; DB 11; Length 609;
 Best Local Similarity 36.6%; Pred. No. 2.6e-18;
 Matches 52; Conservative 16; Mismatches 54; Indels 20; Gaps 4;

QY 13 CLNGGTCVSNKFSNIHWCNCPKKGQHCIDKSKTCYEGNGHFGYRGKASTDTMGRLCL 72
 DB 195 CLNGGSL---LVEDHPLCRCTGTGYFCDDLWATCYEGGLSYRQAGTTSQAPCQ 251

QY 73 PMSATVLOQTY-HAHRSDALQGLGKXNYCRNPNRRPWCYQVGLKPLVQECMVHDC 131
 DB 252 RW---TVEATYRNWTEKQALSWGLGHAFCRNPDNTRPWCYVMSGDRLSWDYCGLEQC 307

QY 132 -----ADGKPSPP 141
 DB 308 QPTFAPLVVPSQESPSQAP 329

RE T 19
 Q9 Y1
 ID Q9BZW1 PRELIMINARY; PRT; 395 AA.
 AC Q9BZW1
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Neofatal thrombolytic agent alpha-form (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dou D.;
 RT "A brain-type plasminogen activator."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.

DR EMBL: AF260825; AAK11956.1; -.
 DR HSP; P00750; 1PK2.
 DR GO: GO:000576; C:extracellular; IEA.
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.
 DR GO: GO:0008233; F:peptidase activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR009003; Cys_Ser_trypsin.
 DR InterPro: IPR001254; Peptidase_S1.
 DR InterPro: IPR000083; Fibrinctnl.
 DR InterPro: IPR001314; Peptidase_S1A.
 DR Pfam: PF00039; fn1; 1.
 DR Pfam: PF00051; kringle; 1.
 DR Pfam: PF00089; trypsin; 1.
 DR PRINTS: PR00722; CHYMOTRYPSIN.
 DR PRINTS: PR00013; FN_Type_II.
 DR PRINTS: PR00018; KRINGLE.
 DR ProDom: PD000395; Kringle; 1.
 DR SMART: SM00058; FN1; 1.
 DR SMART: SM00130; KR; 1.
 DR SMART: SM00020; Tryp_Spc; 1.
 DR PROSITE: PS01253; FIBRONECTIN_1; 1.
 DR PROSITE: PS00021; KRINGLE_1; 1.
 DR PROSITE: PS00070; KRINGLE_2; 1.
 DR PROSITE: PS02400; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
 FT NON_TER 395 395
 SQ SEQUENCE 395 AA; 44323 MW; 3FBD4A3F0B7C1C8 CRC64;

Query Match 27.8%; Score 233; DB 4; Length 395;
 Best Local Similarity 41.2%; Pred. No. 1.1e-16;
 Matches 47; Conservative 12; Mismatches 49; Indels 6; Gaps 3;

QY 30 WCNCPKKGQHCIDKSKTCYEGNGHFGYRGKASTDTMGRLCLPMSATVLOQTYHAHR 89
 DB 33 WCN---GRAQCS-EGNSDCYFGNSAYRGTHSITESGASCLPWNMILIGKVTQNP 87

QY 90 DALQLGLGKXNYCRNPNRRPWCYQVGLKPLVQECMVHDCAD-GKKPSSPPE 142
 DB 88 SAQALGLGKXNYCRNPNRRPWCYQVGLKPLVQECMVHDCAD-GKKPSSPPE 141

RESULT 20
 ID Q81Z25 PRELIMINARY; PRT; 615 AA.
 AC Q81Z25
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Coagulation factor XII-Mie.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wada H.; Nishio K.; Nakatani K.; Kasai Y.; Abe Y.; Nobori T.;
 RT "Molecular characterization of coagulation factor XII-Mie."
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB095845; BAC23095.1; -.
 DR GO: GO:000576; C:extracellular; IEA.
 DR GO: GO:0005509; F:calcium ion binding; IEA.
 DR GO: GO:0004263; F:chymotrypsin activity; IEA.
 DR GO: GO:0004295; F:trypsin activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR009003; Cys_Ser_trypsin.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR000083; Fibrinctnl.
 DR InterPro: IPR000582; FN_Type_II.
 DR InterPro: IPR006210; IEGF.


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D InterPro; IPR000001; Kringle.
D InterPro; IPR001254; Peptidase S1.
D InterPro; IPR001314; Peptidase_S1A.
D Pfam; PF000008; EGF_2.
D Pfam; PF000039; fnl; 1.
D Pfam; PF00040; fn2; 1.
D Pfam; PF00051; kringle; 1.
D Pfam; PF00089; trypsin; 1.
D PRINTS; PR00722; CHYMOTRYPSIN.
D PRINTS; PR00013; ENTYPERII.
D PRINTS; PR00018; KRINGLE.
D ProDom; PD000995; FN_Type_II; 1.
D ProDom; PD000395; Kringle; 1.
D SMART; SM00181; EGF_2.
D SMART; SM00179; EGF_CA; 2.
D SMART; SM00058; FN1_1.
D SMART; SM00059; FN2_1.
D SMART; SM00130; KR; 1.
D SMART; SM00020; Tryp_Spc; 1.
D PROSITE; PS00022; EGF_1; 2.
D PROSITE; PS01186; EGF_2; 1.
D PROSITE; PS01253; FIBRONECTIN_1; 1.
D PROSITE; PS00023; FIBRONECTIN_2; 1.
D PROSITE; PS00021; KRINGLE_1; 1.
D PROSITE; PS00070; KRINGLE_2; 1.
D PROSITE; PS00240; TRYPSIN_DOM; 1.
D PROSITE; PS00134; TRYPSIN_HIS; 1.
D PROSITE; PS00135; TRYPSIN_SER; 1.
D SEQUENCE 615 AA; 67735 MW; 030508870A0C7EDB CRC64;

Query Match 27.8%; Score 233; DB 4; Length 615;
Best Local Similarity 42.3%; Pred. No. 1.8e-16;
Matches 44; Conservative 12; Mismatches 40; Indels 8; Gaps 3;

Q 13 CLNGTCVSNKYFSNIHNCNPKPGGQHCIDKSKTCYEGNGHFYRGKASTDTMGRPCL 72
D 183 CLHGRCLE---VEGRLCHCPVGVTGPFCDVDTKASCYDGRGLSYRGLARTLLSGAPCQ 239

Q 73 PWSATVLCQTY-HAHRSDALQLGLGKYNCRNPDNRRPWCYV 115
D 240 PWSA-----EATYRNVTASQARNWGLGGHAFCRNPDNDIRPWCYV 279

R LT 21
Q 820
I Q8NG20 PRELIMINARY; PRT; 90 AA.
D 01-OCT-2002 (TREMELrel. 22, Created)
D 01-OCT-2002 (TREMELrel. 22, Last sequence update)
D 01-MAR-2003 (TREMELrel. 23, Last annotation update)
D Plasminogen/activator kringle.
D Homo sapiens (Human).
O Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
O Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
O NCBI_TaxID=9606;
R [1]
R SEQUENCE FROM N.A.
R Dou D.;
R "Production of kringle fragment.";
R Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
C -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
D EMBL; AF282882; AAM52248.1; -.
D InterPro; IPR000001; Kringle.
D Pfam; PF00051; kringle; 1.
D PRINTS; PR00018; KRINGLE.
D ProDom; PD000395; Kringle; 1.
D SMART; SM00130; KR; 1.
D PROSITE; PS00021; KRINGLE_1; 1.
D PROSITE; PS00070; KRINGLE_2; 1.
K Glycoprotein; Kringle.
S SEQUENCE 90 AA; 9804 MW; A33887F9FDF4C7B1 CRC64;

Query Match 26.1%; Score 218.5; DB 4; Length 90;

Best Local Similarity 49.4%; Pred. No. 7.9e-16;
Matches 41; Conservative 5; Mismatches 36; Indels 1; Gaps 1;

QY 50 CYEGNGHFYRGKASTDTMGRPCLPWSATVLCQTYHAHRSDALQLGLGKYNCRNPDNRR 109
D 8 CYFGNGSAYRGTHSLTESGASCLPWSNMLIKGVYTAQNPSAQLGLGKHNCRNPDGDA 67

QY 110 RPWCYVQVGLKPLVQECMVHDC 132
D 68 KPWCYT-TNPRKLYDYCDVPQCA 89

RESULT 22
Q90675 PRELIMINARY; PRT; 202 AA.
ID AC Q90675;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tissue-type plasminogen activator (Fragment).
GN TPA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn;
RX MEDLINE=97199025; PubMed=9047000;
RA Johnson A.L., Bridgham J.T., Anthony R.V.;
RT "Expression of avian urokinase and tissue-type plasminogen activator
RT messenger ribonucleic acid during follicle development and atresia.";
RL Biol. Reprod. 56:581-588(1997).
CC -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DR EMBL; U31988; AAA74955.1; -.
DR HSP; P00750; IRTF.
DR MEROPS; S01.232; -.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:004295; F:trypsin activity; IEA.
DR GO; GO:006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 23148 MW; 049DB42941D83AFC CRC64;

Query Match 23.6%; Score 197.5; DB 13; Length 202;
Best Local Similarity 36.9%; Pred. No. 3.4e-13;
Matches 41; Conservative 11; Mismatches 50; Indels 9; Gaps 2;

QY 30 WCNCPK--KFGQHC-----IDKSKTCYEGNGHFYRGKASTDTMGRPCLPWSATVL 80
D 12 WCVVFKAGKVISFCSTPACTVAEDGDCYTGNGLAYRGTSRTKSGFSCLPWNPVFLT 71

QY 81 QCTYHAHRSDALQLGLGKYNCRNPDNRRPWCYVQVGLKPLVQECMVHDC 131
D 72 SKIYTALESQRRALGLGKHNCRNPDGDAQPWCHVKORQLTWECYCDVQC 122

RESULT 23
Q8AXX3

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ID Q8AXX3 PRELIMINARY; PRT; 421 AA.
AC Q8AXX3
DT 01-WAR-2003 (TReMBLrel. 23, Created)
DT 01-WAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Krenenz2.
GN KRM2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22308873; PubMed=12421700;
RA Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;
RT "Kremen proteins interact with Dickkopf1 to regulate anteroposterior
RN CNS patterning";
RL Development 129:5587-5596(2002).
DR EMBL; AY150813; XAN64661.1; -.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF01822; WSC; 1.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00321; WSC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00021; KRINGLE; 1.
DR PROSITE; PS00070; KRINGLE; 2; 1.
SQ SEQUENCE 421 AA; 46274 MW; 74D04DB1682CD15F CRC64;
Query Match 20.8%; Score 174; DB 13; Length 421;
Best Local Similarity 47.4%; Pred. No. 2.5e-10;
Matches 36; Conservative 6; Mismatches 28; Indels 6; Gaps 3;
QY 41 HCEIDSKTCYEGNGHFGYRGKAS-TDTMGRCPLPWSATVLQOTVHAHRSALQLGLGKH 99
Db 23 HPELSE---CFTVNGRDRTGTVSQAGPGTCLYWNQTT--QHLNAGSDPDGELGLGNH 77
QY 100 NYCRRPNDRRRPWCYV 115
Db 78 NYCRRPNDAVQPCVYV 93
RE 24
Q8 26
ID Q8AXY6 PRELIMINARY; PRT; 947 AA.
AC Q8AXY6
DT 01-WAR-2003 (TReMBLrel. 23, Created)
DT 01-WAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Muscle-specific receptor tyrosine kinase MUSK.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20538710; PubMed=11083926;
RA Ip F.C., Glass D.G., Gies D.R., Cheung J., Lai K.O., Fu A.K.,
RA Yancopoulos G.D., Ip N.Y.;
RT "Cloning and characterization of muscle-specific kinase in chicken";
RL Mol. Cell. Neurosci. 16:661-673(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Gies D., Glass D., Yancopoulos G.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY143173; AAN05008.1; -.
DR GO; GO:0016020; C.membrane; IEA.
DR GO; GO:0005874; F.microtubule; IEA.
DR GO; GO:0005524; F.ATP binding; IEA.
DR GO; GO:0004674; F.protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F.protein-tyrosine kinase activity; IEA.
DR GO; GO:0005198; F.structural molecule activity; IEA.
DR GO; GO:0004888; F.transmembrane receptor activity; IEA.
DR GO; GO:0007275; P.development; IEA.
DR GO; GO:0007018; P.microtubule-based movement; IEA.
DR GO; GO:0006468; P.protein amino acid phosphorylation; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008286; Tyr_kinase_AS.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00047; IG; 3.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYTKC; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50835; IG-LIKE; 3.
DR PROSITE; PS00021; KRINGLE; 1.
DR PROSITE; PS00070; KRINGLE; 2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00228; TUBULIN_B_AUTOREG; 1.
DR Receptor; Kinase.
SQ SEQUENCE 947 AA; 105588 MW; E6C3FCC5796CC8BE CRC64;
Query Match 20.8%; Score 174; DB 13; Length 947;
Best Local Similarity 31.1%; Pred. No. 6e-10;
Matches 50; Conservative 15; Mismatches 36; Indels 60; Gaps 10;
QY 4 LHQVPSNCDCLNGGTCVSNKYFSNIHWCNPKKFGQHCIDKSKTCYEGNGHFGYRGKAS 63
Db 441 LHQDPSAC-----THIPFPFKKE-----NITRTCYSGNGQFYGGWAN 478
QY 64 TDTMGRCPLPWSATVLQOTVHAHR-----SDALQLGLGKHNYCRNP-DNRRRPPWC 113
Db 479 VTASGIPCCQKWS-----DQAPHLHRTTPQVFFELSDA-----ENYCNPGGNERPWC 526
QY 114 YVQVGLKPLV--QECMVHDCAG-----KPPSS-----PP 141
Db 527 YTK---DPSVTWEYCVSVPCGDASLSLGRKPKNGETQNLPP 564
RESULT 25
Q7SXB3
ID Q7SXB3 PRELIMINARY; PRT; 263 AA.
AC Q7SXB3
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danilo.
NCBI_TaxID=7955;
[1] SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Body;
MEDLINE=23388257; PubMed=12477932;
Strasberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,
Klauchel S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
Krzyszewski M.J., Skalska U., Smalusi D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2] SEQUENCE FROM N.A.
STRAIN=AB; TISSUE=Body;
Strasberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
EMBL; BC055675; AAH55675.1; --
Hypothetical protein.
SEQUENCE 263 AA; 28777 MW; 8BEBCL178C7C8A58 CRC64;

Query Match 19.8%; Score 166; DB 13; Length 263;
Best Local Similarity 35.7%; Pred. No. 1.1e-09;
Matches 35; Conservative 9; Mismatches 44; Indels 10; Gaps 3;

48 KTCVGNHGFYRGKASTDMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDN 107
23 KDCITNNGEDYRGTKQKTSIGSGTCLSWRLNL-----KPKDSQTGVGDHNCRNPDG 74

108 RRRPWCYVQVGLKPLVQEC-QMVHDCADGKPSPP-PEE 143
75 SNKPWCYVSGSGGKTKKACDIRICQDNQVATEAPAPEE 112

JLT 26
91
Q91691 PRELIMINARY; PRT; 716 AA.
Q91691;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Growth factor Livertine.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1] SEQUENCE FROM N.A.
Ruiz i Altaba A., Thery C.;
Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
-!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
EMBL; U57455.1; AAB52574.1; --
HSP; P00747; 1CEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:peptidase activity; IEA.
GO; GO:0003809; F:thrombin activity; IEA.
GO; GO:0004293; F:trypsin activity; IEA.

DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHIMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS0070; KRINGLE_2; 4.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR Glycoprotein; Hydrolase; Kringle; 1.
SQ SEQUENCE 716 AA; 81971 MW; 508376A0E4398798 CRC64;

Query Match 19.8%; Score 166; DB 13; Length 716;
Best Local Similarity 31.1%; Pred. No. 3.2e-09;
Matches 42; Conservative 11; Mismatches 40; Indels 42; Gaps 6;

QY 30 WC-----NCPKFGGQHCIDKSK-----TCVEGNHGFYRGKASTDMGRPCLP 73
DB 258 WCYTDPNVEKEF---CRITCKQRLSNILITSCPKERGGYRGKANTITSGIPCOR 313

QY 74 WNSAT-----VLQOTYHAHRSALQGLGKHNYCRNPDNRRPWCYVQV-----GL 119
DB 314 WDSQTPQSHRFLPEKYPCKGLD-----ENYCRNPDGSEAPWCTTLPGRMAYCFQI 365

QY 120 KPLVQECMVHDCADG 134
DB 366 KRCKDDVLEPDCVHG 380

RESULT 27
Q8WMR1 PRELIMINARY; PRT; 359 AA.
ID Q8WMR1;
AC Q8WMR1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1] SEQUENCE FROM N.A.
RP Parle-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
RA Polkman J., Waters D.J.;
RT "Angiotensin is Detectable in the Urine of Dogs with Spontaneous Bone
Cancer";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; AY069985; AAL58519.1; --
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 4.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR PRODOM; PD000395; Kringle; 4.

DR SMART; SW00130; KR; 4.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
KW Glycoprotein; Kringle.
FT NON_TER
FT NON_TER
SQ SEQUENCE 359 AA; 41172 MW; 776D35P4AB0BDD9E CRC64;

Query Match 19.8%; Score 165.5; DB 6; Length 359;
Best Local Similarity 29.0%; Pred. No. 1.7e-09;
Matches 42; Conservative 13; Mismatches 43; Indels 47; Gaps 7;

QY 5 HQVPSNCDCLNGGTCVSNKYFSN-----IHWNC-NCPKFGGQHCEIDKSMT-----49
Db 211 NRTPEFPCKN---LDENYCNPDPGETAPWCYTTSNVSRWEHQIPSCSSPTITVEYLD 266
QY 50 -----CYEGNHGFYRGKASTDTMGRPCLPWNSATVLQOTVHAHRSDAL-- 92
Db 267 APASVPPEPTPVVQECYQGNGSKSYRGTSTTTTGRKCOSWSMT-----PHRHETKTP 319
QY 93 ---QLGLGHKNYCRNPNDNRPPWCY 114
Db 320 HPEAGL-TWNYCRNPDAKSPWCY 343

RE J T 28 PRELIMINARY; PRT; 812 AA.
ID Q9RW3 PRELIMINARY; PRT; 812 AA.
AC Q9RW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasmينogen protein precursor (EC 3.4.21.7).
GN PLASMINOGEN
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bangert K., Johnsen A.H., Thorsen S.;
RT "Rat plasminogen: cDNA and gene structure".
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanakas J.J., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
receptor site for plasminogen".
RL J. Biol. Chem. 266:10825-10829 (1991).
CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR ENBL; AJ242649; CAB46014.1; --
DR HSSP; P00747; IPMK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:plasmin activity; IEA.
DR GO; GO:0003809; F:fibrinolysis; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; F:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN_app.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR InterPro; IPR001400; Somatotropin.

DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypan; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; KRingle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY SP; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00338; SOMATOTROPIN_1; 1.
DR PROSITE; PS0240; TRYP SIN_DOM; 1.
DR PROSITE; PS00134; TRYP SIN_HIS; 1.
DR PROSITE; PS00135; TRYP SIN_SER; 1.
KW Glycoprotein; Hydroxylase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL 1 19
FT CHAIN 20 812 PLASMINOGEN.
SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410BEC9E CRC64;

Query Match 19.8%; Score 165.5; DB 11; Length 812;
Best Local Similarity 27.8%; Pred. No. 4.2e-09;
Matches 50; Conservative 22; Mismatches 51; Indels 57; Gaps 12;

QY 5 HQVPSNCDCLNGGTCVSNKYFSN-----IHWNC-NCPKFGGQHCEI-----DKS-- 47
Db 308 NRTPEFPCKN---LEENYCNPDPGETAPWCYTTSQLAWEYCEIFSGSSVSFDQS 363
QY 48 -----KTCEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTVHAHRSALQL-- 94
Db 364 SVLPSTPVVQECYQGNGSKSYRGTSTTTGKKCOSW-----VSMTHSHSKTPANFPDA 418
QY 95 GLGKHNYCRNPNDNRPPWCYVQGLKPLV--QCMMVHCAD-----GKKFSSP 140
Db 419 GL-EMNYCRNPNDNRPPWCYFCT---TDPSVRWEYCNLRKCSCTGGVAESAIVPQVPSAP 474

RESULT 29
Q9RB6 PRELIMINARY; PRT; 393 AA.
ID Q9RB6
AC Q9RB6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to receptor tyrosine kinase-like orphan receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR ENBL; BC005374; AAH06374.1; --
DR HSSP; P00747; ICEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00447; IS; 1.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00130; KR; 1.

DR SMART; SW00130; KR; 4.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
KW Glycoprotein; Kringle.
FT NON_TER
FT NON_TER
SQ SEQUENCE 359 AA; 41172 MW; 776D35P4AB0BDD9E CRC64;

Query Match 19.8%; Score 165.5; DB 6; Length 359;
Best Local Similarity 29.0%; Pred. No. 1.7e-09;
Matches 42; Conservative 13; Mismatches 43; Indels 47; Gaps 7;

QY 5 HQVPSNCDCLNGGTCVSNKYFSN-----IHWNC-NCPKFGGQHCEIDKSMT-----49
Db 211 NRTPEFPCKN---LDENYCNPDPGETAPWCYTTSNVSRWEHQIPSCSSPTITVEYLD 266
QY 50 -----CYEGNHGFYRGKASTDTMGRPCLPWNSATVLQOTVHAHRSDAL-- 92
Db 267 APASVPDEPTPVQECYQGNGSKSYRGTSTTTTGRKCSWSMT-----PHRHETKTP 319
QY 93 ---QLGLGHKNYCRNPNDNRPPWCY 114
Db 320 HPEAGL-TWNYCRNPADAKSPWCY 343

RE J T 28 PRELIMINARY; PRT; 812 AA.
ID Q9RW3 PRELIMINARY; PRT; 812 AA.
AC Q9RW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DE Plasmalogen protein precursor (EC 3.4.21.7).
GN PLASMINOGEN
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Bangert K., Johnsen A.H., Thorsen S.;
RT "Rat plasmalogen: cDNA and gene structure".
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91250378; PubMed=1645711;
RA Kanalas J.J., Makker S.P.;
RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a
receptor site for plasminogen".
RL J. Biol. Chem. 266:10825-10829 (1991).
CC -!- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR ENBL; AJ242649; CAB46014.1; --
DR HSSP; P00747; IPMK.
DR GO; GO:0005576; C:cytoplasmic; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004283; F:protease activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; F:blood coagulation; IEA.
DR GO; GO:0006508; P:proteinolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN_app.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR InterPro; IPR001400; Somatotropin.

DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; KRingle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY SP; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00338; SOMATOTROPIN_1; 1.
DR PROSITE; PS0240; TRYP SIN_DOM; 1.
DR PROSITE; PS00134; TRYP SIN_HIS; 1.
DR PROSITE; PS00135; TRYP SIN_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL 1 19
FT CHAIN 20 812 PLASMINOGEN.
SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410BEC9E CRC64;

Query Match 19.8%; Score 165.5; DB 11; Length 812;
Best Local Similarity 27.8%; Pred. No. 4.2e-09;
Matches 50; Conservative 22; Mismatches 51; Indels 57; Gaps 12;

QY 5 HQVPSNCDCLNGGTCVSNKYFSN-----IHWNC-NCPKFGGQHCEI-----DKS-- 47
Db 308 NRTPEFPCKN---LEENYCNPDPGETAPWCYTTSQLAWEYCEIFSGSSVSFDQS 363
QY 48 -----KTCYEGNHGFYRGKASTDTMGRPCLPWNSATVLQOTVHAHRSALQL-- 94
Db 364 SVLPQTPTVQECYQGNGSKSYRGTSTTTTKKKQSW-----VSMTHSHSKTPANFPDA 418
QY 95 GLGKHNYCRNPDN-RRPWCVYQGLKPLV--QCMMVHCAD-----GKKFSSP 140
Db 419 GL-EMNYCRNPNDQRGPWCFT---TDFSVRWEYCNLRKCRSETGGVAESAIVPQVPSAP 474

RESULT 29
Q9RB6 PRELIMINARY; PRT; 393 AA.
ID Q9RB6
AC Q9RB6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE DE Similar to receptor tyrosine kinase-like orphan receptor 1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: AAH06374.1; --
DR HSSP; P00747; ICEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00047; IS; 1.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00130; KR; 1.

D1	PROSITE; PS00038; FZ; 1.	DR	SMART; SM00408; IGC2; 1.
D1	PROSITE; PS00835; IG LIKE; 1.	DR	SMART; SM00130; KR; 1.
D1	PROSITE; PS00021; KRINGLE 1; 1.	DR	SMART; SM00220; S_TKC; 1.
D1	PROSITE; PS00070; KRINGLE 2; 1.	DR	SMART; SM00219; TYRC; 1.
X1	Glycoprotein; Immunoglobulin domain; Kinase; Kringle; Receptor.	DR	PROSITE; PS00038; FZ; 1.
S1	SEQUENCE 393 AA; 43825 MW; 1F93DCBBBF3855 CRC64;	DR	PROSITE; PS00835; IG LIKE; 1.
		DR	PROSITE; PS00021; KRINGLE 1; 1.
		DR	PROSITE; PS00070; KRINGLE 2; 1.
		DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
		DR	PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
		SQ	SEQUENCE 937 AA; 104118 MW; CB440323CA66EC28 CRC64;
			Query Match 18.9%; Score 158.5; DB 11; Length 937;
			Best Local Similarity 29.7%; Pred. No. 2.7e-08;
			Matches 43; Conservative 14; Mismatches 51; Indels 37; Gaps 7;
			2 NELHQP-----SNDCINGGTCVSNKYPS-----NIHWNC-----PKKFGGQH 41
			236 DETSVKPRDLCDCEILENLVLCQTEYIFARSPNPMILMKLPNCEDLPQPESPEAN 295
			42 C-----EIDSKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLQQTVAHRSAL 92
			296 CIRIGIPWADPINKHKCYNSTGVYRGTVSVTKSGRQCQPWS-----QYPHTHSFTAL 350
			93 QLG--LGKHYCRNPDRRR--PCWY 114
			351 RPELNGGHSYCRNPGNQKEAPWCF 375
			PRELIMINARY; PRT; 937 AA.
			RESULT 31
			Q8BG10 PRELIMINARY; PRT; 937 AA.
			Q8BG10; TISSUE=Adipose tissue;
			STRAIN=C57BL/6J; PubMed=12466851;
			MEDLINE=22354683; PubMed=12466851;
			the FANTOM Consortium,
			the RIKEN Genome Exploration Research Group Phase I & II Team;
			"Analysis of the mouse transcriptome based on functional annotation of
			60,770 full-length cDNAs."
			Nature 420:563-573 (2002).
			EMBL; AK045699; BAC32840.1; --
			EMBL; AK049369; BAC33714.1; --
			MGD; MGI:1347520; Rori.
			GO; GO:0016020; C:membrane; IEA.
			GO; GO:0005524; F:ATP binding; IEA.
			GO; GO:0004674; P:protein serine/threonine kinase activity; IEA.
			GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
			GO; GO:0004888; P:transmembrane receptor activity; IEA.
			GO; GO:0007275; P:development; IEA.
			GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
			InterPro; IPR000024; Fz domain.
			InterPro; IPR003599; IG.
			InterPro; IPR007110; IG-like.
			InterPro; IPR003598; IG c2.
			InterPro; IPR000001; Kringle.
			InterPro; IPR000719; Prot_kinase.
			InterPro; IPR002290; Ser_thr_kinase.
			InterPro; IPR001245; Tyr_kinase.
			InterPro; IPR008266; Tyr_kinase_AS.
			Pfam; PF01392; Fz; 1.
			Pfam; PF00047; Ig; 1.
			Pfam; PF00051; kringle; 1.
			Pfam; PF00069; pkinase.1.
			PRINTS; PR00018; KRINGLE.
			PRINTS; PR00109; TYRKINASE.
			ProDom; PD000395; Kringle; 1.
			ProDom; PD000001; Prot_kinase; 1.
			SMART; SM00409; IG; 1.

DR Pfam, PF00069; pkinase; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000395; Kringle; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00409; IG; 1.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00038; FZ; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS00070; KRINGLE 2; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 SQ SEQUENCE 937 AA; 10408 MW; D6F2D84567D03C69 CRC64;
 Query Match 18.9%; Score 158.5; DB 11; Length 937;
 Best Local Similarity 29.7%; Pred. No. 2.7e-08;
 Matches 43; Conservative 14; Mismatches 51; Indels 37; Gaps 7;
 QY 2 NELHQP-----SNDCINGTGVSNKYFS-----NIHWNC-----PKFGQGH 41
 DB 236 DETSVKPRDLRDECEVLENLQTEYIFARSNPMLMELKLPNCEDLPQEPSEPAAN 295
 QY 42 C-----BIDSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVQLQTYHAHRSDAL 92
 DB 296 CIRGIPVADPINKHKYCNSTGVYRGTVSTKSGRCQPWNS-----QYPHTSHSTAL 350
 QY 93 QLG--LGKHYNCRPNRR--PCWY 114
 DB 351 RPPELNGGHSYCRNPGNKEAPWCF 375
 RE T 32
 ID O46506 PRELIMINARY; PRT; 454 AA.
 AC O46506;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Apolipoprotein a (Fragment).
 GN BABAPOA.
 OS Papio hamadryas (Hamadryas baboon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID=9557;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cox L.A., Jett C., Hixson J.E.;
 RT Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation is Associated with Deletion of a Single Exon in a Null Allele.
 RT Submitted (Oct-1997) to the EMBL/GenBank/DBJ databases.
 CC -/- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -/- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 DR EMBL; AF029691; AAB97886.1; -.
 DR HSSP; P00747; 2PK4.
 DR MEROPS; S01.999; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00051; kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.

DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; TRY SPG; 1.
 DR PROSITE; PS00021; KRINGLE 1; 2.
 DR PROSITE; PS00070; KRINGLE 2; 2.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Glycoprotein; Hydrolase; Kringle; Lipoprotein; Protease;
 KW Serine protease.
 FT NON_TER 1
 SQ SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;
 Query Match 18.9%; Score 158; DB 6; Length 454;
 Best Local Similarity 39.8%; Pred. No. 1.4e-08;
 Matches 35; Conservative 10; Mismatches 31; Indels 12; Gaps 4;
 QY 50 CYEGNGHFYRGKASTDTMGRPCLPWNSATVQLQTYHAHRSDALQLGLGKHNYCRNPDN 107
 DB 102 CYHGDQSYRGSTFTVTGRTCSWSSMTPHQKRTPEHPNDGLTM----NYCRNEDA 156
 QY 108 RRRPWCYVQVGLKPLV--QECMVHDCAD 133
 DB 157 DTGPMCF---MDPSVRWEYCNLTTCSD 181
 RESULT 33
 ID Q9UIR5 PRELIMINARY; PRT; 113 AA.
 AC Q9UIR5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (Fragment).
 GN APOA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21181705; PubMed=11285247;
 RA Ogorekova M., Kraft H.G., Ehnholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians."
 RT Hum. Mol. Genet. 10:815-824(2001).
 CC -/- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR EMBL; AF158663; AAF03680.1; -.
 DR EMBL; AF158662; AAF03680.1; JOINED.
 DR HSSP; P00747; 1PMK.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS00070; KRINGLE 2; 1.
 KW Glycoprotein; Kringle; Lipoprotein.
 FT NON_TER 1
 FT NON_TER 113
 SQ SEQUENCE 113 AA; 12685 MW; F3D65681D9B5253A CRC64;
 Query Match 18.8%; Score 157; DB 4; Length 113;
 Best Local Similarity 34.8%; Pred. No. 4e-09;
 Matches 39; Conservative 13; Mismatches 36; Indels 24; Gaps 6;
 QY 48 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATV--LQTYHAHRSDALQLGLGKHNYCRNP 105
 DB 9 RCYHNGQSYRGSTFTVTGRTCSWSSMTPHRQRTPEHPNDGLTM----NYCRNP 63
 QY 106 DNRERPWCYVQVGLKPLV--QECMVHDCADG-----KKPS-SPPEE 143
 DB 64 DADTGPWCFT---MDPSVRWEYCNLTTCSDTEGTVPVAPPTVIQVPSLGPPE 112

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R1 1LT 34
R2 84
R3 Q7TP84 PRELIMINARY; PRT; 759 AA.
R4 Q7TP84;
R5 01-OCT-2003 (TRENBLrel. 25, Created)
R6 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
R7 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
R8 Abi-346.
R9 Rattus norvegicus (Rat).
R10 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
R11 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
R12 NCBI_TaxID=10116;
R13 [1]
R14 SEQUENCE FROM N.A.
R15 Xu C.S., Li W.Q., Li Y.C., Yan H.M., Chang C.F., Zhao L.F., Ma H.,
R16 Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
R17 Yang K.J., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
R18 "Liver regeneration after PH.";
R19 Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
R20 EMBL; AY325159; AAP92560.1; -.
R21 SEQUENCE 759 AA; 86056 MW; 1422BFAC05C6DFA7 CRC64;
R22
R23 Query Match 18.7%; Score 156.5; DB 11; Length 759;
R24 st Local Similarity 24.2%; Pred. No. 3.6e-08;
R25 tches 53; Conservative 22; Mismatches 49; Indels 95; Gaps 12;
R26
R27 Q 5 HQVPSNCDLNGGTCVSNKYFSN-----IHW-NCPKFGGQHCIEI-----DKS-- 47
R28 316 NRTPEPFCKN---LEBNYCRNPDPGETAPWCYTTSQLRWEYCEIPSCGSSVSPDQSDS 371
R29 48 -----KTCYEGNGHFYRGKASDTMGRCLPWN SATVLOQTYHAHS-----DA 91
R30 372 SVLPQETPVQECYQNGSKYRGTSSTNTGKKQSW-----VSMTHSHSKTPANFPDA 426
R31 92 LQLGLGKH-----NYCRNPDN-RRREWY 114
R32 427 YONLLIQHWRPSVYVYMSLWETFLIHTNQYSVQLKSSGLENNYCRNPDNDQGEWCF 485
R33 115 VQVGLKPLV--QECNVHDCAD-----GKPSPP 140
R34 487 T--TDPFSRWEYCNLKRCSETGGTGVAAESAIVPQVPSAP 522
R35
R36 1LT 35
R37 46
R38 Q15146 PRELIMINARY; PRT; 810 AA.
R39 Q15146;
R40 01-NOV-1996 (TRENBLrel. 01, Created)
R41 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
R42 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
R43 Plasminogen precursor.
R44 Homo sapiens (Human).
R45 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
R46 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
R47 NCBI_TaxID=9606;
R48 [1]
R49 SEQUENCE FROM N.A.
R50 TISSUE=Liver;
R51 Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,
R52 Mitchell D., Robinson J.H.;
R53 "Expression of recombinant human plasminogen and aglycoplasminogen in
R54 HeLa cells.";
R55 Fibrinolysis:0:0-0(1991).
R56 -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
R57 EMBL; M74220; AAA36451.1; -.
R58 HSP; P00747; 2PKA.
R59 GO; GO:0005509; F:calcium ion binding; IEA.
R60 GO; GO:0004263; F:chymotrypsin activity; IEA.
R61 GO; GO:0008233; F:peptidase activity; IEA.
R62 GO; GO:0003809; F:thrombin activity; IEA.
R63 GO; GO:0004295; F:trypsin activity; IEA.

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DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000903; Cys Ser trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00340; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR GlycoProtein; Hydrolase; Kringle; Protease; Serine protease; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 810 PLASMINOGEN.
SQ SEQUENCE 810 AA; 90555 MW; B05C7D4B0D020B3C CRC64;
Query Match 18.7%; Score 156.5; DB 4; Length 810;
Best Local Similarity 28.5%; Pred. No. 3.8e-08;
Matches 49; Conservative 22; Mismatches 52; Indels 49; Gaps 12;
QY 5 HQVPSNCDLNGGTCVSNKYFSN-----IHW-NCP-KKFGGQHCIEI-----DKS----- 47
DB 308 NRTPEPFCKN---LEBNYCRNPDPGETAPWCYTTSQLRWEYCEIPSCDSSPVSTEQIA 363
QY 48 -----KTCYEGNGHFYRGKASDTMGRCLPWN SATVLOQTYHAHS---SDALQ 93
DB 364 PTAPPPLTPVQDCHGQSGYRGTSSTNTGKKQSWSS-----WTHRHQKTPENYPN 418
QY 94 LGLGKHNYCRNPDNRRRWYVQVGLKPLV--QECNVHDCADGKKPS--SPP 141
DB 419 AGL-TMNYCRNPDADKGPWCFT---TDPFSRWEYCNLKKS-GTEASVVAPP 465
RESULT 36
Q8KQ08 PRELIMINARY; PRT; 801 AA.
AC Q8KQ08;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; BC030848; AAH30848.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004574; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0004588; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

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DR InterPro; IPR000024; F2_domain.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR000019; Ser Thr kinase.
 DR InterPro; IPR002290; Ser Thr kinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000395; Kringle; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00130; K3; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00038; FZ; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00021; KRINGLE_2; 1.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 KW Hypothetical protein, ATP-binding; Glycoprotein; Kringle; Transferase.
 FT NON_TER
 SQ SEQUENCE 801 AA; 89201 MW; 3A5928326C8B885D CRC64;
 Query Match 18.4%; Score 154; DB 11; Length 801;
 Best Local Similarity 36.8%; Pred. No. 7e-08; Mismatches 11; Indels 26; Gaps 9;
 Matches 43; Conservative 11; Mismatches 37; Indels 26; Gaps 9;
 QY 32 NC-----PKFGGQHCHIDSKTCYEGNGHYRGKASTDTWGRPCLPWNSATVLOQTYH 85
 DB 156 NCWRIGIPAEIRLGRYH-----QCYNGSGADYRGMASTTXSGHCQCPW-----ALQHP-H 203
 QY 86 AHR--SDALQLGLGHKHYCRNPNRRR-PMCYOVGLKPLVQECMVHDCA--DGKK 136
 DB 204 SRLSLSTPEPELG-GGHAYCRNPGQMEGPCFTQ-KKNVRVELCDVPPCSPRGSK 258
 RE: AT 37
 OL 13
 ID OL18783 PRELIMINARY; PRT; 806 AA.
 AC OL18783
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Plasminogen.
 OS Macropus eugenii (Tamar wallaby).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 OX NCBI_TaxID=9315;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98004511; PubMed=9342350;
 RA Lawn R.M., Schwartz K., Pathy L.;
 RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog."
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
 CC 1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
 DR EMBL; AF012297; BAB65760.1; --
 DR HSP; P00747; SHPG.
 DR MEROPS; S01.233; --
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007596; F:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pr.
 DR Pfam; PF00051; kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF00089; tyrosin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 5.
 DR ProDom; PD000130; KR; 4.
 DR SMART; SM00473; PAN AP; 1.
 DR SMART; SM00020; TYD_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS00240; TRYPsin DOM; 1.
 DR PROSITE; PS00134; TRYPsin HIS; 1.
 DR PROSITE; PS00135; TRYPsin SER; 1.
 KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
 SQ SEQUENCE 806 AA; 90981 MW; 95FAA86DC20064D5 CRC64;
 Query Match 18.4%; Score 154; DB 6; Length 806;
 Best Local Similarity 30.5%; Pred. No. 7.1e-08; Mismatches 9; Indels 38; Gaps 5;
 Matches 39; Conservative 9; Mismatches 42; Indels 38; Gaps 5;
 QY 25 FSNHWCNCPKFGGQHCHIDSKTCYEGNGHYRGKASTDTWGRPCLPWNSATVLOQTY 84
 DB 256 FCNIPRCSSPPPPGPMQ-----CLKGRGENYRGKIATVKSHTCQRWN-----KQTP 304
 QY 85 HAHRSDALQI-----GLCKHYCRNPNRRPWCVV-----QVG 118
 DB 305 HKGNRTPEPNPCRGGLDE-NYCRNPDELEPWCYTTNPVDRQYCAIPSCGTSPTHTDYE 363
 QY 119 LKPLVQEC 126
 DB 364 QSPVQEC 371
 RESULT 38
 Q8C3W2 PRELIMINARY; PRT; 944 AA.
 ID Q8C3W2
 AC Q8C3W2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Receptor tyrosine kinase-like orphan receptor 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Heart;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium.
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,776 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK084752; BAC39273.1; --
 DR MGD; MGI:1347521; Ror2.
 DR GO; GO:0001501; P:skeletal development; IMP.
 DR InterPro; IPR000024; Fz_domain.
 DR InterPro; IPR003599; Ig_c2.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR InterPro; IPR008266; Tyr_pkinase_AS.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF00047; Ig; 1.

Db	RE	68 RPWCYT---MDPSVKEWYCNLTRC 89	131 CAD 133	131 CAD 133
	P7	: : :	369 CTD 371	369 CTD 371
	ID	68 RPWCYT---MDPSVKEWYCNLTRC 89		
	ID	P70006 PRELIMINARY; PRT; 717 AA.		
	AC	P70006; PRELIMINARY; PRT; 717 AA.		
	DT	01-FEB-1997 (TREMELrel. 02, Created)		
	DT	01-FEB-1997 (TREMELrel. 02, Last sequence update)		
	DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)		
	DE	Hepatocyte growth factor-like protein precursor.		
	OS	Xenopus laevis (African clawed frog).		
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;		
	OC	Xenopodinae; Xenopus.		
	OX	NCBI_TaxID=8355;		
	RN	[1]		
	RP	SEQUENCE FROM N.A.		
	RC	TISSUE=Kidney;		
	RX	MEDLINE=96404125; PubMed=8808403;		
	RA	Aberger F., Schmidt G., Richter K.;		
	RT	"The Xenopus homologue of hepatocyte growth factor-like protein is specifically expressed in the presumptive neural plate during gastrulation."		
	RT	Mech. Dev. 54:23-37(1996).		
	RL	-!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.		
	CC	EMBL; Y08734; CAA69989.1; -.		
	DR	HSSP; P00747; 1CEA.		
	DR	MEROPS; S01.977;		
	DR	GO; GO:0005509; F:calcium ion binding; IEA.		
	DR	GO; GO:0004263; F:chymotrypsin activity; IEA.		
	DR	GO; GO:0008233; F:peptidase activity; IEA.		
	DR	GO; GO:0003809; F:thrombin activity; IEA.		
	DR	GO; GO:0004295; F:trypsin activity; IEA.		
	DR	GO; GO:0007596; P:blood coagulation; IEA.		
	DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.		
	DR	InterPro; IPR009003; Cys_Ser_trypsin.		
	DR	InterPro; IPR000001; Kringle.		
	DR	InterPro; IPR003014; PAN.		
	DR	InterPro; IPR003609; Pan app.		
	DR	InterPro; IPR001254; Peptidase S1.		
	DR	InterPro; IPR001314; Peptidase S1A.		
	DR	InterPro; IPR003966; Peptidase_S1A_pr.		
	DR	Pfam; PF00051; kringle; 4.		
	DR	Pfam; PF00024; PAN; 1.		
	DR	Pfam; PF00089; trypsin; 1.		
	DR	PRINTS; PR00722; CHYMOTRYPSIN.		
	DR	PRINTS; PR00018; KRINGLE.		
	DR	PRINTS; PR01505; PROTHROMBIN.		
	DR	ProDom; PD000395; Kringle; 4.		
	DR	SMART; SM00130; KR; 4.		
	DR	SMART; SM00473; PAN AP; 1.		
	DR	SMART; SM00020; TRY SP; 1.		
	DR	PROSITE; PS00021; KRINGLE_1; 4.		
	DR	PROSITE; PS00070; KRINGLE_2; 4.		
	DR	PROSITE; PS00240; TRYPSIN_DOM; 1.		
	KW	Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.		
	FT	SIGNAL 1 28 POTENTIAL		
	FT	CHAIN 29 717 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.		
	SQ	SEQUENCE 717 AA; 82017 MW; 658777A32C8CDD54 CRC64;		
		Query Match 18.2%; Score 152.5; DB 13; Length 717;		
		Best Local Similarity 31.7%; Pred. No. 9e-08;		
		Matches 39; Conservative 13; Mismatches 42; Indels 29; Gaps 6;		
QY	30	WC-----NCPKFGGQHCIDK-----TCYEGNGHYRGKASTDTMGRCLP 73		
Db	259	WCYTDPNVREF-----CHITCKQRISNIEITSTCFKRGEGYRGKANTTSGIFCQR 314		
QY	74	WNSATVLOQTYHAHSDALQL---GLGKHYCRPNDRRRPWCYVQVGLKPLVQECMVHD 130		
Db	315	WDT-----QAPHVHFLEPKYFCKGLDE-NYCRAPVGSAPACFTTLKNWEMAYCFQIKR 369		
		Query Match 18.2%; Score 152; DB 4; Length 567;		
		Best Local Similarity 29.4%; Pred. No. 7.9e-09;		
		Matches 37; Conservative 17; Mismatches 46; Indels 26; Gaps 7;		
QY	30	WC-NCPKFGGQHCIDK-----SKCYEGNGHYRGKASTDTMGRCLPWN 76		
Db	225	WCYTDPQIEREFCDLPRCGSEAPQBEATSVSCFPGKGEYRGKTANTTAGVPCQRWDA 284		
QY	77	ATVLOQTYHAHSDALQLGLG---KINYCNPNDRRRPWCYVQVGLKP--LYQEC-MVHDC 131		
Db	285	-----QIPQHRFTPEKYACKDLRENFNPDGSEAPWCFT---LRPGRVGFYQIRRC 336		
QY	132	ADGKKP 137		
Db	337	TDDVRP 342		
		Query Match 18.2%; Score 152; DB 4; Length 567;		
		Best Local Similarity 29.4%; Pred. No. 7.9e-09;		
		Matches 37; Conservative 17; Mismatches 46; Indels 26; Gaps 7;		

R JLT 43
Q I V4 PRELIMINARY; PRT; 648 AA.
A Q9HIV4;
D 01-MAR-2001 (TRENBLrel. 16, Created)
D 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
D 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
D J1182A14.3 (Similar to MST1 (Macrophage stimulating 1 (Hepatocyte growth factor-like)))
D J1182A14.3.
D Homo sapiens (Human).
O Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
O Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
C NCBI_TaxID=9606;
R [1]
R SEQUENCE FROM N.A.
R Bird C.;
R Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
R -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
C -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
D HMBP; A1137798; CAC17639.1; -.
D HMBP; P00747; SHPG.
D GO; GO:0004263; F:chymotrypsin activity; IEA.
D GO; GO:0008233; F:peptidase activity; IEA.
D GO; GO:0004295; F:trypsin activity; IEA.
D GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
D InterPro: IPR009003; Cyt_Ser_trypsin.
D InterPro: IPR000001; Kringle.
D InterPro: IPR003014; PAN.
D InterPro: IPR003609; Pan app.
D InterPro: IPR001254; Peptidase S1.
D InterPro: IPR001314; Peptidase_S1A.
D Pfam; PF00024; PAN; 1.
D Pfam; PF00051; kringle; 4.
D Pfam; PF00089; trypsin; 1.
D PRINTS; PR00722; CHYMOTRYPSIN.
D PRINTS; PR00018; KRINGLE.
D ProDom; PD000395; Kringle; 4.
D SMART; SM00130; KR; 4.
D SMART; SM00473; PAN_AP; 1.
D SMART; SM00020; Tryp_Spc; 1.
D PROSITE; PS00021; KRINGLE_1; 3.
D PROSITE; PS00070; KRINGLE_2; 4.
D PROSITE; PS00240; TRYPSIN_DOM; 1.
D Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
S SEQUENCE 648 AA; 72781 MW; 4C80770573508463 CRC64;

Query Match 18.2%; Score 152; DB 4; Length 648;
Best Local Similarity 29.4%; Pred. No. 9.1e-08;
Matches 37; Conservative 17; Mismatches 46; Indels 26; Gaps 7;

Q 30 WC-NCPKFGGQHCIDK-----SKTYEGNGHFYRGKASTDTMGRPCLPWS 76
D 205 WCYTTPQIEREFCDLPRGSEAQPROEATSVSCFRGEGYGTANTTTAGVPCQRWDA 264
Q 77 ATVLQOTYHAHSDALQLGLG--KNYCNPNRRRRCYGVGLKP--LVQEC-MVHDC 131
D 265 -----QIPHOHRTPEKYACKDLRENFCEPNPDGSEAPWCFT---LRPGRVGFCYQIIRC 316
Q 132 ADGKKP 137
D 317 TDDVRP 322

R JLT 44
Q I V4 PRELIMINARY; PRT; 930 AA.
A Q8AV69;
D 01-MAR-2003 (TRENBLrel. 23, Created)
D 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
D 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
D Receptor tyrosine kinase Xror2.
C XRO2.

OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RP MSDLINE=2286220; PubMed=12399314;
RX Hikasa H., Shibata M., Hiratani I., Taira M.;
RT "The Xenopus receptor tyrosine kinase Xror2 modulates morphogenetic movements of the axial mesoderm and neuroectoderm via Wnt signalling.";
RT Development 129:5227-5239(2002).
RL EMBL; AB087137; BAC16209.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro: IPR000024; Pz_domain.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR InterPro: IPR008266; Tyr_kinase_AS.
DR Pfam; PF01392; Pz; 1.
DR Pfam; PF00047; ig; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TKG; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00038; Pz; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW Kinase.
SQ SEQUENCE 930 AA; 104081 MW; C68454572411A8B6 CRC64;

Query Match 18.0%; Score 150.5; DB 13; Length 930;
Best Local Similarity 28.0%; Pred. No. 2e-07;
Matches 37; Conservative 18; Mismatches 44; Indels 33; Gaps 8;

Qy 11 CDCNGTCTVSNKY-----FSNIHMCNC-----PKFGGQHC-----EIDKSK 48
D 252 CEVLNDLC-RQSYNTARSNPLILMQLHPNCELPSPESPEANCMRIGIPVEKLNRYQ 310
Qy 49 TCYEGNGHFYRGKASTDTMGRPCLPWSATVLOOTYHAH---RSDALQLGLGHNYCRNP 105
D 311 QCYNGTGTDRGSVSVTKGHQCQCPWS-----HQVPHSHLSNADYFEIG-GGHSYCRNP 364
Qy 106 DNRRR-PWCYVQ 116
D 365 GGQWEGWCFQ 376

RESULT 45
Q7ZTN9 PRELIMINARY;
ID Q7ZTN9 PRT; 709 AA.
AC Q7ZTN9;

DT 01-JUN-2003 (T-EMBLrel. 24, Created)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
 DE 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Similar to macrophage stimulating 1 (Hepatocyte growth factor-like).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR ENBL, BC044008; AAH44008.1; -.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007596; F:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR InterPro; IPR001254; Peptidase S1.
 DR InterPro; IPR001314; Peptidase S1A.
 DR InterPro; IPR001966; Peptidase_S1A_pr.
 DR Pfam; PF00051; kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR PRINTS; PR00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; tryf_Spc; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS00070; KRINGLE_2; 4.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 SQ SEQUENCE 709 AA; 81123 MW; 51C44D8EBD03B76A CRC64;
 Query Match 17.9%; Score 149.5; DB 13; Length 709;
 Best Local Similarity 28.0%; Pred. No. 1.9e-07;
 Matches 44; Conservative 16; Mismatches 58; Indels 39; Gaps 8;
 Qy 15 NGGTC-----VSNKYFSGNIHW-----CNCP-----KKFGQHCEIDKS 47
 Db 127 NGRTQCHWLKFFPHDKHFSPTWPELEENVCNRPDSDEGLWCYTTDKNIRHQYCGIKK 186
 Qy 48 K--TCVEGCHFRGKASTDTMGPRCLPWNSATVLOQTY-HAHRSDALQLGLGKKNYCRN 104
 Db 187 EDVCLTCGDEYRGVSDTESGKQQRWD---LQAPHTFPKPKPKYDPSLDDNYCRN 242
 Qy 105 PDNRPRWCYVQVGLKPLVQ--CMVHDCADGKKPS 139
 Db 243 PDSSRPWCYT---TDPNVEREFCHITKIEQRISN 276
 RE [T 46
 ID Q3UIR8 PRELIMINARY; PRT; 105 AA.
 AC Q3UIR8;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DE 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
 DE Apolipoprotein(a) (fragment).
 GN APOA.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Thery C., Sharpe M.J., Batley S.J., Stern C.D., Gherardi E.;
 RT "Expression of HGF/SF, HGF1/MSP and c-met suggests new functions during early chick development.";
 RL Dev. Genet. 17:90-101(1995).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR ENBL; X84043; CAA58862.1; -.
 DR HSSP; P00747; 1CEA.
 DR MEROPS; S01.977; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 QX NCBI_TaxID=9606;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Ogorelkova M., Kraft H.G., Ehnholm C., Utermann G.;
 RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect Lp(a) plasma concentrations and have different patterns in Africans and Caucasians.";
 RL Hum. Mol. Genet. 10:815-824(2001).
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 DR ENBL; AF158656; AAF03677.1; -.
 DR ENBL; AF158655; AAF03677.1; JOINED.
 DR HSSP; P00747; 2PK4.
 DR InterPro; IPR000001; Kringle.
 DR Pfam; PF00051; kringle; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 KW Glycoprotein; Kringle; Lipoprotein.
 FT NON TER 1 105
 FT NON TER 105 105
 SQ SEQUENCE 105 AA; 11882 MW; 6ECB6C02CD30EFA2 CRC64;
 Query Match 17.7%; Score 148; DB 4; Length 105;
 Best Local Similarity 38.1%; Pred. No. 3.4e-08;
 Matches 32; Conservative 8; Mismatches 36; Indels 8; Gaps 3;
 Qy 50 CYEGNCHFRGKASTDTMGPRCLPWNSATVLOQTYHAHRSDALQLGLGKKNYCRNDR 109
 Db 11 CYHGDGSGYRGFSFTVTGRTCSWSMT---PHHQRTTEYYPNGGLTRNYCRNPD 67
 Qy 110 RPYCVQVGLKPLV--QECMVHDC 131
 Db 68 SPWCYT---MDPNVRWEYCNLTQC 88
 RESULT 47
 ID Q90865 PRELIMINARY; PRT; 704 AA.
 AC Q90865;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Hepatocyte growth factor-like/macrophage stimulating protein.
 GN HGF1/MSP.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RE SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA MEDLINE=96029010; PubMed=7554499;
 RT "Expression of HGF/SF, HGF1/MSP and c-met suggests new functions during early chick development.";
 RL Dev. Genet. 17:90-101(1995).
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
 DR ENBL; X84043; CAA58862.1; -.
 DR HSSP; P00747; 1CEA.
 DR MEROPS; S01.977; -.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.

D: InterPro; IPR001254; Peptidase S1.
D: InterPro; IPR001314; Peptidase_SIA.
D: Pfam; PF00051; kringle_4.
D: Pfam; PF00024; PAN; 1.
D: Pfam; PF00089; trypsin; 1.
D: PRINTS; PR00722; CHYMOTRYPSIN.
D: PRINTS; PR00018; KRINGLE.
D: ProDom; PD000395; Kringle; 4.
D: SMART; SM00130; KR; 4.
D: SMART; SM00473; PAN_AP; 1.
D: SMART; SM00020; Tryp_Spc; 1.
D: PROSITE; PS00021; TRYPSIN_1; 4.
D: PROSITE; PS50070; KRINGLE_2; 4.
D: PROSITE; PS50240; TRYPSIN_DOM; 1.
D: Glycoprotein; Hydroxylase; Kringle; Protease; Serine protease.
S: SEQUENCE 704 AA; 79341 MW; CAB08CC41367C37 CRC64;
Query Match 17.7%; Score 148; DB 13; Length 704;
Best Local Similarity 30.9%; Pred. No. 2.7e-07;
Matches 47; Conservative 12; Mismatches 63; Indels 30; Gaps 10;
Q 5 HQVSNDC--LNGTCVSNKYFSNIHWNCPPK-----FGQHC--RIDSKTCYEG 53
D: 312 HFVPSKYPCKDLQENYC--RNPDSGEAPWCFTTRFGMRVAFCHIRCDDEL--ABECYHG 369
Q 54 NGHYRGKASTDTMGRPCLPWNSAT---VLQQYH--AHSRDLQGLGKHNYCRNPDN 107
D: 370 HGERYHGHVSKTRKIGICORWDATPHVPQISPTTPEAHL-----EKNYCNPDN 420
Q 108 -RRPWCYVQGLKPLVQECMVHDCADGKKPS 138
D: 421 DSHGFWCYTMDPRTFF-DYCAIKPCSGSAVPS 451
R: LT 48
Q: Q8 Q8 PRELIMINARY; PRT; 716 AA.
A: Q91XG8;
D: 01-DEC-2001 (TremBLrel. 19, Created)
D: 01-DEC-2001 (TremBLrel. 19, Last sequence update)
D: 01-OCT-2003 (TremBLrel. 25, Last annotation update)
D: Hepatocyte growth factor-like.
G: MSII OR HGFL
O: Mus musculus (Mouse).
O: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
O: Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
O: NCBI_TaxID=10090;
E: [1]
F: TISSUE=Liver;
R: Strausberg R.;
R: Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
C: -!- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
D: EMBL; BC010551; AAHL0551.1; -.
D: HSP; P00761; 1AN1.
D: MGD; MGI:96080; Met1.
D: GO; GO:0007566; P:embryo implantation; IC.
D: InterPro; IPR00003; Cys_Ser_trypsin.
D: InterPro; IPR000001; Kringle.
D: InterPro; IPR003014; PAN.
D: InterPro; IPR003609; Pan_app.
D: InterPro; IPR001254; Peptidase S1.
D: InterPro; IPR001314; Peptidase_SIA.
D: InterPro; IPR003966; Peptidase_SIA_pr.
D: Pfam; PF00051; kringle; 4.
D: Pfam; PF00024; PAN; 1.
D: Pfam; PF00089; trypsin; 1.
D: PRINTS; PR00722; CHYMOTRYPSIN.
D: PRINTS; PR00018; KRINGLE.
D: PRINTS; PR01505; PROTHROMBIN.
D: ProDom; PD000395; Kringle; 4.
D: SMART; SM00130; KR; 4.
D: SMART; SM00473; PAN_AP; 1.

DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS50070; KRINGLE_2; 4.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
KW Glycoprotein; Hydroxylase; Kringle; Protease; Serine protease.
SQ SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;
Query Match 17.6%; Score 147.5; DB 11; Length 716;
Best Local Similarity 36.5%; Pred. No. 3.1e-07;
Matches 38; Conservative 11; Mismatches 34; Indels 21; Gaps 7;
QY 50 CYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYHAHR-----SDALQLGLGKHNYCRN 104
DB 379 CYHSGEQYRGVSXTRKGVQCHWSSET-----PHKQFTTSAPOAGL-EANFCRN 430
QY 105 PD-NRRRPWCYVQGLKP--LVQECMVHDCADGKKPS--SPPEE 143
DB 431 PDGDSHGWCYT---LDPEILFDYCALQRCDDDPSPILDPDQ 471
RESULT 49
Q9UIR6 PRELIMINARY; PRT; 113 AA.
AC Q9UIR6;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE Agolipoprotein(a) (Fragment).
CN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21181705; PubMed-11285247;
RA Ogorekova W., Kraft H.G., Enholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158661; AAF03679.1; -.
DR EMBL; AF158660; AAF03679.1; JOINED.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12697 MW; 51D4461D9C66312E CRC64;
Query Match 17.6%; Score 147; DB 4; Length 113;
Best Local Similarity 36.0%; Pred. No. 4.7e-08;
Matches 31; Conservative 14; Mismatches 33; Indels 8; Gaps 4;
QY 50 CYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNR 109
DB 11 CYHGDGRSYRGISSTVTGTCQSWSS--MIPHMQRTPENYPNAGL-TENYCRNPDGCK 67
QY 110 RWCYVQGLKPLV--QECMVHDCAD 133
DB 68 QPWCYT---TDFCVRWEYCNLTQCS 90
RESULT 50
Q28398 PRELIMINARY; PRT; 2869 AA.
ID Q28398

AC Q28398;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE Apolipoprotein(a) (Fragment).
OS Erinaceus europaeus (Western European hedgehog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.
OX NCBI_TaxID=9365;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96025778; PubMed=7592577;
RA Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,
RA Byrne C.D., Fong K.J., Meer K., Patthy L.;
RT "The recurring evolution of lipoprotein(a). Insights from cloning of
RT hedgehog apolipoprotein(a).";
RL J. Biol. Chem. 270:24004-24009(1995).
CC -!- SIMILARITY: CONTAINS 31 KRINGLE DOMAINS.
DR EMBL; U33170; AAC48522.1; -.
DR PIR; T18518; T18518.
DR HSSP; P00747; 1PMK.
DR InterPro: IPR000001; Kringle.
DR Pfam: PF00051; kringle; 31.
DR PRINTS; PRO0018; KRINGLE.
DR ProDom; PD000395; Kringle; 31.
DR SMART; SM00130; KG; 31.
DR PROSITE; PS00021; KRINGLE_1; 30.
DR PROSITE; PS00070; KRINGLE_2; 31.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON_TER .1
SQ SEQUENCE 2869 AA; 318601 MW; 9527CEP985A4FE2A CRC64;

ary Match 17.6%; Score 147; DB 6; Length 2869;
st Local Similarity 29.3%; Pred. No. 1.6e-06;
ches 39; Conservative 11; Mismatches 61; Indels 22; Gaps 6;

QY 19 CYSNKFYSNIHNCNCPKFGGQHCIDKSKT-----CYEGNGHFYRGKASTDTMGRP 70
Db 2558 CYTTSAMWEYCSIPA-----CESPTPTLHVVPQCLENGENTQGNWATVSCQP 2611
QY 71 CLFWSATVLOQTYHAHRSDALQLGLGKHNCRPNRRRPMCVYQVGLKPLVQECMVHD 130
Db 2612 CQWRKQTPRHREYTPENYPKSL-PG--NYCRNPDGEIAPWCYT-TNSAVRWEYCSIPT 2667
QY 131 CADGKXPSSPPEE 143
Db 2668 C-----ESSSPPE 2676

Se: h completed: May 25, 2004, 14:57:18
Jo: ime : 24.6871 secs

GenCore version 5.1.6
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C protein - protein search, using sw model

R on: May 25, 2004, 14:43:00 ; Search time 34.9667 Seconds

(without alignments)

1155.508 Million cell updates/sec

T le: US-09-880-503-8

E fect score: 837

S uence: 1 SNEHQVPSNCDLNGGTCV.....QECNVHDCAGKPKSPPEE 143

S ring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

S tched: 1586107 seqs, 282547505 residues

T al number of hits satisfying chosen parameters: 1586107

M inum DB seq length: 0

M inum DB seq length: 2000000000

E t-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

D atabase : A_Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

R	ult	No.	Score	Match	Length	ID	Description
1		837	100.0	143	5	AAR16549	Human uPA
2		837	100.0	337	4	AG75492	Human col
3		837	100.0	337	5	ABP41795	Human ova
4		837	100.0	411	1	AAF50871	Sequence
5		837	100.0	411	2	AAR06244	Urokinase
6		837	100.0	411	2	AAR05117	UK-S3 as
7		837	100.0	411	2	AAR05117	Human nat
8		837	100.0	411	2	AAR10057	Pro-uroki
9		837	100.0	411	2	AAR10058	Pro-uroki
10		837	100.0	411	2	AAR40225	POK. 2/19
11		837	100.0	411	2	AAR62997	Pro-uroki
12		837	100.0	411	2	AAR63008	Pro-uroki
13		837	100.0	411	2	AAR62999	Pro-uroki
14		837	100.0	411	2	AAR62994	Pro-uroki
15		837	100.0	411	2	AAR63003	Pro-uroki
16		837	100.0	411	2	AAR63001	Pro-uroki
17		837	100.0	411	2	AAR63006	Pro-uroki
18		837	100.0	411	2	AAR62992	Pro-uroki
19		837	100.0	411	2	AAR63002	Pro-uroki
20		837	100.0	411	2	AAR63007	Pro-uroki
21		837	100.0	411	2	AAR62995	Pro-uroki
22		837	100.0	411	2	AAR63000	Pro-uroki
23		837	100.0	411	2	AAR63004	Pro-uroki
24		837	100.0	411	2	AAR62996	Pro-uroki
25		837	100.0	411	2	AAR63005	Pro-uroki

ALIGNMENTS

RESULT 1

AAR16549 standard; protein; 143 AA.

AC AAR16549;

09-APR-2002 (first entry)

Human uPA amino terminal fragment (ATP) and connecting peptide.

Human, urokinase-type plasminogen activator; uPA; therapy; hypertension; stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder; microvascular occlusion; angiotensin disorder; pulmonary fibrosis; asthma; tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing; clotting disorder; uterine contraction disorder; respiratory disease; adult respiratory distress syndrome; amino terminal fragment; AIF; male impotence.

26	837	100.0	411	2	AAR62991	Pro-uroki
27	837	100.0	411	2	AAR62998	Pro-uroki
28	837	100.0	411	2	AAR62993	Pro-uroki
29	837	100.0	411	2	AAR92926	Pro-uroki
30	837	100.0	411	3	AAY92836	Urokinase
31	837	100.0	411	5	AAE16544	Human uro
32	837	100.0	412	2	AAR10334	Recombin
33	837	100.0	424	2	AAW24579	Inhibitor
34	837	100.0	430	2	AAW24578	Inhibitor
35	837	100.0	431	1	AAW50114	Sequence
36	837	100.0	431	1	AAW60783	Human uro
37	837	100.0	431	1	AAW70258	Sequence
38	837	100.0	431	1	AAW71491	Modified
39	837	100.0	431	1	AAW71663	Modified
40	837	100.0	431	1	AAW71698	Modified
41	837	100.0	431	1	AAW71699	Modified
42	837	100.0	431	1	AAW80430	Deduced A
43	837	100.0	431	1	AAW81204	Pro-uroki
44	837	100.0	431	1	AAW91886	Sequence
45	837	100.0	431	1	AAW92119	Natural h
46	837	100.0	431	1	AAW94764	Non-glyco
47	837	100.0	431	2	AAW07112	Human pro
48	837	100.0	431	2	AAW04253	Human pro
49	837	100.0	431	2	AAW63141	Full leng
50	837	100.0	431	2	AAW47903	Pro-uroki
51	837	100.0	431	2	AAW33199	Human uri
52	837	100.0	431	2	AAW33198	Human uri
53	837	100.0	431	2	AAW33121	Human uri
54	837	100.0	431	3	AAW50869	Human uro
55	837	100.0	431	3	AAW99591	Human pla
56	837	100.0	431	4	AAW84605	Amino aci
57	837	100.0	431	5	AAE17128	Human uPA
58	837	100.0	431	5	AAU99228	Human pla
59	837	100.0	431	5	AAU99231	Human pla
60	837	100.0	431	5	AAU99229	Human pla
61	837	100.0	431	5	AAU99230	Human pla
62	837	100.0	431	5	AAW99460	sc-uPA. 1
63	837	100.0	431	6	AAE37128	Human uro
64	837	100.0	431	6	ABR55855	Human uro
65	837	100.0	431	6	ABU56547	Lung canc
66	837	100.0	431	6	ABU56708	Lung canc
67	837	100.0	431	6	ABU11076	Human uro
68	837	100.0	431	6	ABR92137	Human cer
69	837	100.0	431	7	ADD46429	Human Pro
70	837	100.0	434	2	AAR20537	Amidated
71	837	100.0	434	2	AAR20538	Amidated
72	837	100.0	436	2	AAR20536	Amidated
73	835	99.8	431	7	ADR25745	Human pro
74	834	99.6	208	2	AAW22747	Metastasi
75	834	99.6	411	2	AAW47958	PUR S261.

OS Homo sapiens.
 PN WO200197752-A2.
 XX 27-DEC-2001.
 XX 13-JUN-2001; 2001WO-US018976.
 XX 20-JUN-2000; 2000US-0212874P.
 XX (TYPE-) UNIV PENNSYLVANIA.
 PA Cines DB, Higazi AA;
 XX WPI; 2002-122240/16.
 XX N-PSDB; AAD27082.
 XX Composition for modulating muscle cell and tissue contractility for
 PT treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 PT comprising domains from urokinase-type plasminogen activator.
 XX Claim 24; Fig. 1H; 117pp; English.
 XX The invention relates to a composition comprising one or more domains of
 CC urokinase-type plasminogen activator (uPA). The composition is used to
 CC modulate the contractility and angiogenic activity of a mammalian muscle,
 CC endothelial cell or tissue. The composition is used for treating stroke,
 CC hypotension, hypertension, atherosclerosis, heart attack, microvascular
 CC occlusions, thrombotic microangiopathies, surgically induced thrombotic
 CC disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 CC invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
 CC diabetic retinopathy, wound healing, clotting disorder, uterine
 CC contraction disorder, male impotence, respiratory disease or condition
 CC such as asthma, adult respiratory distress syndrome, primary pulmonary
 CC hypertension, microvascular thrombotic occlusion, and a disorder
 CC associated with chronic intrapulmonary fibrin formation. The present
 CC sequence is human urokinase-type plasminogen activator (uPA) amino
 CC terminal fragment (ATP) and connecting peptide
 XX Sequence 143 AA;
 XX Query Match 100.0%; Score 837; DB 5; Length 143;
 XX Best Local Similarity 100.0%; Pred. No. 9.9e-56;
 XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60
 DB 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60
 QY 61 KASTDTWGRPCLPWSNATVLQOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
 DB 61 KASTDTWGRPCLPWSNATVLQOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
 QY 121 PLVQECMVHDCADGKKPSPPEE 143
 DB 121 PLVQECMVHDCADGKKPSPPEE 143
 RE IT 2
 AA 5492
 ID AAG75492 standard; protein; 337 AA.
 XX AAG75492;
 XX 03-SEP-2001 (first entry)
 XX Human colon cancer antigen protein SEQ ID NO:6256.
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma; chromosome 10.
 XX Homo sapiens.
 XX

PN WO200122920-A2.
 XX 05-APR-2001.
 XX 28-SEP-2000; 2000WO-US026524.
 XX 29-SEP-1999; 99US-0157137P.
 PR 03-NOV-1999; 99US-0163280P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Ruben SM, Barash SC, Birse CE, Rosen CA;
 PI WPI; 2001-235357/24.
 XX N-PSDB; AAH34897.
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers.
 XX Claim 11; Page 7707-7708; 9803pp; English.
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
 CC proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene therapy
 CC and vaccine production. N and P may be used in the prevention, diagnosis
 CC and treatment of diseases associated with inappropriate P expression. For
 CC example, N and P may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of P by expressing inactive proteins or to
 CC supplement the patient's own production of P. Additionally, N may be used
 CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAH77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1032, 7921 and 7922
 XX Sequence 337 AA;
 XX Query Match 100.0%; Score 837; DB 4; Length 337;
 XX Best Local Similarity 100.0%; Pred. No. 2.1e-55;
 XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60
 DB 27 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 86
 QY 61 KASTDTWGRPCLPWSNATVLQOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
 DB 87 KASTDTWGRPCLPWSNATVLQOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 146
 QY 121 PLVQECMVHDCADGKKPSPPEE 143
 DB 147 PLVQECMVHDCADGKKPSPPEE 169
 RESULT 3
 ABP41795
 ID ABP41795 standard; protein; 337 AA.
 XX ABP41795;
 XX 22-AUG-2002 (first entry)
 XX Human ovarian antigen HVUCB79, SEQ ID NO:2927.
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 XX

inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; neuroprotective; antibody preparation; cytotoxic; immunomodulatory; neuroprotective; antinflammatory; gynaecological; reproductive; chromosome 10q24.

Homo sapiens.

WO200200677-A1.

03-JAN-2002.

07-JUN-2001; 2001WO-US018569.

07-JUN-2000; 2000US-0209467P.

(HUMA-) HUMAN GENOME SCI INC.

Birse CE, Rosen CA;

WPI; 2002-147878/19.

N-PSDB; AB054872.

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological diseases.

Claim 11; SEQ ID NO 2927; 2922pp; English.

The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also encompasses polypeptides 90% identical and polynucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polynucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polynucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenital and acquired immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, respiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and polynucleotides may also be used in screening for compounds which modulate ovarian antigen expression or activity. The polynucleotides may further be used for gene therapy, chromosome mapping, in the identification of individuals and in forensic analysis, and the polypeptides may be used as food additives or to prepare antibodies useful in disease diagnosis, drug targeting and phenotyping. The present sequence represents a human ovarian antigen of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 337; AA;

Query Match 100.0%; Score 837; DB 5; Length 337;

Best Local Similarity 100.0%; Pred. No. 2.1e-55;

atches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNELHQPNSCCLNGTGVSNKYPSNIHWCNPKKFGGQHCIDSKTCYEGNGHYRG 60

27 SNELHQPNSCCLNGTGVSNKYPSNIHWCNPKKFGGQHCIDSKTCYEGNGHYRG 86

61 KASTDTMGRPCLPWSNATVLQOTYHAHRSDALQGLGKHNCRNPNRRRPMCYQVGLK 120

Db 87 KASTDTMGRPCLPWSNATVLQOTYHAHRSDALQGLGKHNCRNPNRRRPMCYQVGLK 146

Qy 121 PLVQECWVHDCADGKKPSPPEE 143

Db 147 PLVQECWVHDCADGKKPSPPEE 169

RESULT 4

AAP50871

ID AAP50871 standard; protein; 411 AA.

AC AAP50871;

XX 30-NOV-1991 (first entry)

XX Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese Patent Application No.37119/84).

XX Thrombolytic agent; plasminogen activator activity; fibrin affinity;

XX enzyme.

XX Homo sapiens.

OS

XX

Key Location/Qualifiers

FT Disulfide-bond 50..131

FT Disulfide-bond 71..113

FT Disulfide-bond 102..126

FT Disulfide-bond 148..279

FT Cleavage-site 158..159

FT /note= "potential cleavage site which generates the two-chain form from the zymogen"

FT Disulfide-bond 189..205

FT Disulfide-bond 197..268

FT Disulfide-bond 293..362

FT Disulfide-bond 325..341

FT Disulfide-bond 352..380

FN EPI39447-A.

XX

XX 02-MAY-1985.

XX 07-SEP-1984; 84EP-00306117.

XX 13-SEP-1983; 83JP-00170354.

XX 17-OCT-1983; 83JP-00195051.

XX (GPEC) GREEN CROSS CORP.

XX Kasai S, Arimura H, Mori K, Suyama T;

XX WPI; 1985-106530/18.

XX New urokinase zymogen - useful as thrombolytic agent.

XX

XX Disclosure; Page 12; 30pp; English.

XX Zymogen AAP50871 is the inactive precursor form of human urokinase.

XX Urokinase zymogen is cleaved into the two-chain form composed of

XX characteristic urokinase H (molecular wt. of 30,000) and L (molecular

XX wt. of 20,000) chains when treated with catalytic amounts of plasmin. The

XX patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a

XX single chain molecular structure, and selective affinity for fibrin. It

XX is a thrombolytic agent which manifests its plasminogen activator

XX activity on cleavage by proteolytic enzymes (e.g. plasmin) and has higher

XX affinity for fibrin than known forms of urokinase

XX

SQ Sequence 411 AA;

Query Match 100.0%; Score 837; DB 1; Length 411;

Best Local Similarity 100.0%; Pred. No. 2.4e-55;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 SNELHQPNSCCLNGTGVSNKYPSNIHWCNPKKFGGQHCIDSKTCYEGNGHYRG 60

1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
121 PLVQECMVHDCADGKPKSPPEE 143
121 PLVQECMVHDCADGKPKSPPEE 143

AA 5244
AA06244 standard; protein; 411 AA.
AA06244;
07-DEC-1990 (first entry)
Urokinase precursor protein.
Urokinase precursor; fibrinolysis; thrombolytic; cerebral thrombosis;
myocardial infarction.
Homo sapiens.
EP380334-A.
01-AUG-1990.
25-JAN-1990; 90EP-00300772.
27-JAN-1989; 89JP-00016406.
17-MAY-1989; 89JP-00121405.
(GREG) GREEN CROSS CORP.
Matsuda H, Ueda Y, Tamanouchi K;
WPI; 1990-233117/31.

Urokinase precursor-lipid composite - used as thrombolytic agent, having
prolonged half-life in the blood, enhanced bio-availability and improved
activity.
Claim 3; Fig 1; 11pp; English.
By forming a precursor-lipid composite, the half-life of this
thrombolytic agent in the blood may be increased, exhibiting improved
activity without abnormal acceleration of fibrinolytic activity. Compound
is useful as a thrombolytic agent in treatment of cerebral thrombosis,
myocardial infarction etc
Sequence 411 AA;

Query Match 100.0%; Score 837; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
121 PLVQECMVHDCADGKPKSPPEE 143
121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 6
AA05117
ID AAR05117 standard; protein; 411 AA.
XX
AC AAR05117;
XX
DT 25-MAR-2003 (revised)
DT 04-OCT-1990 (first entry)
XX
DE UK-S3 as encoded by PUKS3.
XX
KW Urokinase; glycosylation.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 153 /label= synthetic mutation
FT /note= "old seq (Leu)"
FT Misc-difference 155 /label= synthetic mutation
FT /note= "old seq (Pro)"
XX
PN EP370205-A.
XX
PD 30-MAY-1990.
XX
PF 28-SEP-1989; 89EP-00117981.
XX
PR 29-SEP-1988; 88JP-00245705.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Sasaki K, Nishi T, Yasumura S, Sato M, Itoh S;
XX
DR WPI; 1990-165029/22.
DR N-PSDB; AAQ04486.
XX
PT Polypeptide(s) with added carbohydrate chains - formed by modification of
PT aminoacid sequence, used to improve physio:chemical properties and/or
PT activities.
XX
PS Disclosure; Page ?; 30pp; English.
XX
CC The polypeptide is a deriv. of mature urokinase, designated UK-S3 which
CC has 2 amino acid substns. which result in an N-linked glycosylation site
CC giving the new protein improved stability and activity. See also AAR05113
CC -17; (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
CC 2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 411 AA;

Query Match 100.0%; Score 837; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
121 PLVQECMVHDCADGKPKSPPEE 143
121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 7
AAW13634
ID AAW13634 standard; protein; 411 AA.
XX

AAWL3634;
04-JUN-1997 (first entry)
Human native prourokinase.
Human; prourokinase; hPUK; variant; half-life; increase; EGF;
epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
Homo sapiens.
Key Location/Qualifiers
Domain 10..42
/label= EGF domain
/note= "in Claimed variants, at least part of the EGF
domain is deleted (see comments)"
Region 10..19
/label= first_loop
Region 20..31
/label= second_loop
Region 33..42
/label= third_loop
EP398361-A.
22-NOV-1990.
18-MAY-1990; 90EP-00109472.
18-MAY-1989; 89JP-00126433.
22-FEB-1990; 90JP-00042020.
(GREG) GREEN CROSS CORP.
Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H,
Airmura H;
WPI: 1990-350146/47.
N-PSDB; AA161671.
Human pro-urokinase variants - deficient in loop regions of epidermal
growth factor, showing long blood half-life, as fibrinolytic agent.
Disclosure; Fig 1; 22pp; English.
New variants of human prourokinase (hPUK) comprise a hPUK deficient in
(i) at least part of the first loop region of the epidermal growth factor
(EGF) domain; (ii) at least part of the first loop and at least part of
the second loop; or (iii) at least part of the third loop. The hPUK
variants show an increased blood half-life comparable to that of the
whole EGF domain-deficient hPUK variant and urokinase while retaining the
same properties as those of hPUK. They have potent thrombolytic activity
and very little tendency to cause spontaneous bleeding. The present
sequence is that of the wild-type hPUK protein, including the EGF domain
Sequence 411 AA;
Query Match 100.0%; Score 837; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
61 KASTDTMGPRCLPWN SATVLQQT YHAHRS DALQLGLGKHCNYCRNPNRRRPMCVQVGLK 120
61 KASTDTMGPRCLPWN SATVLQQT YHAHRS DALQLGLGKHCNYCRNPNRRRPMCVQVGLK 120
121 PLVQECMVHDCADGKKPSPPEE 143
121 PLVQECMVHDCADGKKPSPPEE 143

RESULT 8
AARI0057
ID AARI0057 standard; protein; 411 AA.
XX
AC AARI0057;
XX
DT 18-MAR-1991 (first entry)
XX
DE Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).
XX
KW pro-urokinase; UK-T4; plasminogen activator; myocardial infarction;
KW cerebral thrombosis.
XX
OS Homo sapiens.
XX
FN EP405285-A.
XX
PD 02-JAN-1991.
XX
PF 18-JUN-1990; 90EP-00111471.
XX
PR 19-JUN-1989; 89JP-00156302.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
PI Yasamura S, Nishi T, Ito S;
XX
WPI: 1991-008678/02.
XX
N-PSDB; AAQ10169.
XX
PT New plasminogen activator almost identical to natural pro-urokinase - is
PT thrombin resistant and used for prophylaxis-treatment of cerebral
PT thrombosis or myocardial infarction.
XX
PS Disclosure; Page 8; 84pp; English.
XX
CC UK-T4 is one example of a plasminogen activator which differs from
CC natural human pro-urokinase at positions 153 and 155 (Ileu substituted by
CC Ser; Pro substituted by Thr, respectively). The derivative has decreased
CC susceptibility to thrombin compared to natural type pro-UK and higher
CC specific activity. See also AAQ10168 and AAQ10170
XX
SQ Sequence 411 AA;
Query Match 100.0%; Score 837; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
DB 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGPRCLPWN SATVLQQT YHAHRS DALQLGLGKHCNYCRNPNRRRPMCVQVGLK 120
DB 61 KASTDTMGPRCLPWN SATVLQQT YHAHRS DALQLGLGKHCNYCRNPNRRRPMCVQVGLK 120
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 121 PLVQECMVHDCADGKKPSPPEE 143

RESULT 9
AARI0058
ID AARI0058 standard; protein; 411 AA.
XX
AC AARI0058;
XX
DT 18-MAR-1991 (first entry)
XX
DE Pro-urokinase derivative UK-S3 with Asn(153) and Thr(155).
XX
KW pro-urokinase; UK-S3; plasminogen activator; myocardial infarction;

KW cerebral thrombosis.

OS Homo sapiens.

PN EP405285-A.

XX 02-JAN-1991.

XX 18-JUN-1990; 90EP-00111471.

XX 19-JUN-1989; 89JP-00156302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Yasamura S, Nishi T, Ito S;

XX MPI; 1991-008678/02.

XX N-PSDB; AAQ10170.

XX New plasminogen activator almost identical to natural pro-urokinase - is thrombin resistant and used for prophylaxis-treatment of cerebral thrombosis or myocardial infarction.

XX Disclosure; Page 9; 84pp; English.

XX UK-S3 is one example of a plasminogen activator which differs from natural human pro-urokinase at positions 153 and 155. (Leu substituted by Asn; Pro substituted by Thr, respectively). The derivative has decreased susceptibility to thrombin compared to natural type pro-UK and higher specific activity. See also AAQ10168 and AAQ10169

XX Sequence 411 AA;

XX Query Match 100.0%; Score 837; DB 2; Length 411;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-55; Mismatches 0; Indels 0; Gaps 0;

XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGTGVSNKYFNSIHWNCNPKKFGGHCIDKSKTCYEGNGHFYRG 60

DB 1 SNELHQPNSCDCLNGTGVSNKYFNSIHWNCNPKKFGGHCIDKSKTCYEGNGHFYRG 60

QY 61 KASDTMTGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHCNCRPNRRPWCYVQVGLK 120

DB 61 KASDTMTGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHCNCRPNRRPWCYVQVGLK 120

QY 121 PLVQECMVHDCADGKPKSPPEE 143

DB 121 PLVQECMVHDCADGKPKSPPEE 143

RE LT 10

AA 0225

XX AAR40225 standard; protein; 411 AA.

XX AAR40225;

XX 10-FEB-1994 (first entry)

XX PUK.

XX Pre-urokinase; thrombolytic; blood; plasmid; PUK.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Region 10..60

XX /notes="Ser, Asn, Pro, Gly, or Tyr in the region 10 to 60 in the N-terminal of the human PUK can be replaced by Thr, Pro or Ala"

XX Domain 10..49

XX /label=EGF

XX Region 10..19

XX /label=Loop_1

FT Region 20..31

FT /label=Loop_2

FT Region 33..42

FT /label=Loop_3

FT Misc-difference 64

FT /notes="Thr encoded by AGT (sic)"

FT Misc-difference 177

FT /note="Thr encoded by TAC (sic)"

XX JP05192142-A.

XX 03-AUG-1993.

XX 20-JAN-1992; 92JP-00030178.

XX 20-JAN-1992; 92JP-00030178.

XX (GREG) GREEN CROSS CORP.

XX WPI; 1993-277461/35.

XX N-PSDB; AAQ48228.

XX Mutant human pre-urokinase - by replacing specified aminoacid(s) in N-terminal for providing longer half-life in blood and higher thrombolytic ability.

XX Claim 1; Page 14-16; 26pp; Japanese.

XX Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or Tyr in the region ranging from residue 10 to 60 in the N-terminal of the human PUK by Thr, Pro or Ala. These mutants have a longer half-life in the blood and a higher thrombolytic ability. For examples see (AAR47956-R47960)

XX Sequence 411 AA;

XX Query Match 100.0%; Score 837; DB 2; Length 411;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-55;

XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGTGVSNKYFNSIHWNCNPKKFGGHCIDKSKTCYEGNGHFYRG 60

DB 1 SNELHQPNSCDCLNGTGVSNKYFNSIHWNCNPKKFGGHCIDKSKTCYEGNGHFYRG 60

QY 61 KASDTMTGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHCNCRPNRRPWCYVQVGLK 120

DB 61 KASDTMTGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHCNCRPNRRPWCYVQVGLK 120

QY 121 PLVQECMVHDCADGKPKSPPEE 143

DB 121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 11

AAR62997

ID AAR62997 standard; protein; 411 AA.

XX AAR62997;

XX 25-MAR-2003 (revised)

XX 21-SEP-1995 (first entry)

XX Pro-urokinase mutant Gly306.

XX Pro-urokinase; thrombolysis; fibrin clot lysis; mutant Gly306;

XX reduced fibrinogenolysis; non-specific plasminogen activation;

XX systemic bleeding.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Disulfide-bond 11..19

FT Region 20..31

FT /label=Loop_2

FT Region 33..42

FT /label=Loop_3

FT Misc-difference 64

FT /notes="Thr encoded by AGT (sic)"

FT Misc-difference 177

FT /note="Thr encoded by TAC (sic)"

XX JP05192142-A.

XX 03-AUG-1993.

XX 20-JAN-1992; 92JP-00030178.

XX 20-JAN-1992; 92JP-00030178.

XX (GREG) GREEN CROSS CORP.

XX WPI; 1993-277461/35.

XX N-PSDB; AAQ48228.

XX Mutant human pre-urokinase - by replacing specified aminoacid(s) in N-terminal for providing longer half-life in blood and higher thrombolytic ability.

XX Claim 1; Page 14-16; 26pp; Japanese.

XX Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or Tyr in the region ranging from residue 10 to 60 in the N-terminal of the human PUK by Thr, Pro or Ala. These mutants have a longer half-life in the blood and a higher thrombolytic ability. For examples see (AAR47956-R47960)

XX Sequence 411 AA;

XX Query Match 100.0%; Score 837; DB 2; Length 411;

XX Best Local Similarity 100.0%; Pred. No. 2.4e-55;

XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGTGVSNKYFNSIHWNCNPKKFGGHCIDKSKTCYEGNGHFYRG 60

DB 1 SNELHQPNSCDCLNGTGVSNKYFNSIHWNCNPKKFGGHCIDKSKTCYEGNGHFYRG 60

QY 61 KASDTMTGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHCNCRPNRRPWCYVQVGLK 120

DB 61 KASDTMTGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHCNCRPNRRPWCYVQVGLK 120

QY 121 PLVQECMVHDCADGKPKSPPEE 143

DB 121 PLVQECMVHDCADGKPKSPPEE 143

F Disulfide-bond 33. .42
F Disulfide-bond 50. .131
F Disulfide-bond 71. .113
F Disulfide-bond 102. .126
F Disulfide-bond 148. .279
F Disulfide-bond 189. .205
F Disulfide-bond 197. .268
F Disulfide-bond 293. .362
F Domain 297. .313
F /note="flexible loop"
F Disulfide-bond 325. .341
F Disulfide-bond 352. .380
X WO9501427-A1
X 12-JAN-1995.
X 28-JUN-1994, 94WO-US007278.
X 02-JUL-1993, 93US-00087163.
X (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
X Liu J, Gurewich V;
X WPI; 1995-060991/08.
X Pro-urokinase mutants - have thrombolytic activity but reduced
X fibrinogenolysis activity and non-specific plasminogen activation.
X Claim 13; Fig 1; 46pp; English.
X AAR62991 is the wild type pro-urokinase, from which the new mutants
X described in AAR62992-R63008 were derived. These mutants retain the
X thrombolytic activity of the wild type protein, useful for the treatment
X of thromboembolism, but have a reduced fibrinogenolysis activity and non-
X specific plasminogen activation. The mutants can therefore be used for
X the lysis of fibrin clots without inducing systemic bleeding, as can be
X the case with the wild type protein. (Updated on 25-MAR-2003 to correct
X PN field.)
X Sequence 411 AA;
X
X Query Match 100.0%; Score 837; DB 2; Length 411;
X Best Local Similarity 100.0%; Pred. No. 2.4e-55; Indels 0; Gaps 0;
X Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
X
X 1 SNELHQPNSNCDLNGGTCVSNKYFSNIHWNCNCPKFGGQHCEIDKSKTCYEGNGHFFYRG 60
X 1 SNELHQPNSNCDLNGGTCVSNKYFSNIHWNCNCPKFGGQHCEIDKSKTCYEGNGHFFYRG 60
X 61 KASTDTMGPRCLPWNASATVLOQTYHAHRSDALQGLGKHNCRNPNRRPWCYVQVGLK 120
X 61 KASTDTMGPRCLPWNASATVLOQTYHAHRSDALQGLGKHNCRNPNRRPWCYVQVGLK 120
X 121 PLVQECMVHDCADGKKPSPPEE 143
X 121 PLVQECMVHDCADGKKPSPPEE 143
X
X RESULT 12
X 63008
X AAR63008 standard; protein; 411 AA.
X
X AAR63008;
X
X 25-MAR-2003 (revised)
X 21-SEP-1995 (first entry)
X
X Pro-urokinase mutant Ser175 His187 His300 Ala301 His313.
X
X Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
X non-specific plasminogen activation; systemic bleeding;

KW mutant Ser175 His187 His300 Ala301 His313.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Disulfide-bond 11. .19
FT Disulfide-bond 13. .31
FT Disulfide-bond 33. .42
FT Disulfide-bond 50. .131
FT Disulfide-bond 71. .113
FT Disulfide-bond 102. .126
FT Disulfide-bond 148. .279
FT Disulfide-bond 189. .205
FT Disulfide-bond 197. .268
FT Disulfide-bond 293. .362
FT Domain 297. .313
FT /note="flexible loop"
FT Disulfide-bond 325. .341
FT Disulfide-bond 352. .380
XX WO9501427-A1.
XX 12-JAN-1995.
XX 28-JUN-1994, 94WO-US007278.
XX 02-JUL-1993, 93US-00087163.
XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
XX Liu J, Gurewich V;
XX WPI; 1995-060991/08.
XX Pro-urokinase mutants - have thrombolytic activity but reduced
XX fibrinogenolysis activity and non-specific plasminogen activation.
XX Claim 16; Fig 1; 46pp; English.
XX AAR62991 is the wild type pro-urokinase, from which the new mutants
XX described in AAR62992-R63008 were derived. These mutants retain the
XX thrombolytic activity of the wild type protein, useful for the treatment
XX of thromboembolism, but have a reduced fibrinogenolysis activity and non-
XX specific plasminogen activation. The mutants can therefore be used for
XX the lysis of fibrin clots without inducing systemic bleeding, as can be
XX the case with the wild type protein. (Updated on 25-MAR-2003 to correct
XX PN field.)
XX Sequence 411 AA;
XX
XX Query Match 100.0%; Score 837; DB 2; Length 411;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-55; Indels 0; Gaps 0;
XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 SNELHQPNSNCDLNGGTCVSNKYFSNIHWNCNCPKFGGQHCEIDKSKTCYEGNGHFFYRG 60
XX 1 SNELHQPNSNCDLNGGTCVSNKYFSNIHWNCNCPKFGGQHCEIDKSKTCYEGNGHFFYRG 60
XX 61 KASTDTMGPRCLPWNASATVLOQTYHAHRSDALQGLGKHNCRNPNRRPWCYVQVGLK 120
XX 61 KASTDTMGPRCLPWNASATVLOQTYHAHRSDALQGLGKHNCRNPNRRPWCYVQVGLK 120
XX 121 PLVQECMVHDCADGKKPSPPEE 143
XX 121 PLVQECMVHDCADGKKPSPPEE 143
XX
XX RESULT 13
XX AAR62999
XX ID AAR62999 standard; protein; 411 AA.
XX
XX AAR62999;
XX

DI 25-MAR-2003 (revised)
 DI 21-SEP-1995 (first entry)
 XX Pro-urokinase mutant His313.
 DE Pro-urokinase; thrombolysis; fibrin clot lysis; mutant His313;
 KW reduced fibrinogenolysis; non-specific plasminogen activation;
 KW systemic bleeding.
 XX Homo sapiens.
 OS
 XX
 FE Key Location/Qualifiers
 FT Disulfide-bond 11..19
 FT Disulfide-bond 13..31
 FT Disulfide-bond 33..42
 FT Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..279
 FT Disulfide-bond 189..205
 FT Disulfide-bond 197..268
 FT Disulfide-bond 293..362
 FT Domain 297..313
 FT /note= "flexible loop"
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380
 XX WO9501427-A1.
 XX
 PD 12-JAN-1995.
 XX
 PF 28-JUN-1994; 94WO-US007278.
 XX
 PF 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 PI Liu J, Gurewich V;
 XX WPI; 1995-060991/08.
 DR
 XX Pro-urokinase mutants - have thrombolytic activity but reduced
 PT fibrinogenolysis activity and non-specific plasminogen activation.
 PT
 PS Claim 11; Fig 1; 46pp; English.
 XX
 CC AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 CC
 SQ Sequence 411 AA;
 Query Match 100.0%; Score 837; DB 2; Length 411;
 st Local Similarity 100.0%; Pred. No. 2.4e-55;
 tches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNEHQVPSNCDCLNGTGVSNKYFNIHWNCNPKFGGQHCIEDKSKTCYEGNGHFRG 60
 DI 1 SNEHQVPSNCDCLNGTGVSNKYFNIHWNCNPKFGGQHCIEDKSKTCYEGNGHFRG 60
 QY 61 KASTDTMGRPCLPWSATVLQOYTHAHRSDALQLGLGKHCYCRNPDRRPPWCYVQVGLK 120
 DI 61 KASTDTMGRPCLPWSATVLQOYTHAHRSDALQLGLGKHCYCRNPDRRPPWCYVQVGLK 120
 QY 121 PLVQECWHDCAADGKXSPPEE 143
 DI 121 PLVQECWHDCAADGKXSPPEE 143

RESULT 14
 AAR62994
 ID AAR62994 standard; protein; 411 AA.
 XX
 XX AAR62994;
 DT 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 XX
 DE Pro-urokinase mutant His299 Ala300.
 XX
 KW Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
 KW non-specific plasminogen activation; systemic bleeding;
 KW mutant His 299 Ala300.
 XX
 OS Homo sapiens.
 XX
 FE Key Location/Qualifiers
 FT Disulfide-bond 11..19
 FT Disulfide-bond 13..31
 FT Disulfide-bond 33..42
 FT Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..279
 FT Disulfide-bond 189..205
 FT Disulfide-bond 197..268
 FT Disulfide-bond 293..362
 FT Domain 297..313
 FT /note= "flexible loop"
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380
 XX WO9501427-A1.
 XX
 PD 12-JAN-1995.
 XX
 PF 28-JUN-1994; 94WO-US007278.
 XX
 PF 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX
 PI Liu J, Gurewich V;
 XX WPI; 1995-060991/08.
 DR
 XX Pro-urokinase mutants - have thrombolytic activity but reduced
 PT fibrinogenolysis activity and non-specific plasminogen activation.
 PT
 PS Claim 7; Fig 1; 46pp; English.
 XX
 CC AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 CC
 SQ Sequence 411 AA;
 Query Match 100.0%; Score 837; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.4e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNEHQVPSNCDCLNGTGVSNKYFNIHWNCNPKFGGQHCIEDKSKTCYEGNGHFRG 60
 DI 1 SNEHQVPSNCDCLNGTGVSNKYFNIHWNCNPKFGGQHCIEDKSKTCYEGNGHFRG 60
 QY 61 KASTDTMGRPCLPWSATVLQOYTHAHRSDALQLGLGKHCYCRNPDRRPPWCYVQVGLK 120

61 KASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKHNCRNPDRRRPWCYVQVLK 120
121 PLVQECMVHDCADGKKPSPPEE 143
121 PLVQECMVHDCADGKKPSPPEE 143

ULT 15
53003
AAR63003 standard; protein; 411 AA.
AAR63003;
25-MAR-2003 (revised)
21-SEP-1995 (first entry)
Pro-urokinase mutant Ser175 His187 His313.
Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
non-specific plasminogen activation; systemic bleeding;
mutant Ser175 His187 His313.
Homo sapiens.

Key Location/Qualifiers
Disulfide-bond 11..19
Disulfide-bond 13..31
Disulfide-bond 33..42
Disulfide-bond 50..131
Disulfide-bond 71..113
Disulfide-bond 102..126
Disulfide-bond 148..279
Disulfide-bond 189..205
Disulfide-bond 197..268
Disulfide-bond 283..362
Domain 297..313
Disulfide-bond 325..341
Disulfide-bond 352..380
WO9501427-A1
12-JAN-1995.
28-JUN-1994; 94WO-US007278.
02-JUL-1993; 93US-00087163.
(NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
Liu J, Gurewich V;
WPI; 1995-060991/08.
Pro-urokinase mutants - have thrombolytic activity but reduced
fibrinogenolysis activity and non-specific plasminogen activation.
Claim 15; Fig 1; 46pp; English.
AAR62991 is the wild type pro-urokinase, from which the new mutants
described in AAR62992-R63008 were derived. These mutants retain the
thrombolytic activity of the wild type protein, useful for the treatment
of thromboembolism, but have a reduced fibrinogenolysis activity and non-
specific plasminogen activation. The mutants can therefore be used for
the lysis of fibrin clots without inducing systemic bleeding, as can be
the case with the wild type protein. (Updated on 25-MAR-2003 to correct
PN field.)
Sequence 411 AA;
Query Match 100.0%; Score 837; DB 2; Length 411;
Est Local Similarity 100.0%; Pred. No. 2.4e-55;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SNELHQPNSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
Db 1 SNELHQPNSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCEIDKSKTCYEGNGHFYRG 60
Qy 61 KASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKHNCRNPDRRRPWCYVQVLK 120
Db 61 KASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKHNCRNPDRRRPWCYVQVLK 120
Qy 121 PLVQECMVHDCADGKKPSPPEE 143
Db 121 PLVQECMVHDCADGKKPSPPEE 143

RESULT 16
AAR63001
ID AAR63001 standard; protein; 411 AA.
XX AAR63001;
AC AAR63001;
XX 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
DT 21-SEP-1995 (first entry)
XX Pro-urokinase mutant Ser175 His187 Ala313.
DE Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
KW non-specific plasminogen activation; systemic bleeding;
KW mutant Ser175 His187 Ala313.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Disulfide-bond 11..19
FT Disulfide-bond 13..31
FT Disulfide-bond 33..42
FT Disulfide-bond 50..131
FT Disulfide-bond 71..113
FT Disulfide-bond 102..126
FT Disulfide-bond 148..279
FT Disulfide-bond 189..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
FT Domain 297..313
FT /note= "flexible loop"
FT Disulfide-bond 325..341
FT Disulfide-bond 352..380
XX WO9501427-A1.
PN 12-JAN-1995.
XX PD 28-JUN-1994; 94WO-US007278.
XX PF 02-JUL-1993; 93US-00087163.
XX PR (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX PA Liu J, Gurewich V;
XX PI WPI; 1995-060991/08.
XX DR Pro-urokinase mutants - have thrombolytic activity but reduced
XX fibrinogenolysis activity and non-specific plasminogen activation.
XX Claim 15; Fig 1; 46pp; English.
XX AAR62991 is the wild type pro-urokinase, from which the new mutants
XX described in AAR62992-R63008 were derived. These mutants retain the
XX thrombolytic activity of the wild type protein, useful for the treatment
XX of thromboembolism, but have a reduced fibrinogenolysis activity and non-
XX specific plasminogen activation. The mutants can therefore be used for
XX the lysis of fibrin clots without inducing systemic bleeding, as can be
XX the case with the wild type protein. (Updated on 25-MAR-2003 to correct
XX PN field.)
XX Sequence 411 AA;
XX Query Match 100.0%; Score 837; DB 2; Length 411;
XX Est Local Similarity 100.0%; Pred. No. 2.4e-55;

CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence 411 AA;
 SQ Query Match 100.0%; Score 837; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.4e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
 DB 1 SNELHQPNSCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
 QY 61 KASTDTMGRPCLPWSATVLQQTTHAHRSDALQLGLGKHNCRPNRRPWCYVQVGLK 120
 DB 61 KASTDTMGRPCLPWSATVLQQTTHAHRSDALQLGLGKHNCRPNRRPWCYVQVGLK 120
 QY 121 PLVQECMVHDCADGKPPSPPEE 143
 DB 121 PLVQECMVHDCADGKPPSPPEE 143
 RE UT 17
 AA 3006
 ID AAR63006 standard; protein; 411 AA.
 AC AAR63006;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 DE Pro-urokinase mutant Ser175 His187 His300 Ala301 Ala313.
 XX Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
 KW non-specific plasminogen activation; systemic bleeding;
 KW mutant Ser175 His187 His300 Ala301 Ala313.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FE Disulfide-bond 11..19
 FT Disulfide-bond 13..31
 FT Disulfide-bond 33..42
 FT Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..279
 FT Disulfide-bond 189..205
 FT Disulfide-bond 197..268
 FT Disulfide-bond 293..362
 FT Domain 297..313
 FT /note= "flexible loop"
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380
 XX WO9501427-A1.
 XX 12-JAN-1995.
 XX 28-JUN-1994; 94WO-US007278.
 XX 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX Liu J, Gurewicz V;
 XX WPI; 1995-060991/08.
 XX Pro-urokinase mutants - have thrombolytic activity but reduced
 XX fibrinogenolysis activity and non-specific plasminogen activation.
 XX Claim 16; Fig 1; 46pp; English.

XX AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence 411 AA;
 SQ Query Match 100.0%; Score 837; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.4e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
 DB 1 SNELHQPNSCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFYRG 60
 QY 61 KASTDTMGRPCLPWSATVLQQTTHAHRSDALQLGLGKHNCRPNRRPWCYVQVGLK 120
 DB 61 KASTDTMGRPCLPWSATVLQQTTHAHRSDALQLGLGKHNCRPNRRPWCYVQVGLK 120
 QY 121 PLVQECMVHDCADGKPPSPPEE 143
 DB 121 PLVQECMVHDCADGKPPSPPEE 143
 RESULT 18
 AAR62992
 ID AAR62992 standard; protein; 411 AA.
 XX
 AC AAR62992;
 XX
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 DE Pro-urokinase mutant Ala300.
 XX Pro-urokinase; thrombolysis; fibrin clot lysis; mutant Ala300;
 KW reduced fibrinogenolysis; non-specific plasminogen activation;
 KW systemic bleeding.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FE Disulfide-bond 11..19
 FT Disulfide-bond 13..31
 FT Disulfide-bond 33..42
 FT Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..279
 FT Disulfide-bond 189..205
 FT Disulfide-bond 197..268
 FT Disulfide-bond 293..362
 FT Domain 297..313
 FT /note= "flexible loop"
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380
 XX WO9501427-A1.
 XX 12-JAN-1995.
 XX 28-JUN-1994; 94WO-US007278.
 XX 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX Liu J, Gurewicz V;

X: WPI; 1995-060991/08.
D: Pro-urokinase mutants - have thrombolytic activity but reduced
X: fibrinogenolysis activity and non-specific plasminogen activation.
P: Claim 5; Fig 1; 46pp; English.
X: AAR62991 is the wild type pro-urokinase, from which the new mutants
C: described in AAR62992-R63008 were derived. These mutants retain the
C: thrombolytic activity of the wild type protein, useful for the treatment
C: of thromboembolism, but have a reduced fibrinogenolysis activity and non-
C: specific plasminogen activation. The mutants can therefore be used for
C: the lysis of fibrin clots without inducing systemic bleeding, as can be
C: the case with the wild type protein. (Updated on 25-MAR-2003 to correct
C: PN field.)
X: Sequence 411 AA;
S: Query Match 100.0%; Score 837; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q: 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCCEIDKSKTCYEGNGHFYRG 60
D: 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCCEIDKSKTCYEGNGHFYRG 60
Q: 61 KASDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRPNDRRRPWCYVOVGLK 120
D: 61 KASDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRPNDRRRPWCYVOVGLK 120
Q: 121 PLVQECMVHDCADGKKPSSPPEE 143
D: 121 PLVQECMVHDCADGKKPSSPPEE 143
R: HT 19
A: 3002
I: AAR63002 standard; protein; 411 AA.
X: AAR63002;
X: 25-MAR-2003 (revised)
D: 21-SEP-1995 (first entry)
X: Pro-urokinase mutant Ser175 His187 Gly306.
X: Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
X: non-specific plasminogen activation; systemic bleeding;
X: mutant Ser175 His187 Gly306.
X: Homo sapiens.
X: Key Location/Qualifiers
F: Disulfide-bond 11..19
F: Disulfide-bond 13..31
F: Disulfide-bond 33..42
F: Disulfide-bond 50..131
F: Disulfide-bond 71..113
F: Disulfide-bond 102..126
F: Disulfide-bond 148..279
F: Disulfide-bond 189..205
F: Disulfide-bond 197..268
F: Disulfide-bond 293..362
F: Domain 297..313
F: Disulfide-bond 325..341
F: Disulfide-bond 352..380
X: WO9501427-A1
X: 12-JAN-1995.
X: /note= "flexible loop"

PF 28-JUN-1994; 94WO-US007278.
XX
PR 02-JUL-1993; 93US-00087163.
XX
PA (NEWB-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Liu J, Gurewich V;
XX
DR WPI; 1995-060991/08.
XX
PT Pro-urokinase mutants - have thrombolytic activity but reduced
PT fibrinogenolysis activity and non-specific plasminogen activation.
XX
PS Claim 15; Fig 1; 46pp; English.
XX
CC AAR62991 is the wild type pro-urokinase, from which the new mutants
CC described in AAR62992-R63008 were derived. These mutants retain the
CC thrombolytic activity of the wild type protein, useful for the treatment
CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
CC specific plasminogen activation. The mutants can therefore be used for
CC the lysis of fibrin clots without inducing systemic bleeding, as can be
CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 411 AA;
Query Match 100.0%; Score 837; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Q: 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCCEIDKSKTCYEGNGHFYRG 60
D: 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCCEIDKSKTCYEGNGHFYRG 60
Q: 61 KASDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRPNDRRRPWCYVOVGLK 120
D: 61 KASDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRPNDRRRPWCYVOVGLK 120
Q: 121 PLVQECMVHDCADGKKPSSPPEE 143
D: 121 PLVQECMVHDCADGKKPSSPPEE 143
RESULT 20
AAR63007
ID AAR63007 standard; protein; 411 AA.
XX
AC AAR63007;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
DE Pro-urokinase mutant Ser175 His187 Ala300 Ala301 His313.
XX
KW Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
KW non-specific plasminogen activation; systemic bleeding;
KW mutant Ser175 His187 Ala300 Ala301 His313.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Disulfide-bond 11..19
FT Disulfide-bond 13..31
FT Disulfide-bond 33..42
FT Disulfide-bond 50..131
FT Disulfide-bond 71..113
FT Disulfide-bond 102..126
FT Disulfide-bond 148..279
FT Disulfide-bond 189..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
FT Domain 297..313
FT /note= "flexible loop"

FT Disulfide-bond 325. .341
 FT Disulfide-bond 352. .380
 XX WO9501427-A1.
 XX 12-JAN-1995.
 XX 28-JUN-1994; 94WO-US007278.
 XX 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX Liu J, Gurewich V;
 XX WPI; 1995-060991/08.
 XX Pro-urokinase mutants - have thrombolytic activity but reduced
 FT fibrinogenolysis activity and non-specific plasminogen activation.
 XX Claim 16; Fig 1; 46pp; English.
 XX AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence 411 AA;
 XX Query Match 100.0%; Score 837; DB 2; Length 411;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-55;
 XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 DB 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 QY 61 KASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 DB 61 KASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 QY 121 PLVQECMVHDCADGKPPSPPEE 143
 DB 121 PLVQECMVHDCADGKPPSPPEE 143
 RE DT 21
 AA 2995
 ID AAR62995 standard; protein; 411 AA.
 XX AAR62995;
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 XX Pro-urokinase mutant Ala300 Ala301.
 XX Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
 KW non-specific plasminogen activation; mutant Ala300 Ala301;
 KW systemic bleeding.
 XX Homo sapiens.
 OS Key Location/Qualifiers
 PH Disulfide-bond 11. .19
 FT Disulfide-bond 13. .31
 FT Disulfide-bond 33. .42
 FT Disulfide-bond 50. .131
 FT Disulfide-bond 71. .113

FT Disulfide-bond 102. .126
 FT Disulfide-bond 148. .279
 FT Disulfide-bond 189. .205
 FT Disulfide-bond 197. .268
 FT Disulfide-bond 293. .362
 FT Domain 297. .313
 FT /note= "flexible loop"
 FT Disulfide-bond 325. .341
 FT Disulfide-bond 352. .380
 XX WO9501427-A1.
 XX 12-JAN-1995.
 XX 28-JUN-1994; 94WO-US007278.
 XX 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX Liu J, Gurewich V;
 XX WPI; 1995-060991/08.
 XX Pro-urokinase mutants - have thrombolytic activity but reduced
 FT fibrinogenolysis activity and non-specific plasminogen activation.
 XX Claim 9; Fig 1; 46pp; English.
 XX AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence 411 AA;
 XX Query Match 100.0%; Score 837; DB 2; Length 411;
 XX Best Local Similarity 100.0%; Pred. No. 2.4e-55;
 XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 DB 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
 QY 61 KASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 DB 61 KASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 QY 121 PLVQECMVHDCADGKPPSPPEE 143
 DB 121 PLVQECMVHDCADGKPPSPPEE 143
 RESULT 22
 AAR63000
 ID AAR63000 standard; protein; 411 AA.
 XX AAR63000;
 AC AAR63000;
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 XX Pro-urokinase mutant Ser175 His187.
 XX Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
 KW non-specific plasminogen activation; systemic bleeding;
 KW mutant Ser175 His187.
 XX Homo sapiens.
 OS

ID XX AAR62996 standard; protein; 411 AA.
 AC AAR62996;
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 XX Pro-urokinase mutant His300 Ala301.
 DE Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
 KW non-specific plasminogen activation; mutant His300 Ala301;
 XX systemic bleeding.
 OS Homo sapiens.
 XX
 FE Key Location/Qualifiers
 FT Disulfide-bond 11..19
 FT Disulfide-bond 13..31
 FT Disulfide-bond 33..42
 FT Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..205
 FT Disulfide-bond 189..268
 FT Disulfide-bond 293..362
 FT Domain 297..313
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380
 XX WO9501427-A1.
 PN 12-JAN-1995.
 XX 28-JUN-1994; 94WO-US007278.
 XX 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX Liu J, Gurewich V;
 XX WPI; 1995-060991/08.
 XX Pro-urokinase mutants - have thrombolytic activity but reduced
 FT fibrinogenolysis activity and non-specific plasminogen activation.
 XX Claim 9; Fig 1; 46pp; English.
 CC AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence 411 AA;
 CC
 Query Match 100.0%; Score 837; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.4e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDLNGTGVSNKYFSNIHWCNPKFKGGQHCIEIDKSKTCYEGNGHFRG 60
 DT 1 SNELHQPNSCDLNGTGVSNKYFSNIHWCNPKFKGGQHCIEIDKSKTCYEGNGHFRG 60
 QY 61 KASTDTMGPCPLPWSATVLTQTYHAHRSDALQLGLGKHNCRNPNRRRRCWYVQVGLK 120
 DT 61 KASTDTMGPCPLPWSATVLTQTYHAHRSDALQLGLGKHNCRNPNRRRRCWYVQVGLK 120

QY 121 PLVQECWVHDCADGKXPSPPEE 143
 DB 121 PLVQECWVHDCADGKXPSPPEE 143
 RESULT 25
 AAR63005
 ID AAR63005 standard; protein; 411 AA.
 XX AAR63005;
 AC AAR63005;
 XX 25-MAR-2003 (revised)
 DT 21-SEP-1995 (first entry)
 XX Pro-urokinase mutant Ser175 His187 Ala300 Ala301 Ala313.
 DE Pro-urokinase; thrombolysis; fibrin clot lysis; reduced fibrinogenolysis;
 KW non-specific plasminogen activation; systemic bleeding;
 KW mutant Ser175 His187 Ala300 Ala301 Ala313.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT Disulfide-bond 11..19
 FT Disulfide-bond 13..31
 FT Disulfide-bond 33..42
 FT Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..205
 FT Disulfide-bond 189..268
 FT Disulfide-bond 293..362
 FT Domain 297..313
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380
 XX WO9501427-A1.
 PN 12-JAN-1995.
 XX 28-JUN-1994; 94WO-US007278.
 XX 02-JUL-1993; 93US-00087163.
 XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.
 XX Liu J, Gurewich V;
 XX WPI; 1995-060991/08.
 XX Pro-urokinase mutants - have thrombolytic activity but reduced
 FT fibrinogenolysis activity and non-specific plasminogen activation.
 XX Claim 16; Fig 1; 46pp; English.
 CC AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX Sequence 411 AA;
 CC
 Query Match 100.0%; Score 837; DB 2; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2.4e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDLNGTGVSNKYFSNIHWCNPKFKGGQHCIEIDKSKTCYEGNGHFRG 60

1 SNEHQVPSNCDCLNGTGVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFRG 60
61 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNCRNPNRRRPWCYVQVGLK 120
61 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNCRNPNRRRPWCYVQVGLK 120
121 PLVQECMVHDCADGKPKSPPEE 143
121 PLVQECMVHDCADGKPKSPPEE 143

LT 26
52991
AAR62991 standard; protein; 411 AA.
AAR62991;
25-MAR-2003 (revised)
21-SEP-1995 (first entry)
Pro-urokinase.
Pro-urokinase; thrombolysis; fibrin clot lysis.
Homo sapiens.
Key Location/Qualifiers
Disulfide-bond 11..19
Disulfide-bond 13..31
Disulfide-bond 33..42
Disulfide-bond 50..131
Disulfide-bond 71..113
Disulfide-bond 102..126
Disulfide-bond 148..279
Disulfide-bond 189..205
Disulfide-bond 197..268
Disulfide-bond 293..362
Domain 297..313
Disulfide-bond 325..341
Disulfide-bond 352..380
WO9501427-A1.
12-JAN-1995.
28-JUN-1994; 94WO-US007278.
02-JUL-1993; 93US-00087163.
(NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
Liu J, Gurewich V;
WPI; 1995-060991/08.
Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation.
Disclosure; Fig 1; 46pp; English.
AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-specific plasminogen activation. The mutants can therefore be used for the lysis of fibrin clots without inducing systemic bleeding, as can be the case with the wild type protein. (Updated on 25-MAR-2003 to correct PN field.)
Sequence 411 AA;

Query Match 100.0%; Score 837; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2.4e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNEHQVPSNCDCLNGTGVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFRG 60
Db 1 SNEHQVPSNCDCLNGTGVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFRG 60
QY 61 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNCRNPNRRRPWCYVQVGLK 120
Db 61 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNCRNPNRRRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGKPKSPPEE 143
Db 121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 27
AAR62998
ID AAR62998 standard; protein; 411 AA.
XX
AC AAR62998;
XX
DT 25-MAR-2003 (revised)
DT 21-SEP-1995 (first entry)
XX
DE Pro-urokinase mutant Ala313.
XX
KW Pro-urokinase; thrombolysis; fibrin clot lysis; mutant Ala313;
KW reduced fibrinogenolysis; non-specific plasminogen activation;
KW systemic bleeding.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Disulfide-bond 11..19
FT Disulfide-bond 13..31
FT Disulfide-bond 33..42
FT Disulfide-bond 50..131
FT Disulfide-bond 71..113
FT Disulfide-bond 102..126
FT Disulfide-bond 148..279
FT Disulfide-bond 189..205
FT Disulfide-bond 197..268
FT Disulfide-bond 293..362
Domain 297..313
FT /note= "flexible loop"
FT Disulfide-bond 325..341
FT Disulfide-bond 352..380
XX
PN WO9501427-A1.
XX
PD 12-JAN-1995.
XX
PF 28-JUN-1994; 94WO-US007278.
XX
PR 02-JUL-1993; 93US-00087163.
XX
PA (NEWE-) NEW ENGLAND DEACONESS HOSPITAL.
XX
PI Liu J, Gurewich V;
XX
WPI; 1995-060991/08.
XX
PT Pro-urokinase mutants - have thrombolytic activity but reduced fibrinogenolysis activity and non-specific plasminogen activation.
PS Claim 11; Fig 1; 46pp; English.
XX
CC AAR62991 is the wild type pro-urokinase, from which the new mutants described in AAR62992-R63008 were derived. These mutants retain the thrombolytic activity of the wild type protein, useful for the treatment of thromboembolism, but have a reduced fibrinogenolysis activity and non-

CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX Sequence 411 AA;

XX Query Match 100.0%; Score 837; DB 2; Length 411;
 XX St Local Similarity 100.0%; Pred. No. 2.4e-55;
 XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 60
 Db 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 60
 Qy 61 KASTDTMGRCLPWNATVLOQTYHAHRSDALQGLGKHNCRPNRRPWCYVQVGLK 120
 Db 61 KASTDTMGRCLPWNATVLOQTYHAHRSDALQGLGKHNCRPNRRPWCYVQVGLK 120
 Qy 121 PLVQECMVHDCADGKPPSPPEE 143
 Db 121 PLVQECMVHDCADGKPPSPPEE 143

RE 28

AA 2993
 ID AAR62993 standard; protein; 411 AA.

XX AAR62993;

XX 25-MAR-2003 (revised)

DT 21-SEP-1995 (first entry)

XX Pro-urokinase mutant His300.

XX Pro-urokinase; thrombolysis; fibrin clot lysis; mutant His300;
 KW reduced fibrinogenolysis; non-specific plasminogen activation;
 KW systemic bleeding.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 11..19
 FT Disulfide-bond 13..31
 FT Disulfide-bond 33..42
 FT Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..279
 FT Disulfide-bond 189..205
 FT Disulfide-bond 197..268
 FT Disulfide-bond 293..362
 FT Domain 297..313
 FT /note= "flexible loop"
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380

XX WO9501427-A1.

XX 12-JAN-1995.

XX 28-JUN-1994; 94WO-US007278.

XX 02-JUL-1993; 93US-00087163.

XX (NEW-) NEW ENGLAND DEACONESS HOSPITAL.

XX Liu J, Gurewicz V;

XX WPI; 1995-060991/08.

XX Pro-urokinase mutants - have thrombolytic activity but reduced
 PT fibrinogenolysis activity and non-specific plasminogen activation.

XX Claim 5; Fig 1; 46pp; English.

XX AAR62991 is the wild type pro-urokinase, from which the new mutants
 CC described in AAR62992-R63008 were derived. These mutants retain the
 CC thrombolytic activity of the wild type protein, useful for the treatment
 CC of thromboembolism, but have a reduced fibrinogenolysis activity and non-
 CC specific plasminogen activation. The mutants can therefore be used for
 CC the lysis of fibrin clots without inducing systemic bleeding, as can be
 CC the case with the wild type protein. (Updated on 25-MAR-2003 to correct
 CC PN field.)

XX Sequence 411 AA;

XX Query Match 100.0%; Score 837; DB 2; Length 411;
 XX St Local Similarity 100.0%; Pred. No. 2.4e-55;
 XX Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 60
 Db 1 SNEHQVPSNCDCLNGGTCVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 60
 Qy 61 KASTDTMGRCLPWNATVLOQTYHAHRSDALQGLGKHNCRPNRRPWCYVQVGLK 120
 Db 61 KASTDTMGRCLPWNATVLOQTYHAHRSDALQGLGKHNCRPNRRPWCYVQVGLK 120
 Qy 121 PLVQECMVHDCADGKPPSPPEE 143
 Db 121 PLVQECMVHDCADGKPPSPPEE 143

RESULT 29

AAR62926

ID AAR62926 standard; protein; 411 AA.

XX AAR62926;

XX 03-AUG-1996 (first entry)

XX Pro-urokinase.

XX Pro-urokinase; plasminogen activator; fusion drug; drug delivery;
 KW platelet; cardiovascular disease; thrombolytic.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..132
 FT /label= A-chain
 FT Domain 1..45
 FT /label= Growth_factor_domain
 FT Disulfide-bond 11
 FT /note= "disulfide between Cys11 and Cys19"
 FT Disulfide-bond 13
 FT /note= "disulfide bond between Cys13 and Cys31"
 FT Disulfide-bond 33
 FT /note= "disulfide bond between Cys33 and Cys42"
 FT Domain 46..132
 FT /label= Kringle_domain
 FT Disulfide-bond 50
 FT /note= "disulfide bond between Cys50 and Cys131"
 FT Disulfide-bond 71
 FT /note= "disulfide bond between Cys71 and Cys113"
 FT Disulfide-bond 102
 FT /note= "disulfide bond between Cys102 and Cys126"
 FT Region 133..158
 FT /label= Linker_region
 FT Disulfide-bond 148
 FT /note= "disulfide bond between Cys148 and Cys279"
 FT Cleavage-site 156..157
 FT /note= "thrombin cleavage site"
 FT Cleavage-site 158..159
 FT /note= "plasmin cleavage site"

121 PLVQECMVHDCADGKKPSSPPEE 143
122 PLVQECMVHDCADGKKPSSPPEE 144

ULT 33
24579
AAW24579 standard; protein; 424 AA.
AAW24579;
25-MAR-2003 (revised)
11-NOV-1997 (first entry)
Inhibitor resistant modified urokinase.

Urokinase; inhibitor resistant; plasminogen; human; whey acid protein;
plasminogen activator inhibitor-1; plasminogen activator; protease; WAP;
plasmin; proteolytic enzyme; clot lysis; heart attack; heart muscle.

Homo sapiens.
Synthetic.

Key Location/Qualifiers
Peptide 1..19
Protein /note= "whey acid protein signal peptide"
Domain /note= "urokinase"
Domain 20..64
Domain /note= "E-domain"
Domain 61..150
Domain /note= "Kringle-1 domain"
Domain 179..424
Domain /note= "P-domain"
Misc-difference 197..198
/note= "site of 6 residue (Arg-His-Arg-Gly-Ser)
deletion"

US5648253-A.
15-JUL-1997.
08-SEP-1992; 92US-00942157.
20-DEC-1990; 90US-00631673.
(TSIT-) TSI CORP.

Wei C;
WPI; 1997-372062/34.
N-PSDB; AAT80076.

Deletion-modified urokinase protein - with increased resistance to
inhibition by plasminogen activator inhibitor-1.
Claim 2; Col; 16pp; English.

This sequence represents the modified full length urokinase of the
invention, including the whey acid protein (WAP) signal peptide. This
sequence had residues 179-184 of the wild type urokinase sequence (see
AAW24578) deleted. This modified urokinase cleaves plasminogen, and has a
lower binding affinity for plasminogen activator inhibitor-1 than the
corresponding unmodified urokinase. Urokinase is one of two types of
mammalian plasminogen activators (PA), the other being tissue type PA.
PA catalyze the conversion of the circulating zymogen plasminogen to the
broad spectrum protease plasmin by limited proteolysis. The modified
urokinase can be used for clot lysis, specifically to dissolve heart
attack-causing clots before they cause permanent damage to heart muscle.
The urokinase mutant is more resistant to inhibition by plasminogen
activator inhibitors than the unmodified urokinase. It can be selectively
expressed and secreted from the mammary glands of transgenic animals.

CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 424 AA;

Query Match 100.0%; Score 837; DB 2; Length 424;
Best Local Similarity 100.0%; Pred. No. 2.5e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCBEIDKSKTCYEGNGHFYRG 60
Db 20 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCBEIDKSKTCYEGNGHFYRG 79
Qy 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKKNYCNPNRRPWCYVOVGLK 120
Db 80 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKKNYCNPNRRPWCYVOVGLK 139
Qy 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 140 PLVQECMVHDCADGKKPSSPPEE 162

RESULT 34
AAW24578

ID AAW24578 standard; protein; 430 AA.

XX AC AAW24578;

DT 25-MAR-2003 (revised)
DT 11-NOV-1997 (first entry)

XX Inhibitor resistant urokinase.

XX Urokinase; inhibitor resistant; plasminogen; human; whey acid protein;
XX plasminogen activator inhibitor-1; plasminogen activator; protease; WAP;
XX plasmin; proteolytic enzyme; clot lysis; heart attack; heart muscle.

OS Homo sapiens.
OS Synthetic.

Key Location/Qualifiers
Peptide 1..19
Protein /note= "whey acid protein signal peptide"
Domain /note= "urokinase"
Domain 20..64
Domain /note= "E-domain"
Domain 61..150
Domain /note= "Kringle-1 domain"
Domain 179..430
Domain /note= "P-domain"
Misc-difference 198..203
/note= "deleted in modified urokinase of the invention"

US5648253-A.

15-JUL-1997.

08-SEP-1992; 92US-00942157.

20-DEC-1990; 90US-00631673.

(TSIT-) TSI CORP.

Wei C;

WPI; 1997-372062/34.

N-PSDB; AAT80075.

Deletion-modified urokinase protein - with increased resistance to
inhibition by plasminogen activator inhibitor-1.

Disclosure; Col 15-18; 16pp; English.

XX

CC This sequence represents the full length urokinase, including the whey
CC acid protein (WAP) signal peptide. This sequence has residues 179-184 of
CC the urokinase sequence deleted to create the modified urokinase of the
CC invention. The modified urokinase (see AAW24579) cleaves plasminogen, and
CC has a lower binding affinity for plasminogen activator inhibitor-1 than
CC the corresponding unmodified urokinase. Urokinase is one of two types of
CC mammalian plasminogen activators (PA), the other being tissue type PA.
CC PAs catalyze the conversion of the circulating zymogen plasminogen to the
CC broad spectrum protease plasmin by limited proteolysis. The modified
CC urokinase can be used for clot lysis, specifically to dissolve heart
CC attack-causing clots before they cause permanent damage to heart muscle.
CC The urokinase mutant is more resistant to inhibition by plasminogen
CC activator inhibitors than the unmodified urokinase. It can be selectively
CC expressed and secreted from the mammary glands of transgenic animals.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 430 AA;

Query Match 100.0%; Score 837; DB 2; Length 430;
Best Local Similarity 100.0%; Pred. No. 2.5e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 60
DB 20 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 79
QY 61 KASTDTMGRCPLPNSATVLTQTYHAHRSALQGLGKINYCRNPNRRRPPWCYVQVGLK 120
DB 80 KASTDTMGRCPLPNSATVLTQTYHAHRSALQGLGKINYCRNPNRRRPPWCYVQVGLK 139
QY 121 PLVQECWVHDCADGKPKSPPEE 143
DB 140 PLVQECWVHDCADGKPKSPPEE 162

RE UT 35
AA 0114
ID AAP50114 standard; protein; 431 AA.
AC AAP50114;
XX
DT 27-SEP-1991 (first entry)
DE
DE Sequence encoded by the signal sequence and noncoding region of the pro-
DE UK structural gene (Sequence II).
XX Enzyme; thrombosis therapy; embolic disease; single-chain pro-urokinase.
XX Homo sapiens.

Key Location/Qualifiers
Peptide 1..20
Domain 21..177 /label= signal peptide
Domain 179..431 /label= A chain
Domain 179..431 /label= B chain
XX EP154272-A.
XX 11-SEP-1985.
XX 23-FEB-1985; 85JP-00102031.
XX 27-FEB-1984; 84JP-00037119.
XX 31-JAN-1985; 85JP-00017969.
XX (GREC) GREEN; CROSS CORP.
XX Hiramatsu R, Kaneda T, Nagai M, Rimura H, Nishida M, Suyama T;
XX WPI; 1985-224693/37.
XX N-PSDB; AAN50118.

XX Glycosylated single-chain pro-urokinase - prepd. by cultivating animal
PT cells transformed by DNA prepd. from m RNA.
XX Disclosure; Page 8-10; 64pp; English.
XX The inventors claim a method of producing single-chain pro-urokinase by
CC using as template, mRNA obtd. from cells of an established human kidney-
CC derived cell line. The urokinase is used to treat thrombosis and embolic
CC diseases as well as in the treatment of diseases in combination with
CC anticancer agents
XX Sequence 431 AA;

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 60
DB 21 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNCPKFGGQHCIDKSKTCYEGNGHFGYRG 80
QY 61 KASTDTMGRCPLPNSATVLTQTYHAHRSALQGLGKINYCRNPNRRRPPWCYVQVGLK 120
DB 81 KASTDTMGRCPLPNSATVLTQTYHAHRSALQGLGKINYCRNPNRRRPPWCYVQVGLK 140
QY 121 PLVQECWVHDCADGKPKSPPEE 143
DB 141 PLVQECWVHDCADGKPKSPPEE 163

RESULT 36
AAP60783
ID AAP60783 standard; protein; 431 AA.
XX AAP60783;
XX
XX 25-MAR-2003 (revised)
DT 23-OCT-1991 (first entry)
XX Human urokinase.
XX E.coli; high molecular urokinase.
XX Homo sapiens.
Key Location/Qualifiers
Protein 21..431
XX JP61181377-A.
XX 14-AUG-1986.
XX 25-JAN-1985; 85JP-00011032.
XX 25-JAN-1985; 85JP-00011032.
XX (NISC) NISSAN CHEM IND LTD.
XX (HODO) HODOGAYA CHEM IND CO LTD.
XX (SAGA) SAGAMI CHEM RES CENTRE.
XX (CENG) CENTRAL GLASS CO LTD.
XX (NIPS) NIPPON SODA CO.
XX (TOIJ) TOYO SODA MFG CO LTD.
XX WPI; 1986-254744/39.
XX N-PSDB; AAN60703.
XX Human urokinase gene - has N-end of aminoacid sequence coded by codon
PT used in Escherichia coli.
XX Disclosure; Fig 2; 19pp; Japanese.
XX The claimed gene product may be expressed in a transformed E.coli host,
CC

for the efficient production of high molecular human urokinase. The N-terminal of the protein expressed by the transforming plasmid is replaced with a codon frequently used in E.coli. (Updated on 25-MAR-2003 to correct PA field.)

Sequence 431 AA;

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Every Match .. 100.0%; Score 837; DB 1; Length 431;
t Local Similarity 100.0%; Pred. No. 2.6e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 SNEHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKFFGGQHCETDKSKTCYEGNGHYRG 60
21 SNEHQVPSNCDCLNGGTCVSNKYPSNIHWCNCPKFFGGQHCETDKSKTCYEGNGHYRG 60

61 KASTDTMGRPCLPWNSATVLOOTYHAHRSDALQLGLGKHNYCRNPDNRPPWCYVQVGLK 1200

81 KASTDTMGRPCLPWNSATVLQOTYAHRS DALQLGLKHNYCRNPDNRRRPPWCVVVGLK 140

121 PLVQECMVHDCADGKKPSSPPEE 143

141 PLVQECMVHDCADGKPSPPPEE 163

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0258

AAFP70258

ADP70358.

1 OCT 20 / 1955

25-MAR-2003 11:11 (revised)

19-MAY-1991 (first entry)

Sentence of h

[illegible]

Cardiovascular disease treatment; fr

protease.

Home sapiens

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[illegible]

Peptide	1:1:20	1:1:100	1:1:500
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2	100	100	100
3	100	100	100
4	100	100	100
5	100	100	100
6	100	100	100
7	100	100	100
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9	100	100	100
10	100	100	100
11	100	100	100
12	100	100	100
13	100	100	100
14	100	100	100
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17	100	100	100
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26	100	100	100
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60	100	100	100
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63	100	100	100
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83	100	100	100
84	100	100	100
85	100	100	100
86	100	100	100
87	100	100	100
88	100	100	100
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90	100	100	100
91	100	100	100
92	100	100	100
93	100	100	100
94	100	100	100
95	100	100	100
96	100	100	100

Protein	21	431
/label= leader		

/label= prouokinase

EP231883-A.

12-AUG-1987

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29-JAN-1987; 87EP-00101209.

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31-JAN-1986; 86JF-00017734.
30-JAN-1987. 87JP-00018626

[illegible]

(SAGA) SAGAMI CHEM RES CENTRE.

(NIPPON) NIPPON SODA CO. CENTRAL CITY CO. INC.

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCEIDKSKTCYEGNGHFFYRG 60
DB 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCEIDKSKTCYEGNGHFFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGKPPSPPEE 143
DB 141 PLVQECMVHDCADGKPPSPPEE 163

RESULT 39
AA 1663
ID AAP71663 standard; protein; 431 AA.

AC AAP71663;
XX 30-APR-1991 (first entry)
XX Modified prourokinase.
XX Prourokinase; fibrin; PUK.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= sig_peptide
FT Protein 21..431
FT /label= mat_protein
FT Misc-difference 178..178
FT /note= "amino acid other than LYS"

XX EP236040-A.
XX 09-SEP-1987.
XX 24-FEB-1987; 87EP-00301567.
XX 26-FEB-1986; 86US-00833179.
XX 19-FEB-1987; 87US-00012023.
XX (COLB) COLLABORATIVE RES INC.
XX Vovis GF, Mao JI;
XX WPI; 1987-251560/36.
XX N-PSDB; AAN71338.

XX Amino acid modified form of prourokinase - having high fibrin selectively
XX and resistant to cleavage to the two-chain form.
XX Disclosure; Fig 1; 18pp; Japanese.

XX The amino acid LYS at position 158 of the mature protein (see tag b) is
XX replaced by another amino acid, achieved by site-directed mutagenesis or
XX by chemical modification. The modified PUK has a single polypeptide chain,
XX high fibrin activity and is resistant to cleavage to the two-chain form
XX to an extent greater than its original unmodified form. The therapeutic
XX specificity of single-chain PUK can be increased without decreasing
XX fibrinolytic activity. The single chain form can have high fibrin
XX activity and thus does not cause general bleeding in the body but rather
XX can be localised to the site of the blood clot directly. See also
XX AAN71368-69

XX Sequence 431 AA;

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-55;

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCEIDKSKTCYEGNGHFFYRG 60
DB 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCEIDKSKTCYEGNGHFFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGKPPSPPEE 143
DB 141 PLVQECMVHDCADGKPPSPPEE 163

RESULT 40
AA 1698
ID AAP71698 standard; protein; 431 AA.

AC AAP71698;
XX 30-APR-1991 (first entry)
XX Modified prourokinase (MET/SER).
XX Prourokinase; fibrin; PUK.
XX Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..20
FT /label= sig_peptide
FT Protein 21..431
FT /label= mat_protein
XX EP236040-A.

XX 09-SEP-1987.
XX 24-FEB-1987; 87EP-00301567.
XX 26-FEB-1986; 86US-00833179.
XX 19-FEB-1987; 87US-00012023.
XX (COLB) COLLABORATIVE RES INC.

XX Vovis GF, Mao JI;
XX WPI; 1987-251560/36.
XX N-PSDB; AAN71368.

XX Amino acid modified form of prourokinase - having high fibrin selectively
XX and resistant to cleavage to the two-chain form.
XX Disclosure; Fig 1; 18pp; Japanese.

XX The amino acid LYS at position 158 of the mature protein is replaced by
XX MET and the amino acid ILE at position 160 is replaced by SER, achieved
XX by site-directed mutagenesis or by chemical modification. The modified PUK
XX has a single polypeptide chain, high fibrin activity and is resistant to
XX cleavage to the two-chain form to an extent greater than its original
XX unmodified form. The therapeutic specificity of single-chain PUK can be
XX increased without decreasing fibrinolytic activity. The single chain form
XX can have high fibrin activity and thus does not cause general bleeding in
XX the body but rather can be localised to the site of the blood clot
XX directly. See also AAN71368-69 and AAN71338

XX Sequence 431 AA;

atches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 1 SNELHQPNSCDCLNGTGVSNKYPNSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60

D 21 SNELHQPNSCDCLNGTGVSNKYPNSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 80

Q 61 KASTDTMGRCPLPWSNATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 120

D 81 KASTDTMGRCPLPWSNATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 140

Q 121 PLVQECMVHDCADGKKPSSPPEE 143

D 141 PLVQECMVHDCADGKKPSSPPEE 163

F JLT 41

A /1699

I AAP71699 standard; protein; 431 AA.

X AAP71699;

X 30-APR-1991 (first entry)

X Modified prourokinase (ALA).

X Prourokinase; fibrin; PUK.

X Homo sapiens.

Key Location/Qualifiers

Peptide : 1..20

Protein /label= sig_peptide

21..431

/label= mat_protein

EP236040-A.

09-SEP-1987.

24-FEB-1987; 87EP-00301567.

26-FEB-1986; 86US-00833179.

19-FEB-1987; 87US-00012023.

(COLB) COLLABORATIVE RES INC.

Vovis GF, Mao JI;

WPI; 1987-251560/36.

N-PSDB; AAN71369.

Amino acid modified form of prourokinase - having high fibrin selectively and resistant to cleavage to the two-chain form.

Disclosure; Fig 1; 18pp; Japanese.

The amino acid LYS at position 158 of the mature protein (bases 610-612) is replaced by another amino acid (ALA), achieved by site-directed mutagenesis. The modified PUK has a single polypeptide chain, high fibrin activity and is resistant to cleavage to the two-chain form to an extent greater than its original unmodified form. The therapeutic specificity of single-chain PUK can be increased without decreasing fibrinolytic activity. The single chain form can have high fibrin activity and thus does not cause general bleeding in the body but rather can be localised to the site of the blood clot directly. See also AAN71368-69

Sequence 431 AA;

very Match 100.0%; Score 837; DB 1; Length 431;

est Local Similarity 100.0%; Pred. No. 2.6e-55;

atches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 1 SNELHQPNSCDCLNGTGVSNKYPNSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60

Db 21 SNELHQPNSCDCLNGTGVSNKYPNSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 80

QY 61 KASTDTMGRCPLPWSNATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 120

Db 81 KASTDTMGRCPLPWSNATVLOQTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143

Db 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 42

AAP80430

ID AAP80430 standard; protein; 431 AA.

XX AAP80430;

XX 25-MAR-2003 (revised)

DT 14-SEP-1990 (first entry)

XX Deduced AA sequence of the single chain urokinase plasminogen activator (SCU-PA) cDNA insert prepared from human Hep3 cells.

DE Single chain urokinase plasminogen activator (SCU-PA); human Hep3 cells;

DE glyceroldehyde-3-phosphate dehydrogenase gene; thrombosis prevention;

XX thrombosis treatment.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..20

FT Protein 21..411

FN EP288435-A.

XX 26-OCT-1988.

PD 11-APR-1988; 88EP-00810234.

XX 15-APR-1987; 87GB-00009081.

XX 16-JUN-1987; 87GB-00014059.

PR 04-DEC-1987; 87IE-00003299.

XX (CIBA) CIBA GEIGY AG.

XX Meyhack B, Heim J, Burgi R;

XX WPI; 1988-301440/43.

DR N-PSDB; AAN80981.

XX Prodn. of human single chain urokinase-type plasminogen activator - by

PT culturing yeast strain transformed with hybrid vector contg. yeast

PT expression control sequences.

XX Example 1; Fig 2; 48pp; English.

XX The patent is for the prodn. of human single chain urokinase-type

CC plasminogen activator (UTPA). Mutants of scu-PA are especially those

CC which render the protein protease resistant. Such scu-PA mutants are

CC covalently modified at sites of proteolysis by proteases occurring in

CC blood such as thrombin or plasmin, so that they are no longer susceptible

CC to protease hydrolysis at these locations. The target sites include

CC Lys135 to Lys136 (cleavage at this site generates the so-called low

CC molecular weight form of scu-PA or LUK), Arg156 to Phe157 (susceptible to

CC thrombin attack) and Lys158 to Ile159 (cleavage at this site by plasmin

CC generates tuc-PA). Suitable scu-PA mutants have site specific

CC substitutions, insertions or deletions of residues at one or more of

CC these target sites. Especially preferred are those mutants in which one

CC amino acid residue or both amino acid residues forming the target sites

CC are deleted or in which at least one of these amino acid residues is

CC replaced by another amino acid residue so that the resulting mutants are

CC resistant to proteolytic attack. The UTPA proteins exhibit the biological

CC activity of natural human UTPA without any refolding procedure being
CC necessary. They can be used as for known PAs in humans for the prevention
CC or treatment of thrombosis or other conditions where it is desired to
CC produce local fibrinolytic or proteolytic activity. (Updated on 25-MAR-
CC 2003 to correct PR field.)
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-55; Indels 0; Gaps 0;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIEDKSKTCYEGNGHFFYRG 60
DE 21 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIEDKSKTCYEGNGHFFYRG 80
QY 61 KASDTMTGRCLPWSNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVOVGLK 120
DB 81 KASDTMTGRCLPWSNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVOVGLK 140
QY 121 PLVQECWVHDCADGKKPSPPEE 143
DB 141 PLVQECWVHDCADGKKPSPPEE 163

RESULT 44
AAP91886
ID AAP91886 standard; protein; 431 AA.
XX
AC AAP91886;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 16-APR-1990 (first entry)
XX
DE Pro-urokinase with signal sequence.
XX
KW pro-urokinase (pro-UK); plasminogen activator; pUK33; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /label= signal peptide
FT Protein 21..431
FT /label= pro-urokinase
XX
PN EP265874-A.
XX
PD 04-MAY-1988.
XX
PF 23-OCT-1987; 87EP-00115600.
XX
PE 23-OCT-1986; 86JP-00253078.
XX
PA (GREG) GREEN CROSS CORP.
XX
PI Amatsuji Y, Okabayashi K, Nagai M, Arimura H, Suyama T;
XX
WPI; 1988-121000/18.
XX
N-PSDB; AAN81558.
XX

XX Glycosylated single-chain pro-urokinase prodn. - by cultivating DHFR gene
XX -deficient CHO-K1 cells transformed with a plasmid contg. CDNA, SV40
XX promoter and DHFR gene.
XX
XX Disclosure; Page ?; 19pp; English.
XX

XX The Arg at position 2 is encoded by TGA(sic). Possible error in the
XX specification. Should read CGA? The pro-UK gene was derived from plasmid
XX pUK33. The cDNA was synthesised using urokinase mRNA isolated from a
XX human kidney cell line. Pro-UK was cloned into a SV40 promoter-contg.
XX plasmid, down- stream of the promoter. This plasmid was then ligated to
XX a DHFR- gene contg. plasmid so that pro-UK and DHFR are inserted in

CC opposite directions. The recombinant plasmid was used to transform CHO-K1
CC cell derived DHFR gene-deficient host cells to produce glycosylated
CC single-chain pro-UK. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 431 AA;

Query Match 100.0%; Score 837; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 2.6e-55; Indels 0; Gaps 0;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIEDKSKTCYEGNGHFFYRG 60
DB 21 SNELHQVPSNCDCLNGGTCVSNKYFNSNIHWNCNCPKFGGQHCIEDKSKTCYEGNGHFFYRG 80
QY 61 KASDTMTGRCLPWSNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVOVGLK 120
DB 81 KASDTMTGRCLPWSNATVLOQTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVOVGLK 140
QY 121 PLVQECWVHDCADGKKPSPPEE 143
DB 141 PLVQECWVHDCADGKKPSPPEE 163

RESULT 44
AAP91886
ID AAP91886 standard; protein; 431 AA.
XX
AC AAP91886;
XX
DT 25-MAR-2003 (revised)
DT 31-OCT-2002 (revised)
DT 16-APR-1990 (first entry)
XX
DE Sequence of pro-urokinase.
XX
KW Low mol. wt. plasminogen activator; pro-urokinase; dissolve blood clot.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 21..431
FT /note= "Mature pro-urokinase."
FT Region 170..179
FT /note= "Preferred initiation region for the low mol. wt. plasminogen activators."
XX
PN EP316068-A.
XX
PD 17-MAY-1989.
XX
PF 07-OCT-1988; 88EP-00309417.
XX
PE 09-OCT-1987; 87US-00107370.
XX
PA 27-SEP-1988; 88US-00248727.
XX
PI (COLB) COLLABORATIVE RES INC.
XX
WPI; 1989-146601/20.
XX
N-PSDB; AAN91740.
XX

XX Modified low mol. wt. plasminogen activator - formed of amino acids
XX comprising the amino acid portion of pro-urokinase from 150 to 411.
XX
XX Fig 1; Page -; 27pp; English.
XX

XX A low mol. wt. polypeptide plasminogen activator (PA) is claimed which is
XX formed from amino acids 150-411 of pro-urokinase. The preferred initiation
XX region for the low mol. wt. PA is indicated (see FT). A low mol wt. PA
XX can be injected into blood in the body in vivo to dissolve clots without
XX harm. (Updated on 31-OCT-2002 to add missing OS field.) (Updated on 25-
XX MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI

C field.)
 X Sequence 431 AA;
 S Query Match 100.0%; Score 837; DB 1; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Q 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCIEDKSKTCYEGNGHFYRG 60
 D 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCIEDKSKTCYEGNGHFYRG 80
 Q 61 KASTDTMGPRCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPNRRRRCWCVQVGLK 120
 D 81 KASTDTMGPRCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPNRRRRCWCVQVGLK 140
 Q 121 PLVQECMVHDCADGKXPSPPEE 143
 D 141 PLVQECMVHDCADGKXPSPPEE 163
 R JLT 45
 A 92119
 I AAP92119 standard; protein; 431 AA.
 X AAP92119;
 A 25-MAR-2003 (revised)
 D 29-JUN-1990 (first entry)
 X Natural human prourokinase.
 D Human prourokinase; antithrombotic; derivative.
 X Homo sapiens.
 X Key Location/Qualifiers
 F Misc-difference 1 /note= "Optional in new deriv."
 F Misc-difference 2 /note= "Incorporated into new deriv."
 F Misc-difference 135 /note= "May be replaced by a non-basic AA in new deriv."
 F Misc-difference 156 /note= "Undefined residue in new deriv."
 F Misc-difference 157 /note= "Pro, Gly, Ala or Val in new deriv."
 F Misc-difference 158 /note= "Lys or Arg in new deriv."
 F WO8901513-A.
 X 23-FEB-1989.
 F 18-AUG-1988; 88WO-JP000815.
 X 19-AUG-1987; 87JP-00204149.
 X (SAGA) SAGAMI CHEM RES CENTRE.
 X (CENG) CENTRAL GLASS CO LTD.
 X (HODO) HODOGAYA CHEM KK.
 X (NIPS) NIPPON SODA CO.
 X (NISC) NISSAN CHEM IND LTD.
 X Kobayashi Y.; Omori M, Yamada C;
 X WPI; 1989-068869/09.
 D N-PSDB; AAN91075.
 X Antithrombotic fast-acting pro-urokinase deriv. - produced by culture of
 X E coli transformant contg. new plasmid of PMUT9Q family.
 X Disclosure; Fig 1; 75pp; Japanese.

XX A human prourokinase (PU) deriv. is new which is based upon residues 2-
 CC 155 of natural human prourokinase. The new deriv. is produced by E. coli
 CC J103/PMUT9Q-RPK in culture. It is a fast-acting drug for the treatment
 CC and prevention of thrombosis. (Updated on 25-MAR-2003 to correct PA
 CC field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX SQ Sequence 431 AA;
 Query Match 100.0%; Score 837; DB 1; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCIEDKSKTCYEGNGHFYRG 60
 DB 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCIEDKSKTCYEGNGHFYRG 80
 QY 61 KASTDTMGPRCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPNRRRRCWCVQVGLK 120
 DB 81 KASTDTMGPRCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPNRRRRCWCVQVGLK 140
 QY 121 PLVQECMVHDCADGKXPSPPEE 143
 DB 141 PLVQECMVHDCADGKXPSPPEE 163
 RESULT 46
 AAP94764
 ID AAP94764 standard; protein; 431 AA.
 XX AAP94764;
 XX 25-MAR-2003 (revised)
 DT 27-JUN-1990 (first entry)
 XX Non-glycosylated prourokinase.
 DE Prourokinase; CGE 195; plasminogen activator; blood clot lysis.
 KW Homo sapiens.
 OS Key Location/Qualifiers
 FH Region 1..20
 FT /label= signal sequence
 XX EF299706-A.
 XX PD 18-JAN-1989.
 XX PF 12-JUL-1988; 88EP-00306334.
 XX PR 13-JUL-1987; 87US-00072426.
 PR 29-JUN-1988; 88US-00211279.
 XX (COLB) COLLABORATIVE RES INC.
 XX Baltimore D, Moir DT, Broeze RJ;
 WPI; 1989-017204/03.
 DR N-PSDB; AAN93079.
 XX New non glycosylated, secreted plasminogen activator - pref. with
 PT asparagine replaced or deleted, useful for treating blood clots,
 PT expressed in non mammalian cells.
 XX Disclosure; Page; 26pp; English.
 XX myocardial infarction. DNA encoding the protein was sequenced from
 CC plasmid pCGS195, a subclone of two inserts isolated by screening a cDNA
 CC library prep. from kidney cell RNA. One of the original inserts, clone
 CC CGF31 (tag c) started in the middle of the signal sequence. Mutants of
 CC the sequence, pref. in which gcc (Ala) replaces aat (Aan) at nucleotides
 CC 1002-1004 (residue 302) are used to transform hosts for the prodn. of non

CC -glycosylated, pro-urokinase. (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 431 AA;
 SC Query Match 100.0%; Score 837; DB 1; Length 431;
 st Local Similarity 100.0%; Pred. No. 2.6e-55;
 ches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFRG 60
 DB 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFRG 80

QY 61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
 DB 81 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
 DB 141 PLVQECMVHDCADGKKPSSPPEE 163

RE LT 47
 AA 112
 ID AAR07112 standard; protein; 431 AA.
 XX AAR07112;
 AC AAR07112;
 XX 25-MAR-2003 (revised)
 DT 24-JAN-1991 (first entry)
 XX Human pro-Urokinase encoded by plasmid pUK1.
 DE Human pro-Urokinase; transgenic mice.
 XX pro-Urokinase; transgenic mice.
 OS Synthetic.
 XX EP390592-A.
 PN 03-OCT-1990.
 XX 30-MAR-1990; 90EP-00303445.
 XX 31-MAR-1989; 89JP-00078574.
 PR (KYOW) KYOWA-HAKKO KOGYO KK.
 PA (EXPE-) CENT INST EXPER ANIMALS.
 PA (JIKK-) JIKKEN DOBUTSU CHUO KENK.
 XX Sekine S, Ito S, Katsuki M;
 PI WPI; 1990-299492/40.
 XX N-PSDB; AAQ06049.
 DE Prodn. of recombinant protein, esp. human pro-urokinase - from milk of
 XX transgenic animals using promoter of bovine alpha S1 casein chromosomal
 PT gene.
 PT Example; Table 1; 55pp; English.
 PS E.coli strain C600SF8 was transformed with recombinant plasmid containing
 XX ds DNA derived from human pharynx cancer cell strain Detroit 562. 10000
 CC colonies were screened and one positive clone was identified. Plasmid
 CC pUK1 was isolated and found to contain the coding region and 3' non-
 CC coding region of pro-UK downstream of Cys(41). Four silent substitutions
 CC were identified c.f. Holmes et al., Biotechnology, vol.3, p.923 (1985) as
 CC follows: (sic) Asn(254), AAC to AAT; Leu(340), CTA to CTG; Pro(345), CCC
 CC to CCA; Gln(346), CAA to CAG. See also AAQ06045-Q06048 and AAQ06392.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX Sequence 431 AA;
 SC Query Match 100.0%; Score 837; DB 2; Length 431;
 st Local Similarity 100.0%; Pred. No. 2.6e-55;

Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFRG 60
 DB 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFRG 80

QY 61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
 DB 81 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
 DB 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 48
 AAR04253
 ID AAR04253 standard; protein; 431 AA.
 XX AAR04253;
 AC AAR04253;
 XX 25-MAR-2003 (revised)
 DT 12-SEP-1990 (first entry)
 XX Human pro-urokinase from the cDNA of clone pcUK176.
 DE Human pro-urokinase; pro-urokinase; E. coli; Ptp promoter; MS-2 RBS.
 XX Non-glycosylated; pro-urokinase; E. coli; Ptp promoter; MS-2 RBS.
 OS Synthetic.
 XX EP365894-A.
 PN 02-MAY-1990.
 XX 06-OCT-1989; 89EP-00118586.
 XX 11-OCT-1988; 88GB-00023833.
 XX (FARM) FARMITALIA ERBA SPA CARLO.
 XX Brandazza A, Sarmientos P, Orsini G;
 XX WPI; 1990-133447/18.
 DR N-PSDB; AAQ04107.
 XX Non-glycosylated pro-urokinase prodn. - using E coli B strains and E coli
 PT promoter PTP and Shine-Dalgarno sequence MS-2.
 XX Disclosure; Page ?; -pp; English.
 XX SER residue at position 21 is the start of the mature proUK. Non-
 CC glycosylated proUK (MW 45kD) produced by E.coli B strain containing the
 CC sequence. See also AAQ04101-07. (Updated on 25-MAR-2003 to correct PA
 CC field.)
 XX Sequence 431 AA;
 SC Query Match 100.0%; Score 837; DB 2; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFRG 60
 DB 21 SNEHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFRG 80

QY 61 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
 DB 81 KASTDTMGRPCLPWNATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
 DB 141 PLVQECMVHDCADGKKPSSPPEE 163

F ULT 49
 A 63141
 AAR63141 standard; protein; 431 AA.
 AAR63141;
 25-MAR-2003 (revised)
 09-JUN-1995 (first entry)
 Full length human urokinase protein.
 Human urokinase glycoproteins; cardiovascular diseases;
 pulmonary embolism.
 Homo sapiens;
 Key Location/Qualifiers
 Sig_peptide 1..20
 Disulfide-bond 70..151
 Disulfide-bond 91..133
 Disulfide-bond 122..146
 Disulfide-bond 168..299
 Cleavage-site 179..180
 /note= "cleavage of this site produces a bioactive two
 chain form of urokinase"
 Disulfide-bond 209..225
 Disulfide-bond 217..288
 Disulfide-bond 313..382
 Disulfide-bond 345..361
 Disulfide-bond 372..400
 EP620279-A1.
 19-OCT-1994.
 14-APR-1983; 94EP-00104777.
 15-APR-1982; 82US-00368773.
 14-MAR-1983; 82US-00474930.
 14-APR-1983; 83EP-00103629.
 (GETH) GENENTECH INC.
 Heyneker HL, Holmes WE, Vehar GA;
 WPI; 1994-318362/40.
 N-PSDB; AAQ73483.
 Prodn. of human urokinase glycoproteins - using a recombinant expression
 system used for the treatment of vascular diseases or conditions.
 Claim 1; Fig 4; 41pp; English.
 AAQ73483 is the cDNA sequence which encodes AAR63141 the full length
 54000 dalton human urokinase (UK) protein. This cDNA was used in the
 construction of a plasmid capable of transforming either yeast or
 vertebrate cells, enabling them to produce the 54000 dalton human UK
 protein. The UK glycoprotein produced could then be used in the treatment
 of cardiovascular diseases, including pulmonary embolism. The UK produced
 using this method had the advantage of a specific activity towards fibrin
 and extant thrombi, not demonstrated previously with UK isolated from
 natural sources. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 PR field.)
 Sequence 431 AA;
 Query Match 100.0%; Score 837; DB 2; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SNELHQVPSNCDCLNGTGVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60
 AAR63141 standard; protein; 431 AA.
 AAR63141;
 25-MAR-2003 (revised)
 09-JUN-1995 (first entry)
 Full length human urokinase protein.
 Human urokinase glycoproteins; cardiovascular diseases;
 pulmonary embolism.
 Homo sapiens;
 Key Location/Qualifiers
 Sig_peptide 1..20
 Disulfide-bond 70..151
 Disulfide-bond 91..133
 Disulfide-bond 122..146
 Disulfide-bond 168..299
 Cleavage-site 179..180
 /note= "cleavage of this site produces a bioactive two
 chain form of urokinase"
 Disulfide-bond 209..225
 Disulfide-bond 217..288
 Disulfide-bond 313..382
 Disulfide-bond 345..361
 Disulfide-bond 372..400
 EP620279-A1.
 19-OCT-1994.
 14-APR-1983; 94EP-00104777.
 15-APR-1982; 82US-00368773.
 14-MAR-1983; 82US-00474930.
 14-APR-1983; 83EP-00103629.
 (GETH) GENENTECH INC.
 Heyneker HL, Holmes WE, Vehar GA;
 WPI; 1994-318362/40.
 N-PSDB; AAQ73483.
 Prodn. of human urokinase glycoproteins - using a recombinant expression
 system used for the treatment of vascular diseases or conditions.
 Claim 1; Fig 4; 41pp; English.
 AAQ73483 is the cDNA sequence which encodes AAR63141 the full length
 54000 dalton human urokinase (UK) protein. This cDNA was used in the
 construction of a plasmid capable of transforming either yeast or
 vertebrate cells, enabling them to produce the 54000 dalton human UK
 protein. The UK glycoprotein produced could then be used in the treatment
 of cardiovascular diseases, including pulmonary embolism. The UK produced
 using this method had the advantage of a specific activity towards fibrin
 and extant thrombi, not demonstrated previously with UK isolated from
 natural sources. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 PR field.)
 Sequence 431 AA;
 Query Match 100.0%; Score 837; DB 2; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 SNELHQVPSNCDCLNGTGVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60

Db 21 SNELHQVPSNCDCLNGTGVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 80
 Qy 61 KASTDTMGPRPCLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
 Db 81 KASTDTMGPRPCLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 140
 Qy 121 PLVQECMWHDCADGKKPSSPPPEE 143
 Db 141 PLVQECMWHDCADGKKPSSPPPEE 163
 RESULT 50
 AAR47903
 ID AAR47903 standard; protein; 431 AA.
 XX
 AC AAR47903;
 DT 13-JUL-1994 (first entry)
 XX
 DE Pro-urokinase derivative.
 XX
 KW Pro-urokinase; half-life; thrombolytic; thrombosis; fibrinolytic; factor.
 XX
 OS Homo sapiens.
 XX
 PN JP05336965-A.
 XX
 PD 21-DEC-1993.
 XX
 PF 17-OCT-1991; 91JP-00269615.
 XX
 PR 17-OCT-1991; 91JP-00269615.
 XX
 PA (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 DR WPI; 1994-030907/04.
 XX
 DR N-PSDB; AAQ55772.
 XX
 PT Novel human pro-urokinase deriva. having long half-life - with high
 PT thrombolytic activity, useful for treatment of thrombosis.
 XX
 PS Disclosure; Page 15-17; 29pp; Japanese.
 CC
 CC Sequences (AAQ55771-72) are pro-urokinase derivatives. The products have
 CC an inserted sugar moiety having an amino acid substituted, depleted or
 CC inserted variant around the thrombin cleavage site. They also have a long
 CC half-life allowing them to be used in the treatment of thrombosis.
 XX
 SQ Sequence 431 AA;
 Query Match 100.0%; Score 837; DB 2; Length 431;
 Best Local Similarity 100.0%; Pred. No. 2.6e-55;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 SNELHQVPSNCDCLNGTGVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60
 Db 21 SNELHQVPSNCDCLNGTGVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 80
 Qy 61 KASTDTMGPRPCLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
 Db 81 KASTDTMGPRPCLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 140
 Qy 121 PLVQECMWHDCADGKKPSSPPPEE 143
 Db 141 PLVQECMWHDCADGKKPSSPPPEE 163
 Search completed: May 25, 2004, 14:53:01
 Job time : 36.9657 secs

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C protein - protein search, using sw model

Run on: May 25, 2004, 14:53:05 ; Search time 26.0684 Seconds
(without alignments)
1530.046 Million cell updates/sec

Title: US-09-880-503-8

Effect score: 837

Source: 1. SNEHLQVPSNCCLNGGTCV.....QECMVHDCADGKPSPEE 143

String table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Aligned: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0

Minimum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database: Published Applications AA:

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US02_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	837	100.0	143	9	US-09-880-503-8
2	837	100.0	337	14	US-10-106-698-6266
3	837	100.0	337	15	US-10-264-049-2927
4	837	100.0	411	9	US-09-880-503-3
5	837	100.0	431	9	US-09-264-486B-1
6	837	100.0	431	12	US-10-411-037-34
7	837	100.0	431	12	US-10-411-026-34
8	837	100.0	431	13	US-10-076-421-2
9	837	100.0	431	14	US-10-171-311-184
10	837	100.0	431	14	US-10-193-656-4
11	837	100.0	431	14	US-10-301-822-161
12	837	100.0	431	14	US-10-131-985-21
13	837	100.0	431	14	US-10-295-027-414
14	837	100.0	431	15	US-10-295-027-1275
15	837	100.0	431	16	US-10-410-962-34

ALIGNMENTS

RESULT 1

US-09-880-503-8

; Sequence 8, Application US/09880503

; Patent No. US20020131964A1

; GENERAL INFORMATION:

; APPLICANT: CINES, Douglas B

; APPLICANT: HIGAZI, Abd Al-Roof

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

837	100.0	431	16	US-10-411-049-34	Sequence 34, Appl
837	100.0	437	12	US-10-087-192-594	Sequence 594, Appl
835	99.8	431	14	US-10-247-671-149	Sequence 149, Appl
827	98.8	411	15	US-10-407-821-2	Sequence 2, Appl
821	98.1	431	12	US-10-282-174-562	Sequence 562, Appl
815	97.4	445	15	US-10-360-101-266	Sequence 266, Appl
793	94.7	135	9	US-09-880-503-4	Sequence 4, Appl
793	94.7	138	9	US-09-884-186-12	Sequence 12, Appl
793	94.7	138	14	US-10-237-667-12	Sequence 12, Appl
793	94.7	138	14	US-10-237-708-12	Sequence 12, Appl
793	94.7	138	14	US-10-237-866-12	Sequence 12, Appl
793	94.7	138	14	US-10-237-871-12	Sequence 12, Appl
793	94.7	138	14	US-10-237-634-12	Sequence 12, Appl
793	94.7	138	16	US-10-702-536-12	Sequence 12, Appl
793	94.7	138	16	US-10-702-636-12	Sequence 12, Appl
793	94.7	403	9	US-09-880-503-6	Sequence 6, Appl
595.5	71.1	432	15	US-10-401-077-1	Sequence 1, Appl
559	68.0	432	12	US-10-087-192-591	Sequence 591, Appl
554	66.2	96	9	US-09-880-503-9	Sequence 9, Appl
510	60.9	88	9	US-09-880-503-1	Sequence 1, Appl
505	60.3	322	12	US-10-424-999-21	Sequence 21, Appl
505	60.3	322	12	US-10-425-000-41	Sequence 41, Appl
505	60.3	322	15	US-10-233-675A-21	Sequence 21, Appl
501	59.9	91	12	US-10-424-999-37	Sequence 37, Appl
501	59.9	221	12	US-10-424-999-36	Sequence 36, Appl
501	59.9	687	12	US-10-424-999-17	Sequence 17, Appl
501	59.9	687	12	US-10-425-000-37	Sequence 37, Appl
501	59.9	687	15	US-10-233-675A-17	Sequence 17, Appl
500	59.7	87	12	US-10-424-999-9	Sequence 9, Appl
500	59.7	87	12	US-10-425-000-29	Sequence 29, Appl
500	59.7	87	15	US-10-233-675A-9	Sequence 9, Appl
499	59.6	86	12	US-10-424-999-5	Sequence 5, Appl
499	59.6	86	12	US-10-424-999-62	Sequence 62, Appl
499	59.6	86	12	US-10-425-000-97	Sequence 97, Appl
499	59.6	86	15	US-10-233-675A-5	Sequence 5, Appl
498	59.5	688	12	US-10-424-999-18	Sequence 18, Appl
498	59.5	688	15	US-10-425-000-38	Sequence 38, Appl
498	59.5	688	12	US-10-233-675A-18	Sequence 18, Appl
498	59.5	689	12	US-10-424-999-13	Sequence 13, Appl
498	59.5	689	15	US-10-425-000-33	Sequence 33, Appl
498	59.5	689	12	US-10-233-675A-13	Sequence 13, Appl
496	59.3	91	12	US-10-424-999-35	Sequence 35, Appl
496	59.3	221	12	US-10-424-999-34	Sequence 34, Appl
495	59.1	87	12	US-10-424-999-10	Sequence 10, Appl
495	59.1	87	12	US-10-425-000-30	Sequence 30, Appl
495	59.1	87	15	US-10-233-675A-10	Sequence 10, Appl
495	59.1	672	12	US-10-424-999-15	Sequence 15, Appl
495	59.1	672	12	US-10-425-000-35	Sequence 35, Appl
495	59.1	672	15	US-10-233-675A-15	Sequence 15, Appl
495	59.1	674	12	US-10-424-999-14	Sequence 14, Appl
495	59.1	674	12	US-10-425-000-34	Sequence 34, Appl
495	59.1	674	15	US-10-233-675A-14	Sequence 14, Appl
494	59.0	86	12	US-10-424-999-1	Sequence 1, Appl
494	59.0	86	15	US-10-233-675A-1	Sequence 1, Appl
494	59.0	322	12	US-10-424-999-20	Sequence 20, Appl
494	59.0	322	15	US-10-425-000-40	Sequence 40, Appl
494	59.0	322	15	US-10-233-675A-20	Sequence 20, Appl
489	58.4	86	12	US-10-424-999-7	Sequence 7, Appl
489	58.4	86	15	US-10-233-675A-7	Sequence 7, Appl

; TITLE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880,503
 ; PRIOR FILING DATE: 2001-06-13
 ; RIOR APPLICATION NUMBER: US 60/212,847
 ; RIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 143
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US 9-880-503-8

Query Match 100.0%; Score 837; DB 9; Length 143;
 Best Local Similarity 100.0%; Pred. No. 2.4e-76;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
 Db 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
 QY 61 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 Db 61 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 QY 121 PLVQECWVHDCADGKPPSPPEE 143
 Db 121 PLVQECWVHDCADGKPPSPPEE 143

RESULT 2
 US 9-106-698-6266
 ; Sequence 6266, Application US/10106698
 ; Publication No. US20030109690A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
 ; CURRENT APPLICATION NUMBER: US/10/106,698
 ; PRIOR FILING DATE: 2002-03-27
 ; RIOR APPLICATION NUMBER: PCT/US00/26524
 ; RIOR FILING DATE: 2000-09-28
 ; RIOR APPLICATION NUMBER: US 60/157,137
 ; RIOR FILING DATE: 1999-09-29
 ; RIOR APPLICATION NUMBER: US 60/163,280
 ; RIOR FILING DATE: 1999-11-03
 ; NUMBER OF SEQ ID NOS: 8564
 ; SOFTWARE: PatentIn Ver. 3.0
 ; SEQ ID NO 6266
 ; LENGTH: 337
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US 9-106-698-6266

Query Match 100.0%; Score 837; DB 14; Length 337;
 Best Local Similarity 100.0%; Pred. No. 6.1e-76;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
 Db 27 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 86
 QY 61 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 Db 87 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 146
 QY 121 PLVQECWVHDCADGKPPSPPEE 143
 Db 147 PLVQECWVHDCADGKPPSPPEE 169

RESULT 3

US-10-264-049-2927
 ; Sequence 2927, Application US/10264049
 ; Publication No. US20040005579A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Birse et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: P4133P1
 ; CURRENT APPLICATION NUMBER: US/10/264,049
 ; CURRENT FILING DATE: 2002-10-04
 ; PRIOR APPLICATION NUMBER: PCT/US01/18569
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: US 60/209,467
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 4360
 ; SOFTWARE: PatentIn Ver. 3.1
 ; SEQ ID NO 2927
 ; LENGTH: 337
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-264-049-2927

Query Match 100.0%; Score 837; DB 15; Length 337;
 Best Local Similarity 100.0%; Pred. No. 6.1e-76;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
 Db 27 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 86
 QY 61 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 Db 87 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 146
 QY 121 PLVQECWVHDCADGKPPSPPEE 143
 Db 147 PLVQECWVHDCADGKPPSPPEE 169

RESULT 4
 US-09-880-503-3
 ; Sequence 3, Application US/09880503
 ; Patent No. US20020131964A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CINES, Douglas B
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
 ; FILE OF INVENTION: TISSUE CONTRACTABILITY
 ; FILE REFERENCE: 9596-331
 ; CURRENT APPLICATION NUMBER: US/09/880,503
 ; CURRENT FILING DATE: 2001-06-13
 ; PRIOR APPLICATION NUMBER: US 60/212,847
 ; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-503-3

Query Match 100.0%; Score 837; DB 9; Length 411;
 Best Local Similarity 100.0%; Pred. No. 7.6e-76;
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
 Db 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
 QY 61 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 Db 61 KASTDTMGPRCLPWNATVLTQTYHAHRSDALQLGLGKHNCRNPNRRPWCYVQVGLK 120
 QY 121 PLVQECWVHDCADGKPPSPPEE 143

Db 121 PLVQECMVHDCADGKKPSSPPEE 143
|||||
RESULT 5
US-09-264-468B-1
; Sequence 1, Application US/09264468B
; Patent No. US20020106775A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Jieyi
; APPLICANT: Nienaber, Vicki L.
; APPLICANT: Henkin, Jack
; APPLICANT: Smith, Richard A.
; APPLICANT: Walzer, Karl A.
; APPLICANT: Severin, Jean M.
; APPLICANT: Edalji, Rouniton
; APPLICANT: Johnson Jr., Robert W.
; APPLICANT: Holzman, Thomas F.
; TITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
; FILE REFERENCE: 6310.US.P1
; CURRENT APPLICATION NUMBER: US/09/264,468B
; CURRENT FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 09/036,361
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Leader sequence
; NAME/KEY: VARIANT
; LOCATION: (279)...(279)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: VARIANT
; LOCATION: (302)...(302)
; OTHER INFORMATION: Xaa = any amino acid
US-09-264-468B-1

Query Match 100.0%; Score 837; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCHEIDKSKTCYEGNGHFGYRG 60
|||
Db 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCHEIDKSKTCYEGNGHFGYRG 80
|||
QY 61 KASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
|||
Db 81 KASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 140
|||
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
|||
Db 141 PLVQECMVHDCADGKKPSSPPEE 163
|||

RESULT 6
US-10-411-037-34
; Sequence 34, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bows, Calvin
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; TITLE OF INVENTION: GALACTOSIDASE A

; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-34

Query Match 100.0%; Score 837; DB 12; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCHEIDKSKTCYEGNGHFGYRG 60
|||
Db 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNPKKFGQHCHEIDKSKTCYEGNGHFGYRG 80
|||
QY 61 KASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
|||
Db 81 KASTDTMGRCPLPWN SATVLOQTYHAHRS DALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 140
|||
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
|||
Db 141 PLVQECMVHDCADGKKPSSPPEE 163
|||

RESULT 7
US-10-411-026-34
; Sequence 34, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; TITLE OF INVENTION: METHODS
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-34

Query Match
Best Local Similarity 100.0%; Score 837; DB 12; Length 431;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCHEIDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCHEIDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVOVGLK 120
Db 81 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVOVGLK 140
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 8
US-10-076-421-2
; Sequence 2, Application US/10076421
; Publication No. US20020193304A1
; GENERAL INFORMATION:
; APPLICANT: WADA, MANABU
; APPLICANT: WADA, NAKO
; TITLE OF INVENTION: ANTI-HIV AGENTS
; FILE REFERENCE: HAYAK-9
; CURRENT APPLICATION NUMBER: US/10/076,421
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: JP 2001-42655
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: JP 2001-184284
; PRIOR FILING DATE: 2001-06-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-421-2

Query Match
Best Local Similarity 100.0%; Score 837; DB 13; Length 431;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCHEIDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCHEIDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVOVGLK 120
Db 81 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVOVGLK 140
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 9
US-10-171-311-184
; Sequence 184, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Giatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoersh, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-184

Query Match
Best Local Similarity 100.0%; Score 837; DB 14; Length 431;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCHEIDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCHEIDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVOVGLK 120
Db 81 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVOVGLK 140
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 10
US-10-193-656-4
; Sequence 4, Application US/10193656
; Publication No. US20030096733A1
; GENERAL INFORMATION:
; APPLICANT: NY, Tor
; APPLICANT: HOLMDAHL, Rikard
; APPLICANT: LI, Jihan
; TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
; FILE REFERENCE: 3810/10577-US3
; CURRENT APPLICATION NUMBER: US/10/193,656
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/304,461
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/304,490
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,182
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P00749
; DATABASE ENTRY DATE: 1986-07-21
; RELEVANT RESIDUES: (1)...(431)
US-10-193-656-4

Query Match
Best Local Similarity 100.0%; Score 837; DB 14; Length 431;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFYRG 60
DB 21 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFYRG 80

QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNTCRNPDNRPRPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNTCRNPDNRPRPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
DB 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 11
US-10-301-822-161
; Sequence 161, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Bursart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MP001-0292RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-161

Query Match 100.0%; Score 837; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFYRG 60
DB 21 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFYRG 80

QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNTCRNPDNRPRPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNTCRNPDNRPRPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
DB 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 12
US-10-131-985-21
; Sequence 21, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V

; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-21

Query Match 100.0%; Score 837; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFYRG 60
DB 21 SNELHQPNSCDLNGGTCVSNKYFSNIHWNCNPKKFGGQHCCEIDKSKTCYEGNGHFYRG 80

QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNTCRNPDNRPRPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNTCRNPDNRPRPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
DB 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 13
US-10-295-027-414
; Sequence 414, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250

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; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 414
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-414

Query Match      100.0%; Score 837; DB 15; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWN SATVLQQTTHAHRSDALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
Db 81 KASTDTMGRPCLPWN SATVLQQTTHAHRSDALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 140
QY 121 PLVQECWHDCAADGKPKSSPPEE 143
Db 141 PLVQECWHDCAADGKPKSSPPEE 163

RESULT 14
US-10-295-027-1275
; Sequence 1275, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Nataasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-013500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1275
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; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1275

Query Match      100.0%; Score 837; DB 15; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWN SATVLQQTTHAHRSDALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
Db 81 KASTDTMGRPCLPWN SATVLQQTTHAHRSDALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 140
QY 121 PLVQECWHDCAADGKPKSSPPEE 143
Db 141 PLVQECWHDCAADGKPKSSPPEE 163

RESULT 15
US-10-410-962-34
; Sequence 34, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-34

Query Match      100.0%; Score 837; DB 16; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWN SATVLQQTTHAHRSDALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 120
Db 81 KASTDTMGRPCLPWN SATVLQQTTHAHRSDALQLGLGKHNYCRNPDNRPRPWCYVQVGLK 140
```

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QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 16
US-10-411-049-34
; Sequence 34, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bowe, Caryn
; TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; PRIOR FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-049-34

Query Match 100.0%; Score 837; DB 16; Length 431;
Best Local Similarity 100.0%; Pred. No. 8e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
Db 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 80

QY 61 KASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 120
Db 81 KASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 17
US-10-087-192-594
; Sequence 594, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 52945200122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
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; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-594

Query Match 100.0%; Score 837; DB 12; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.1e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
Db 27 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 86

QY 61 KASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 120
Db 87 KASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 146

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 147 PLVQECMVHDCADGKKPSSPPEE 169

RESULT 18
US-10-247-671-149
; Sequence 149, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
US-10-247-671-149

Query Match 99.8%; Score 835; DB 14; Length 431;
Best Local Similarity 99.3%; Pred. No. 1.3e-75;
Matches 142; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
Db 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 80

QY 61 KASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 120
Db 81 KASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRRPPWCYVQVGLK 140

QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 163
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RESULT 19


```
US-10-407-821-2
; Sequence 2, Application US/10407821
; Publication No. US20030219386A1
; GENERAL INFORMATION:
; APPLICANT: IDELL, STEVEN
; TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
; TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
; TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURITIS IN RABBITS
; FILE REFERENCE: UTSN:022US
; CURRENT APPLICATION NUMBER: US/10/407,821
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/414,202
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/370,466
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-407-821-2

Query Match      98.8%; Score 827; DB 15; Length 411;
Best Local Similarity 99.3%; Pred. No. 7,7e-75;
Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
DB 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWSNATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRRCVYQVGLK 120
DB 61 KASTDTMGRPCLPWSNATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRRCVYQVGLK 120
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 121 LLVQECMVHDCADGKKPSPPEE 143

RESULT 20
US-10-282-174-562
; Sequence 562, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Vellicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph B.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Aleister J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lytne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
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; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 562
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARIANT
; LOCATION: 15, 58, 141, 214, 231, 274, 366
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-282-174-562

Query Match      98.1%; Score 821; DB 12; Length 431;
Best Local Similarity 98.6%; Pred. No. 3.2e-74;
Matches 141; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 60
DB 21 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWSNATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRRCVYQVGLK 120
DB 81 KASTDTMGRPCLPWSNATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRRCVYQVGLK 140
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 141 XLVQECMVHDCADGKKPSPPEE 163

RESULT 21
US-10-360-101-266
; Sequence 266, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 266
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of urokinase
US-10-360-101-266

Query Match      97.4%; Score 815; DB 15; Length 445;
Best Local Similarity 97.3%; Pred. No. 1.3e-73;
Matches 143; Conservative 0; Mismatches 0; Indels 4; Gaps 2;

QY 1 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFY 58
DB 21 SNELHQPNSCCLNGGTCVSNKYPSNIHWCNCPKFKGGQHCIEDKSKTCYEGNGHFY 80
QY 59 RGKASTDTMGRPCLPWSNATVLOQTY--HAHRSDALQLGLGKHNYCRNPDNRRRRCVYQ 116
DB 81 RGKASTDTMGRPCLPWSNATVLOQTYFTHAHRSDALQLGLGKHNYCRNPDNRRRRCVYQ 140
QY 117 VGLKPLVQECMVHDCADGKKPSPPEE 143
DB 141 VGLKPLVQECMVHDCADGKKPSPPEE 167

RESULT 22
US-09-880-503-4
; Sequence 4, Application US/09880503
; Patent No. US20020131964A1
```

GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Root
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-503-4

Query Match 94.7%; Score 793; DB 9; Length 135;
Best Local Similarity 100.0%; Pred. No. 6e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHVPNSCDCLNGTGVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
Db 1 SNELHVPNSCDCLNGTGVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
QY 61 KASTDTMGRPCLPWSATVLTQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
Db 61 KASTDTMGRPCLPWSATVLTQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGK 135
Db 121 PLVQECMVHDCADGK 135

RESULT 23
US-09-884-186-12
Sequence 12, Application US/09884186
Patent No. US2002015101A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085

FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-984-186-12

Query Match 94.7%; Score 793; DB 9; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.2e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHVPNSCDCLNGTGVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
Db 4 SNELHVPNSCDCLNGTGVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 63
QY 61 KASTDTMGRPCLPWSATVLTQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 120
Db 64 KASTDTMGRPCLPWSATVLTQTYHAHRSDALQLGLGKHNYCRNPNRRRPPWCYVQVGLK 123
QY 121 PLVQECMVHDCADGK 135
Db 124 PLVQECMVHDCADGK 138

RESULT 24
US-10-237-667-12
Sequence 12, Application US/10237667
Publication No. US20030022308A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,667
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-708-12

Query Match 94.7%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.2e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCEIDKSKTCYEGNGHFYRG 60
DB 4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCEIDKSKTCYEGNGHFYRG 63
QY 61 KASDTMTGRPCLPWNSATVLQOQTYHAHRS DALQLGLGKKNYCRNPDNRPRPCVYQVGLK 120
DB 64 KASDTMTGRPCLPWNSATVLQOQTYHAHRS DALQLGLGKKNYCRNPDNRPRPCVYQVGLK 123
QY 121 PLVQECMVHDCADGK 135
DB 124 PLVQECMVHDCADGK 138

RESULT 25
US-10-237-708-12
Sequence 12, Application US/10237708
Publication No. US20030036170A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,708
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PC7/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.

NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-708-12

Query Match 94.7%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.2e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCEIDKSKTCYEGNGHFYRG 60
DB 4 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCEIDKSKTCYEGNGHFYRG 63
QY 61 KASDTMTGRPCLPWNSATVLQOQTYHAHRS DALQLGLGKKNYCRNPDNRPRPCVYQVGLK 120
DB 64 KASDTMTGRPCLPWNSATVLQOQTYHAHRS DALQLGLGKKNYCRNPDNRPRPCVYQVGLK 123
QY 121 PLVQECMVHDCADGK 135
DB 124 PLVQECMVHDCADGK 138

RESULT 26
US-10-237-866-12
Sequence 12, Application US/10237866
Publication No. US20030036171A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,866
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PC7/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.

REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-866-12

Query Match 94.7%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.2e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60
Db 4 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 63
QY 61 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
Db 64 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 123
QY 121 PLVQECMVHDCADGK 135
Db 124 PLVQECMVHDCADGK 138

RESULT 27
US-10-237-871-12
Sequence 12, Application US/10237871
Publication No. US20030036172A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,871
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619

REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-871-12

Query Match 94.7%; Score 793; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.2e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 60
Db 4 SNELHQPNSCDCLNGGTCVSNKYFSNIHWNCNPKKFGGQHCIEDKSKTCYEGNGHFYRG 63
QY 61 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
Db 64 KASTDTMGPRCLPWSATVLOQTYHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVGLK 123
QY 121 PLVQECMVHDCADGK 135
Db 124 PLVQECMVHDCADGK 138

RESULT 28
US-10-237-624-12
Sequence 12, Application US/10237624
Publication No. US20030082747A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSER: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US


```
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-702-636-12

Query Match          94.7%; Score 793; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 6.2e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDLNGGTCVSNKYFSNIHWCNCPKFGQHQCEIDKSKTCYEGNGHFYRG 60
Db 4 SNELHQVPSNCDLNGGTCVSNKYFSNIHWCNCPKFGQHQCEIDKSKTCYEGNGHFYRG 63
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRREPCVYQVGLK 120
Db 64 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRREPCVYQVGLK 123
QY 121 PLVQECMVHDCADGK 135
Db 124 PLVQECMVHDCADGK 138

RESULT 31
US-09-880-503-6
; Sequence 6, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-6

Query Match          94.7%; Score 793; DB 9; Length 403;
Best Local Similarity 100.0%; Pred. No. 2e-71;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDLNGGTCVSNKYFSNIHWCNCPKFGQHQCEIDKSKTCYEGNGHFYRG 60
Db 1 SNELHQVPSNCDLNGGTCVSNKYFSNIHWCNCPKFGQHQCEIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRREPCVYQVGLK 120
Db 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRREPCVYQVGLK 120
QY 121 PLVQECMVHDCADGK 135
Db 121 PLVQECMVHDCADGK 135

RESULT 32
US-10-401-077-1
; Sequence 1, Application US/10401077
; Publication No. US20040002137A1
; GENERAL INFORMATION:
; APPLICANT: Hung, Paul Porwen
; APPLICANT: Wu, Bryan T. H.
```

```
; TITLE OF INVENTION: HUMAN TISSUE UROKINASE TYPE PLASMINOGEN
; TITLE OF INVENTION: ACTIVATOR PRODUCTION
; FILE REFERENCE: 12133-006001
; CURRENT APPLICATION NUMBER: US/10/401,077
; CURRENT FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/371,013
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-401-077-1

Query Match          71.1%; Score 595.5; DB 15; Length 650;
Best Local Similarity 77.9%; Pred. No. 2.4e-51;
Matches 106; Conservative 7; Mismatches 18; Indels 5; Gaps 3;

QY 3 ELHQVF-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGQHQCEIDKSKTCYEGNGHFY 58
Db 77 QCHSVFVKSCSEPERCFNGGTCQALYFSDF-VCCQPEGAGKCCEDTATCYEGNGHFY 135
QY 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRREPCVYQV 118
Db 136 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRREPCVYQV 195
QY 119 LKPLVQECMVHDCADG 134
Db 196 LKPLVQECMVHDCSEG 211

RESULT 33
US-10-087-192-591
; Sequence 591, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 591
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-591

Query Match          68.0%; Score 569; DB 12; Length 433;
Best Local Similarity 70.4%; Pred. No. 7.2e-49;
Matches 95; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 9 SNCDCLNGGTCVSNKYFSNIHWCNCPKFGQHQCEIDKSKTCYEGNGHFYRGKASTDTMG 68
Db 30 SNCGCQGGVCVSYKYFSRIRRCSCPRKFGQHQCEIDKSKTCYHNGNDSYRGKANTDTKG 89
QY 69 RPLCPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRREPCVYQVGLPLVQECMV 128
Db 90 RPLCAWNAFVLOKYPNAHRPDALSLGLGKHNYCRNPDNRREPCVYQVGLRQFVQECMV 149
QY 129 HDCADGKSPSSPPEE 143
Db 150 HDCSLSKSPSSSDVQ 164
```

```
RESULT 34
US-09-880-503-9
; Sequence 9, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-9
Query Match 66.2%; Score 554; DB 9; Length 96;
Best Local Similarity 100.0%; Pred. No. 4.6e-48; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 107
Db 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 60

QY 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 143
Db 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96

RESULT 35
US-09-880-503-1
; Sequence 1, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-1
Query Match 60.9%; Score 510; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.1e-43; Indels 0; Gaps 0;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 107
Db 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 60

QY 108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135
Db 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88

RESULT 36
US-10-424-999-21
; Sequence 21, Application US/10424999
```

```
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 21
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein human abrogen
US-10-424-999-21
Query Match 60.3%; Score 505; DB 12; Length 322;
Best Local Similarity 92.6%; Pred. No. 1.4e-42; Indels 0; Gaps 0;
Matches 87; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPD 106
Db 1 AKTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPD 60

QY 107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSP 140
Db 61 NRRRPWCYVQVGLKPLVQECMVHDCADRLPRGP 94

RESULT 37
US-10-425-000-41
; Sequence 41, Application US/10425000
; Publication No. US20040052777A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
; TITLE OF INVENTION: Angiogenesis
; FILE REFERENCE: ST01027-B
; CURRENT APPLICATION NUMBER: US/10/425,000
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 41
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human derived fusion protein
US-10-425-000-41
Query Match 60.3%; Score 505; DB 12; Length 322;
Best Local Similarity 92.6%; Pred. No. 1.4e-42; Indels 0; Gaps 0;
Matches 87; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPD 106
Db 1 AKTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPD 60

QY 107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSP 140
Db 61 NRRRPWCYVQVGLKPLVQECMVHDCADRLPRGP 94
```

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RESULT 38
US-10-233-675A-21
; Sequence 21, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/233,675A
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein human abrogen
US-10-233-675A-21

Query Match 60.3%; Score 505; DB 15; Length 322;
Best Local Similarity 92.6%; Pred. No. 1.4e-42;
Matches 87; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPD 106
DB 1 AKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPD 60

QY 107 NRRPWCYVQGLKPLVQECMVHDCADGKPSPP 140
DB 61 NRRPWCYVQGLKPLVQECMVHDCADRLPRGP 94

RESULT 39
US-10-424-999-37
; Sequence 37, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Abrogen D43
US-10-424-999-37

Query Match 59.9%; Score 501; DB 12; Length 91;
Best Local Similarity 92.6%; Pred. No. 9.2e-43;
Matches 88; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 39 GQCEIDKSKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGK 98
DB 1 GSH-----MAKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGK 56

QY 99 HNYCRNPDNRRPWCYVQVGLKPLVQECMVHDCAD 133
DB 1 AKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPD 106
```

```
Db 57 HNYCRNPDNRRPWCYVQVGLKPLVQECMVHDCAD 91

RESULT 40
US-10-424-999-36
; Sequence 36, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TrxA-Abrogen D43 fusion protein
US-10-424-999-36

Query Match 59.9%; Score 501; DB 12; Length 221;
Best Local Similarity 92.6%; Pred. No. 2.4e-42;
Matches 88; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 39 GQCEIDKSKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGK 98
DB 131 GSH-----MAKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGK 186

QY 99 HNYCRNPDNRRPWCYVQVGLKPLVQECMVHDCAD 133
DB 187 HNYCRNPDNRRPWCYVQVGLKPLVQECMVHDCAD 221

RESULT 41
US-10-424-999-17
; Sequence 17, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein human abrogen
US-10-424-999-17

Query Match 59.9%; Score 501; DB 12; Length 687;
Best Local Similarity 97.9%; Pred. No. 8.2e-42;
Matches 86; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPD 106
DB 1 AKTCYEGNGHFGYRGKASTDTMGRCPLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPD 60
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QY 107 NRRPWCYVQVGLKPLVQECWVHDCADG 134
Db 61 NRRPWCYVQVGLKPLVQECWVHDCADG 88

RESULT 42
US-10-425-000-37
; Sequence 37, Application US/10425000
; Publication No. US20040052777A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blancher, Francis
; TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
; FILE REFERENCE: ST01027-B
; CURRENT APPLICATION NUMBER: US/10/425,000
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human derived fusion protein
US-10-425-000-37

Query Match 59.9%; Score 501; DB 12; Length 687;
Best Local Similarity 97.7%; Pred. No. 8.2e-42;
Matches 86; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKKNYCRNPD 106
Db 1 AKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKKNYCRNPD 60

QY 107 NRRPWCYVQVGLKPLVQECWVHDCADG 134
Db 61 NRRPWCYVQVGLKPLVQECWVHDCADG 88

RESULT 43
US-10-233-675A-17
; Sequence 17, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027
; CURRENT APPLICATION NUMBER: US/10/233,675A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein human abrogen
US-10-233-675A-17

Query Match 59.9%; Score 501; DB 15; Length 687;
Best Local Similarity 97.7%; Pred. No. 8.2e-42;
Matches 86; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKKNYCRNPD 106
Db 1 AKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKKNYCRNPD 60

QY 107 NRRPWCYVQVGLKPLVQECWVHDCADG 134
Db 61 NRRPWCYVQVGLKPLVQECWVHDCADG 88

RESULT 44
US-10-424-999-9
; Sequence 9, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blancher, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human abrogen as secreted from pMB063 (abrogen D43)
US-10-424-999-9

Query Match 59.7%; Score 500; DB 12; Length 87;
Best Local Similarity 98.9%; Pred. No. 1.1e-42;
Matches 86; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKKNYCRNPD 106
Db 1 AKTCYEGNGHFYRGKASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKKNYCRNPD 60

QY 107 NRRPWCYVQVGLKPLVQECWVHDCAD 133
Db 61 NRRPWCYVQVGLKPLVQECWVHDCAD 87

RESULT 45
US-10-425-000-29
; Sequence 29, Application US/10425000
; Publication No. US20040052777A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blancher, Francis
; TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
; FILE REFERENCE: ST01027-B
; CURRENT APPLICATION NUMBER: US/10/425,000
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human abrogen (D43)
US-10-425-000-29

Query Match 59.7%; Score 500; DB 12; Length 87;

Best Local Similarity 98.3%; Pred. No. 1.1e-42;
Matches 86; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	47	SKTCYEGNGHFYRGKASTDTMG	PCLPWSATVLQQT	YHAHRS	DALQLGLGK	NYCRNP	105
	:	:	:	:	:	:	
Db	1	AKTCYEGNGHFYRGKASTDTMG	PCLPWSATVLQQT	YHAHRS	DALQLGLGK	NYCRNP	60

QY 107 NRRPWCYVQGLKPLVQECMVHDCAD 133

DD 81. NARRPNCIVQVGLKFLVQECMVHDCAD 87

RESULT 46
US-10-233-675A-9
; Sequence 9, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Them to Inhibit Angiogenesis

```

, , CURRENT APPLICATION NUMBER: US/10/233,675A
, , CURRENT FILING DATE: 2002-09-04
, , PRIOR APPLICATION NUMBER: 60/316,300
, , PRIOR FILING DATE: 2001-09-04
, , NUMBER OF SEQ ID NOS: 27
, , SOFTWARE: PatentIn version 3.1
, , SEQ ID NO 9:
, , LENGTH: 87
, , TYPE: PRT
, , ORGANISM: Artificial Sequence
, , FEATURE:
, , OTHER INFORMATION: human derived fusion protein

```

Query Match	59.7%	Score 500;	DB 15;	Length 87;
Best Local Similarity	98.9%	Pred. No. 1.1e-42;		
Matches 86;	Conservative	1;	Mismatches 0;	Indels 0;
			Gaps	0;

QY 47 SKTCYEGNGHFVRGKASTDTMGPRCLPNNSATVLTQTYHAHRSDALQLGLGKINYCRNPD 105
:
Db 1 AKTCYEGNGHFVRGKASTDTMGPRCLPNNSATVLTQTYHAHRSDALQLGLGKINYCRNPD 60

QY 107 NRRRPNCTVOVGLKPLVQECNVHDCAD 133

LD 61 NRRRPFWCYVVGGLKFLVQECMVHDCAD 87

RESULT 47
US-10-424-999-5
; Sequence 5, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Using Them to Inhibit Angiogenesis

```

: : CURRENT APPLICATION NUMBER: US/10/424,999
: :
: : CURRENT FILING DATE: 2003-04-29
: : PRIOR APPLICATION NUMBER: 10/233,675
: : PRIOR FILING DATE: 2002-09-04
: : NUMBER OF SEQ ID NOS: 70
: : SOFTWARE: PatentIn version 3.2
: : SEQ ID NO 5
: : LENGTH: 86
: : TYPE: PRT
: : ORGANISM: Artificial Sequence
: : FEATURE:
: : OTHER INFORMATION: Human abroten

```

US-10-424-999-5

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Query Match      59.6%; Score 499; DB 12; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	48	KTCYEGNGHFYRGKASTDTWGRPCLPWNSATVLQOTYHAHRSDAIQGLGKHNYCRNPDN	107
<hr/>			
Db	1	KTCYEGNGHFYRGKASTDTWGRPCLPWNSATVLQOTYHAHRSDAIQGLGKHNYCRNPDN	60

QY 108 RRPWCYVQGLXPLVOECMVHDCAD 133
| | | | | | | | | | | | | |
Db 61 RRPWCYVQGLXPLVOECMVHDCAD 86

```

RESULT 48
US-10-424-999-62
; Sequence 62, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Branche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Using Them to Inhibit Angiogenesis

```

```

? ? PRIORITY: 09-10-27-86
? ? CURRENT APPLICATION NUMBER: US/10/424,999
? ? CURRENT FILING DATE: 2003-04-29
? ? PRIOR APPLICATION NUMBER: 10/233,675
? ? PRIOR FILING DATE: 2002-09-04
? ? NUMBER OF SEQ ID NOS: 70
? ? SOFTWARE: PatentIn version 3.2
? ? SEQ ID NO 62
? ? LENGTH: 86
? ? TYPE: prt
? ? ORGANISM: Artificial Sequence
? ? FEATURE:
? ? OTHER INFORMATION: Human kringle domain ATF-Kringle (Abrogen)
US-10-424-999-62

```

```
Query Match          59.6%; Score 499; DB 12; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 48 KTCYEGNCHFYRCKASTDTMGRPCLPWNSATVLTQTYHAHRS DALQLGLGKHNYCRNPDN 107
|||||
Dp 1 KTCYEGNGHFYRCKASTDTMGRPCLPWNSATVLTQTYHAHRS DALQLGLGKHNYCRNPDN 60
|||||

Qy 108 RRRPWCYVQVGLKPLVQECMWHDCAD 133
|||||
Dk 61 RRRPWCYVQVGLKPLVQECMWHDCAD 85
|||||

```

RESULT 49
US-10-425-000-97
; Sequence 97, Application US/10425000
; Publication No. US20040052777A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
; TITLE OF INVENTION: Angiogenesis
; FILE REFERENCE: ST01027B
; CURRENT APPLICATION NUMBER: US/10/425,000
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 86
; TYPE: PRT

```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human kringle domain ATP-Kringle (Abrogen)
US-10-425-000-97

Query Match          59.6%; Score 499; DB 12; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPDN 107
Db 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPDN 60

QY 108 RRRPWCYVQVGLKPLVQECMWHDCAD 133
Db 61 RRRPWCYVQVGLKPLVQECMWHDCAD 86

RESULT 50
US-10-233-675A-5
; Sequence 5, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Them To Inhibit Angiogenesis
; FILE REFERENCE: ST01027
; CURRENT APPLICATION NUMBER: US/10/233,675A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5:
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human derived abrogen
US-10-233-675A-5

Query Match          59.6%; Score 499; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.4e-42;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPDN 107
Db 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKHNCRNPDN 60

QY 108 RRRPWCYVQVGLKPLVQECMWHDCAD 133
Db 61 RRRPWCYVQVGLKPLVQECMWHDCAD 86

Search completed: May 25, 2004, 15:03:48
Job time : 27.0684 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2004, 14:48:05 ; Search time 9.90096 Seconds
(without alignments)
745.636 Million cell updates/sec

Title: US-09-880-503-8

Perfect score: 837

Sequence: 1 SNEIHQVPSNCDLNGTGV.....QECMVHDCADGKPSPEE 143

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	837	100.0	200	4 US-09-101-272G-73
2	837	100.0	208	4 US-09-101-272G-98
3	837	100.0	411	1 US-08-087-163-1
4	837	100.0	411	1 US-08-286-748B-18
5	837	100.0	411	1 US-08-153-799-18
6	837	100.0	411	4 US-09-403-736-2
7	837	100.0	430	1 US-07-942-157A-3
8	837	100.0	431	4 US-09-101-272G-1
9	837	100.0	431	6 5188829-1
10	827	98.8	411	3 US-09-181-816-1
11	826	98.7	411	2 US-08-560-098A-48
12	821.5	98.1	430	6 5219569-2
13	813	97.1	157	3 US-08-142-590B-25
14	793	94.7	138	2 US-08-797-689-12
15	793	94.7	138	4 US-09-984-186-12
16	788	94.1	194	4 US-09-101-272G-80
17	788	94.1	201	4 US-09-101-272G-96
18	559	66.8	432	2 US-08-560-098A-47
19	558	65.7	365	1 US-08-093-741-83
20	558	65.7	365	1 US-08-720-012-83
21	558	66.7	393	2 US-08-560-098A-44
22	558	66.7	393	3 US-08-967-024C-24
23	558	66.7	393	3 US-08-967-024C-25
24	513	61.3	89	4 US-09-101-272G-62
25	335.5	40.1	477	2 US-08-560-098A-51
26	328.5	39.2	527	1 US-07-609-510B-16
27	328.5	39.2	527	2 US-08-811-949-39

28	328.5	39.2	527	5	PCT-US91-01025A-2	Sequence 2, Appl
29	328.5	39.2	527	6	5185259-8	Patent No. 5185259
30	328.5	39.2	527	6	5520913-1	Patent No. 5520913
31	328.5	39.2	546	6	5200340-6	Patent No. 5200340
32	328.5	39.2	562	2	US-08-811-949-43	Sequence 43, Appl
33	328.5	39.2	562	2	US-08-560-098A-50	Sequence 50, Appl
34	328.5	39.2	562	2	US-08-883-795A-38	Sequence 38, Appl
35	328.5	39.2	562	4	US-09-703-695A-4	Sequence 4, Appl
36	328.5	39.2	562	6	5185259-3	Patent No. 5185259
37	328.5	39.2	562	6	5200340-2	Patent No. 5200340
38	328.5	39.2	562	6	5344773-2	Patent No. 5344773
39	321.5	38.4	562	6	5244676-5	Sequence 15, Appl
40	300	35.8	233	3	US-08-438-745-15	Sequence 17, Appl
41	300	35.8	233	3	US-08-438-745-17	Sequence 15, Appl
42	300	35.8	233	3	US-09-219-019-15	Sequence 17, Appl
43	300	35.8	233	3	US-09-219-019-17	Sequence 15, Appl
44	300	35.8	233	5	PCT-US94-05669A-15	Sequence 17, Appl
45	300	35.8	233	5	PCT-US94-05669A-17	Sequence 15, Appl
46	300	35.8	235	3	US-08-438-745-13	Sequence 13, Appl
47	300	35.8	235	3	US-09-219-019-13	Sequence 13, Appl
48	300	35.8	235	5	PCT-US94-05669A-13	Sequence 13, Appl
49	293	35.0	49	4	US-08-747-915-5	Sequence 5, Appl
50	293	35.0	49	4	US-09-285-783-5	Sequence 5, Appl
51	288	34.4	48	3	US-09-219-019-22	Sequence 22, Appl
52	268	32.0	44	2	US-08-747-915-1	Sequence 1, Appl
53	268	32.0	44	4	US-09-285-783-1	Sequence 1, Appl
54	262	31.3	655	1	US-08-148-910-12	Sequence 12, Appl
55	262	31.3	655	1	US-08-448-937A-12	Sequence 12, Appl
56	230.5	27.5	437	2	US-08-811-949-49	Sequence 49, Appl
57	230.5	27.5	437	2	US-08-811-949-51	Sequence 51, Appl
58	230.5	27.5	437	2	US-08-811-949-55	Sequence 55, Appl
59	230.5	27.5	437	2	US-08-811-949-57	Sequence 57, Appl
60	230.5	27.5	472	2	US-08-811-949-63	Sequence 63, Appl
61	224.5	26.8	356	1	US-08-427-640-8	Sequence 8, Appl
62	224	26.8	326	4	US-09-411-977-3	Sequence 3, Appl
63	220.5	26.3	378	4	US-09-553-498-10	Sequence 10, Appl
64	220.5	26.3	378	4	US-09-618-869-10	Sequence 10, Appl
65	219.5	26.2	389	2	US-08-811-949-67	Sequence 67, Appl
66	218.5	26.1	355	1	US-08-137-116-1	Sequence 1, Appl
67	218.5	26.1	355	1	US-08-217-618-1	Sequence 2, Appl
68	218.5	26.1	355	1	US-08-427-640-2	Sequence 2, Appl
69	218.5	26.1	355	1	US-08-217-617A-1	Sequence 1, Appl
70	218.5	26.1	355	1	US-08-217-616-1	Sequence 1, Appl
71	218.5	26.1	355	2	US-08-811-949-45	Sequence 45, Appl
72	218.5	26.1	355	2	US-08-811-949-47	Sequence 47, Appl
73	218.5	26.1	355	2	US-08-811-949-53	Sequence 53, Appl
74	218.5	26.1	355	3	US-08-794-528-1	Sequence 1, Appl
75	218.5	26.1	355	6	5223256-1	Patent No. 5223256

ALIGNMENTS

RESULT 1
US-09-101-272G-73
; Sequence 73, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent version 3.1
; SEQ ID NO 73
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

OTHER INFORMATION: ATF domain of uPA
US-09-101-272G-73

Query Match 100.0%; Score 837; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 6.1e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 60
DB 21 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 141 PLVQECMVHDCADGKKPSPPEE 163

RESULT 2
US-09-101-272G-98
Sequence 98, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patent version 3.1
SEQ ID NO 98
LENGTH: 208
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ATFI-ML chimeric protein
US-09-101-272G-98

Query Match 100.0%; Score 837; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.4e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 60
DB 2 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 61
QY 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
DB 62 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 121
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 122 PLVQECMVHDCADGKKPSPPEE 144

RESULT 3
US-08-087-163-1
Sequence 1, Application US/08087163
Patent No. 5472692
GENERAL INFORMATION:
APPLICANT: Liu, Jian-Ning
TITLE OF INVENTION: PRO-UKINASE MUTANTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts

OTHER INFORMATION: ATF domain of uPA
US-09-101-272G-73

Query Match 100.0%; Score 837; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 6.1e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 60
DB 21 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
DB 81 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 141 PLVQECMVHDCADGKKPSPPEE 163

RESULT 2
US-09-101-272G-98
Sequence 98, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101,272G
CURRENT FILING DATE: 1998-07-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patent version 3.1
SEQ ID NO 98
LENGTH: 208
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ATFI-ML chimeric protein
US-09-101-272G-98

Query Match 100.0%; Score 837; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 6.4e-76;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 60
DB 2 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 61
QY 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
DB 62 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 121
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 122 PLVQECMVHDCADGKKPSPPEE 144

RESULT 3
US-08-087-163-1
Sequence 1, Application US/08087163
Patent No. 5472692
GENERAL INFORMATION:
APPLICANT: Liu, Jian-Ning
TITLE OF INVENTION: PRO-UKINASE MUTANTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts

COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04353/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-087-163-1

Query Match 100.0%; Score 837; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 60
DB 1 SNELHVPSCDCLNGTGVSNKYFNSNIHWCNPKKFGGQHCHEIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
DB 61 KASTDTMGRPCLPWNSATVLTQYTHAHRSDALQLGLGKKNYCRNPNRRRPPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGKKPSPPEE 143
DB 121 PLVQECMVHDCADGKKPSPPEE 143

RESULT 4
US-08-286-748B-18
Sequence 18, Application US/08286748B
Patent No. 5755542
GENERAL INFORMATION:
APPLICANT: Victor Gurewlich
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
OF DRUGS BY PLATELETS FOR THE TREATMENT OF
CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,748B
FILING DATE: August 5, 1994
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/013001
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-286-748B-18

Query Match 100.0%; Score 837; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
DB 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOOTYHAHRSALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
DB 61 KASTDTMGRPCLPWNSATVLOOTYHAHRSALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGKPKSPPEE 143
DB 121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 5
US-08-153-799-18
Sequence 18, Application US/08153799
Patent No. 5766883
GENERAL INFORMATION:
APPLICANT: Ballance, David J
APPLICANT: Goodey, Andrew R
TITLE OF INVENTION: Polypeptides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: R Hain Swope, BOC Health Care Inc
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,799
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847975
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8909916.2
FILING DATE: 29-APR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB90/00650
FILING DATE: 26-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/775952
FILING DATE: 29-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Swope, R Hain
REGISTRATION NUMBER: 24864
REFERENCE/DOCKET NUMBER: 92H832
TELEPHONE: (908) 665 2400
TELEFAX: (908) 771 6159
TELEX: 219484
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 411 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-799-18

Query Match 100.0%; Score 837; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
DB 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOOTYHAHRSALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
DB 61 KASTDTMGRPCLPWNSATVLOOTYHAHRSALQLGLGKHNYCRNPNRRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGKPKSPPEE 143
DB 121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 6
US-09-403-736-2
Sequence 2, Application US/09403736
Patent No. 6638502
GENERAL INFORMATION:
APPLICANT: Aventis S.A.
APPLICANT: LI, Hong
APPLICANT: LU, He
APPLICANT: GRISCELLI, Frank
APPLICANT: OPOLO, Paule
APPLICANT: SORIA, Claudine
APPLICANT: RAGOT, Thierry
APPLICANT: LEGRAND, Yves
APPLICANT: SORIA, Jeanette
APPLICANT: MABILAT, Christelle
APPLICANT: PERRICAUD, Michel
APPLICANT: YEH, Patrice
TITLE OF INVENTION: Adenovirus-Mediated Intratumoral Delivery Of An Angiogenesis Ant
FILE REFERENCE: A2778A-US
CURRENT APPLICATION NUMBER: US/09/403,736
CURRENT FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/EP98/02491
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 60/044,980
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: humanurokinase
US-09-403-736-2

Query Match 100.0%; Score 837; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 1.4e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHFYRG 60

Db 1 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNPKKFGQHCEIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKNCYCRNPNRRPWCYVQVGLK 120
Db 61 KASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKNCYCRNPNRRPWCYVQVGLK 120
QY 121 PLVQECMVHDCADGKPKSPPEE 143
Db 121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 7
US-07-942-157A-3
; Sequence 3, Application US/07942157A
; Patent No. 5648253
; GENERAL INFORMATION:
; APPLICANT: Wei, Cha-Mer
; TITLE OF INVENTION: Inhibitor-Resistant Urokinase
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kilpatrick & Cody
; STREET: 1100 Peachtree Street Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/942,157A
; FILING DATE: 19920908
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/631673
; FILING DATE: 20-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET INFORMATION: TS1108Cont.
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)815-6508
; TELEFAX: (404)815-6555
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..19
; OTHER INFORMATION: /label= peptide
; OTHER INFORMATION: /note= "MAP signal"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 198..203
; OTHER INFORMATION: /label= modified
; OTHER INFORMATION: /note= "six amino acids deleted in mutant"
US-07-942-157A-3

Query Match 100.0%; Score 837; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNPKKFGQHCEIDKSKTCYEGNGHFYRG 60
Db 20 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNPKKFGQHCEIDKSKTCYEGNGHFYRG 79
QY 61 KASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKNCYCRNPNRRPWCYVQVGLK 120

Db 80 KASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKNCYCRNPNRRPWCYVQVGLK 139
QY 121 PLVQECMVHDCADGKPKSPPEE 143
Db 140 PLVQECMVHDCADGKPKSPPEE 162

RESULT 8
US-09-101-272G-1
; Sequence 1, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (21)..()
; OTHER INFORMATION:
; NAME/KEY: misc_feature
; LOCATION: (20)..()
; OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)
US-09-101-272G-1

Query Match 100.0%; Score 837; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNPKKFGQHCEIDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNPKKFGQHCEIDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKNCYCRNPNRRPWCYVQVGLK 120
Db 81 KASTDTMGRPCLPWSATVLOQTYHAHRSDALQGLGKNCYCRNPNRRPWCYVQVGLK 140
QY 121 PLVQECMVHDCADGKPKSPPEE 143
Db 141 PLVQECMVHDCADGKPKSPPEE 163

RESULT 9
5188829-1
; Patent No. 5188829
; APPLICANT: KOBAYASHI, YO-ICHI; OMORI, MUNEXI; YAMADA, CHIKAKO
; TITLE OF INVENTION: RAPIDLY ACTING PROUROKINASE
; NUMBER OF SEQUENCES: 23
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/340,007
; FILING DATE: 18-AUG-1988
; SEQ ID NO:1:
; LENGTH: 431
5188829-1

Query Match 100.0%; Score 837; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.5e-75;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNPKKFGQHCEIDKSKTCYEGNGHFYRG 60
Db 21 SNELHQPNSCDCLNGTGVSNKYFNSNIHWCNPKKFGQHCEIDKSKTCYEGNGHFYRG 80

QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 120
Db 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 140
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 163

RESULT 10

US-09-181-816-1
; Sequence 1, Application US/09181816
; Patent No. 6277818
; GENERAL INFORMATION:
; APPLICANT: NAZAR, Andrew P.
; APPLICANT: JONES, Terence R.
; TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
; TITLE OF INVENTION: PLASMINOGEN ACTIVATOR RECEPTOR
; FILE REFERENCE: 329042000300 SIDN 1-7
; CURRENT APPLICATION NUMBER: US/09/181,816
; CURRENT FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 411
; TYPE: PRI
; ORGANISM: Homo sapiens
US-09-181-816-1

Query Match 98.8%; Score 827; DB 3; Length 411;
Best Local Similarity 99.3%; Pred. No. 1.4e-74;
Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
Db 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 120
Db 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 120
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 121 PLVQECMVHDCADGKKPSSPPEE 143

RESULT 11

US-08-560-098A-48
; Sequence 48, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WNEBTD, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560.098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-560-098A-48

Query Match 98.7%; Score 826; DB 2; Length 411;
Best Local Similarity 99.3%; Pred. No. 1.7e-74;
Matches 142; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
Db 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 120
Db 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 120
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 121 PLVQECMVHDCADGKKPSSPPEE 143

RESULT 12

5219569-2
; Patent No. 5219569
; APPLICANT: BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
; GORDON A.
; TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/766,858
; FILING DATE: 16-AUG-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 725,468
; FILING DATE: 22-APR-1985
; SEQ ID NO: 2
; LENGTH: 430
5219569-2

Query Match 98.1%; Score 821.5; DB 6; Length 430;
Best Local Similarity 99.3%; Pred. No. 5.1e-74;
Matches 142; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 60
Db 21 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWCNCPKFGQGHCEIDKSKTCYEGNGHFYRG 80
QY 61 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 120
Db 81 KASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNYCRNPNRRRPPWCVQVGLK 140
QY 121 PLVQECMVHDCADGKKPSSPPEE 143
Db 141 PLVQECMVHDCADGKKPSSPPEE 162

RESULT 13

US-08-142-590B-25
; Sequence 25, Application US/08142590B
; Patent No. 6120765

GENERAL INFORMATION:
APPLICANT: HIBINO, Toshihiko; TAKAHASHI, Tadabito; HORII, Izumi; and GOETINCK,
TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/142,590B
FILING DATE: 25-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,318
FILING DATE: 02-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Paul L.
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: MGP-009CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-142-590B-25

Query Match 97.1%; Score 813; DB 3; Length 157;
Best Local Similarity 97.2%; Pred. No. 1.1e-73;
Matches 139; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIDKSKTCYEGNGHFYRG 60
DB 1 SNELHQVPSNCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIDKSKTCYEGNGHFYRG 60
QY 61 KASTDTMGSPCLPWSATVLOQTYHAHRSALQLGLGKHNYCRNPDNRRPWCYQVGLK 120
DB 61 KASTDTMGSPCLPWSATVLOQTYHAHRSALQLGLGKHNYCRNPDNRRPWCYQVGLK 120
QY 121 PLVQECMVHDCADGKPKSPPEE 143
DB 121 PLVQECMVHDCADGKPKSPPEE 143

RESULT 14
US-08-797-689-12
Sequence 12, Application US/08797689
Patent No. 5876969
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville

GENERAL INFORMATION:
APPLICANT: HIBINO, Toshihiko; TAKAHASHI, Tadabito; HORII, Izumi; and GOETINCK,
TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-797-689-12

Query Match 94.7%; Score 793; DB 2; Length 138;
Best Local Similarity 100.0%; Pred. No. 9.7e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQVPSNCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIDKSKTCYEGNGHFYRG 60
DB 4 SNELHQVPSNCCLNGGTCVSNKYFSNIHWCNCPKFKGGQHCIDKSKTCYEGNGHFYRG 63
QY 61 KASTDTMGSPCLPWSATVLOQTYHAHRSALQLGLGKHNYCRNPDNRRPWCYQVGLK 120
DB 64 KASTDTMGSPCLPWSATVLOQTYHAHRSALQLGLGKHNYCRNPDNRRPWCYQVGLK 123
QY 121 PLVQECMVHDCADGK 135
DB 124 PLVQECMVHDCADGK 138

RESULT 15
US-09-984-186-12
Sequence 12, Application US/09984186
Patent No. 6686179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/984,186
  FILING DATE: 29-Oct-2001
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US/08/797,689
  FILING DATE: 31-JAN-1997
  APPLICATION NUMBER: US 08/256,927
  FILING DATE: 28-JUL-1994
  APPLICATION NUMBER: FR 92/01064
  FILING DATE: 31-JAN-1992
  APPLICATION NUMBER: PCT/FR93/00085
  FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
  NAME: Smith Ph.D., Julie K.
  REGISTRATION NUMBER: P-38,619
  REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (610) 454-3839
  TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 138 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
  SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-984-186-12

Query Match          94.7%; Score 793; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 9.7e-72;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHIFYRG 60
Db 4 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHIFYRG 63
QY 61 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
Db 64 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 123
QY 121 PLVQECMVHDCADGK 135
Db 124 PLVQECMVHDCADGK 138

RESULT 16
US-09-101-272G-80
; Sequence 80, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101.272G
; PRIOR FILING DATE: 1998-07-08
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ATFHI chimeric protein
US-09-101-272G-80

Query Match          94.1%; Score 788; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHIFYRG 60
Db 2 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHIFYRG 61
QY 61 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
Db 62 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 121
QY 121 PLVQECMVHDCADG 134
Db 122 PLVQECMVHDCADG 135

RESULT 17
US-09-101-272G-96
; Sequence 96, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101.272G
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ATFHI-CL chimeric protein
US-09-101-272G-96

Query Match          94.1%; Score 788; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 4.7e-71;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHIFYRG 60
Db 2 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGQHCIEDKSKTCYEGNGHIFYRG 61
QY 61 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 120
Db 62 KASTDTMGRPCLPWN SATVLQOTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVGLK 121
QY 121 PLVQECMVHDCADG 134
Db 122 PLVQECMVHDCADG 135

RESULT 18
US-08-560-098A-47
; Sequence 47, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WNEEDT, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEPPENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
```

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/
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/560,098A
/ FILING DATE: 17-NOV-1995
/ PRIORITY APPLICATION DATA:
/ PRIORITY APPLICATION NUMBER: P 44 40 892.7
/ FILING DATE: 17-NOV-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: EVANS, Joseph D.
/ REGISTRATION NUMBER: 26,269
/ REFERENCE/DOCKET NUMBER: 148/42448
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 628-8800
/ TELEFAX: (202) 628-8844
/ INFORMATION FOR SEQ ID NO: 47:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 432 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-560-098A-47

Query Match          56.7%; Score 559; DB 2; Length 432;
Best Local Similarity 77.1%; Pred. No. 7.5e-48;
Matches 101; Conservative 8; Mismatches 16; Indels 6; Gaps 1;

QY 13 CLNGGTCVSNKVFNSIHWNCPCFKFGQHCEDKSKTCYEGNGHYRGKASTDTMGPRCL 72
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 40 CVTGECPKPSHNNGDPEIEEY-----LQISKTCYEGNGHYRGKASTDTMGPRCL 93

QY 73 PWSATVLOQTHAHRSDALQGLGKHNYCRNPNRRPWCYVQVGLKPLVQECMVHDC 132
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 94 PWSATVLOQTHAHRSDALQGLGKHNYCRNPNRRPWCYVQVGLKPLVQECMVHDC 153

QY 133 DGKTPSSPPEE 143
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 154 DGKTPSSPPEE 164

RESULT 19
US-08-093-741-83
; Sequence 83, Application US/08093741
; Patent No. 5681721
; GENERAL INFORMATION:
; APPLICANT: STEFFENS, GERD J.
; APPLICANT: WENNDT, STEPHAN
; APPLICANT: SCHNEIDER, JOHANNES
; APPLICANT: HEINZEL-WIELAND, REGINA
; APPLICANT: SAUNDERS, DEREK J.
; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
; INHIBITING EFFECT
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N. W. Suite 700
; CITY: Washington, D.C.
; COUNTRY: U.S.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,741
; FILING DATE: 20-JUL-1993
; PRIORITY APPLICATION DATA:
; PRIORITY APPLICATION NUMBER: US 08/093,741
; FILING DATE: 20-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/41345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 83:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P43 23 754.1
FILING DATE: 15-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/41345
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-093-741-83

Query Match          66.7%; Score 558; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHYRGKASTDTMGPRCLPWSATVLOQTHAHRSDALQGLGKHNYCRNPD 106
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SKTCYEGNGHYRGKASTDTMGPRCLPWSATVLOQTHAHRSDALQGLGKHNYCRNPD 60

QY 107 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 NRRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97

RESULT 20
US-08-720-012-83
; Sequence 83, Application US/08720012
; Patent No. 5747291
; GENERAL INFORMATION:
; APPLICANT: STEFFENS, GERD J.
; APPLICANT: WENNDT, STEPHAN
; APPLICANT: SCHNEIDER, JOHANNES
; APPLICANT: HEINZEL-WIELAND, REGINA
; APPLICANT: SAUNDERS, DEREK J.
; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
; INHIBITING EFFECT
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N. W. Suite 700
; CITY: Washington, D.C.
; COUNTRY: U.S.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720,012
; FILING DATE: 27-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,741
; FILING DATE: 20-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/41345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 83:
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SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-720-012-83

Query Match 66.7%; Score 558; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 7.8e-48;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPD 106
1 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPD 60

Db

QY 107 NRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 143
61 NRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 97

Db

RESULT 21
US-08-560-098A-44
Sequence 44, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WNEEDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
TITLE OF INVENTION: Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560.098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-098A-44

Query Match 66.7%; Score 558; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.5e-48;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPD 106
2 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPD 61

Db

QY 107 NRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 143

QY

Db 62 NRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 98

RESULT 22
US-08-967-024C-24
Sequence 24, Application US/08967024C
Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: WNEEDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOSHA, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 665.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-024C-24

Query Match 66.7%; Score 558; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.5e-48;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPD 106
2 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPD 61

Db

QY 107 NRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 143
62 NRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 98

Db

RESULT 23
US-08-967-024C-25
Sequence 25, Application US/08967024C
Patent No. 6133011
GENERAL INFORMATION:
APPLICANT: WNEEDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOSHA, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
;; STREET: 1200 G Street, N.W., Suite 700
;; CITY: Washington
;; STATE: DC
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/967,024C
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: P 44 42 665.8
;; FILING DATE: 30-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D.
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 148/42444
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 25:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 393 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-967-024C-25

Query Match 66.7%; Score 558; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 8.5e-48;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPD 106
DB 2 SKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPD 61

QY 107 NRRRPWCYQVGLKPLVQECMVHDCADGKKPSPPEE 143
DB 62 NRRRPWCYQVGLKPLVQECMVHDCADGKKPSPPEE 98

RESULT 24
US-09-101-272G-62
; Sequence 62, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 62
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
; US-09-101-272G-62

Query Match 61.3%; Score 513; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 4.8e-44;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRN 102
DB 1 EIDKSKTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRN 60

QY 103 RNPENRRPWCYQVGLKPLVQECMVHDC 131
DB 61 RNPENRRPWCYQVGLKPLVQECMVHDC 89

RESULT 25
US-08-560-098A-51
; Sequence 51, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WENDT, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-560-098A-51

Query Match 40.1%; Score 335.5; DB 2; Length 477;
Best Local Similarity 46.3%; Pred. No. 1.6e-25;
Matches 62; Conservative 17; Mismatches 50; Indels 5; Gaps 2;

QY 3 ELHOVP-----SNCDLNGGTCVENKVFNSIHWNCNCPKFGQHCIEDKSKTCYEGNGHFY 58
DB 78 QCHTVPVKSCSELRCFNGTCWQASFSDF-VQCCKPGYTKQCEVDTHATCYKDQGVY 136

QY 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPDNRRPWCYQV 118
DB 137 RGTWSTESGAQCINMNSNLTRTNGRRSDAITLQGNHNYCRPNDRNNSKWCYVKA 196

QY 119 LKPLVQECMVHDC 132
DB 197 SKFILEFCSPVCS 210

RESULT 26


```
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US91-01025A-2

Query Match          39.2%; Score 328.5; DB 5; Length 527;
Best Local Similarity 46.3%; Pred. No. 8.9e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

Qy 3 ELHQP-SNCD---CLNGGTCVSNKYFNSNIHWCNPKKFGGQHCCEIDKSKTCYEGNGHGY 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 42 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPEGFAGKCCCEIDTRATCYEDQGISY 100
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 101 RGTWSTAESGAECTNWNSSALAQPYSGRRPDALRLGLGNHNYCRNPDNRDRSKPWCYVFXA 160
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 119 LKPLVQECMVHDCADG 134
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 161 GKYSEFCSTPACSEG 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 29
5185259-8
; Patent No. 5185259
; APPLICANT: GOEDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
; VEHAR, GORDON A.
; TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
; ACTIVATOR
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/489,855
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 12,694
; FILING DATE: 09-FEB-1987
; APPLICATION NUMBER: 483,052
; FILING DATE: 07-APR-1983
; APPLICATION NUMBER: 398,003
; FILING DATE: 14-JUL-1982
; APPLICATION NUMBER: 374,860
; FILING DATE: 05-MAY-1982
; SEQ ID NO: 8:
; LENGTH: 527
5185259-8

Query Match          39.2%; Score 328.5; DB 6; Length 527;
Best Local Similarity 46.3%; Pred. No. 8.9e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

Qy 3 ELHQP-SNCD---CLNGGTCVSNKYFNSNIHWCNPKKFGGQHCCEIDKSKTCYEGNGHGY 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 42 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPEGFAGKCCCEIDTRATCYEDQGISY 100
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 101 RGTWSTAESGAECTNWNSSALAQPYSGRRPDALRLGLGNHNYCRNPDNRDRSKPWCYVFXA 160
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 119 LKPLVQECMVHDCADG 134
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 161 GKYSEFCSTPACSEG 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 30
5520913-1
; Patent No. 5520913
; APPLICANT: ANDERSON, STEPHEN; BENNETT, WILLIAM F.; BORSTEIN,
; DAVID; HIGGINS, DEBORAH L.; PAONI, NICHOLAS F.; ZOLLER, MARK J.
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR HAVING
; ZYMOGENIC PROPERTIES
; NUMBER OF SEQUENCES: 35
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/88,451
; FILING DATE: 06-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 770,510
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: 384,608
; FILING DATE: 24-JUL-1989
; APPLICATION NUMBER: 240,856
; FILING DATE: 02-SEP-1986
; SEQ ID NO: 1:
; LENGTH: 527
5520913-1

Query Match          39.2%; Score 328.5; DB 6; Length 527;
Best Local Similarity 46.3%; Pred. No. 8.9e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

Qy 3 ELHQP-SNCD---CLNGGTCVSNKYFNSNIHWCNPKKFGGQHCCEIDKSKTCYEGNGHGY 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 42 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPEGFAGKCCCEIDTRATCYEDQGISY 100
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 101 RGTWSTAESGAECTNWNSSALAQPYSGRRPDALRLGLGNHNYCRNPDNRDRSKPWCYVFXA 160
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 119 LKPLVQECMVHDCADG 134
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 161 GKYSEFCSTPACSEG 176
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 31
5200340-6
; Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
; ACTIVATORS
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/53,412
; FILING DATE: 22-MAY-1987
; SEQ ID NO: 6:
; LENGTH: 546
5200340-6

Query Match          39.2%; Score 328.5; DB 6; Length 546;
Best Local Similarity 46.3%; Pred. No. 9.2e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

Qy 3 ELHQP-SNCD---CLNGGTCVSNKYFNSNIHWCNPKKFGGQHCCEIDKSKTCYEGNGHGY 58
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 77 QCHSVPVKSCSEPCFNGGTCQALYFSDP-VQCPEGFAGKCCCEIDTRATCYEDQGISY 135
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 59 RGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVG 118
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 136 RGTWSTAESGAECTNWNSSALAQPYSGRRPDALRLGLGNHNYCRNPDNRDRSKPWCYVFXA 195
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 119 LKPLVQECMVHDCADG 134
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 196 GKYSEFCSTPACSEG 211
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 32
US-08-811-949-43
; Sequence 43, Application US/08811949
; Patent No 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
```

APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949

FILING DATE: 05-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 18-966-0

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 562 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-811-949-43

Query Match 39.2%; Score 328.5; DB 2; Length 562;
Best Local Similarity 46.3%; Pred. No. 9.5e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

QY 3 ELHOVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFY 58

Db 77 QCHSVPVKSCSEPRCFNGGTCQALYFSDP-VQCPEGFAGKCEIDTRATCYEQGISY 135

QY 59 RGKASTDTMGRCLPWN SATVLQOYTHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVG 118

Db 136 RGTWSTAESGAECTNWNSSALAKPYSGRRPDALRLGLGNHNYCRNPNDRDSKPCWYVKA 195

QY 119 LKPLVQECMVHDCADG 134

Db 196 GKYSSEFCSTPACSEG 211

RESULT 33
US-08-560-098A-50
Sequence 50, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:

APPLICANT: WENDEL, Stephan

APPLICANT: HEINZEL-WIELAND, Regina

APPLICANT: STEFFENS, Gerd Josef

TITLE OF INVENTION: Proteins having Fibrinolytic and

Coagulation-inhibiting Properties

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Evenson, McKeown, Edwards & Lenahan

STREET: 1200 G Street, N.W., Suite 700

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/560,098A

FILING DATE: 17-NOV-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: P 44 40 892.7

FILING DATE: 17-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: EVANS, Joseph D.

REGISTRATION NUMBER: 26,269

REFERENCE/DOCKET NUMBER: 148/42448

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 628-8800

TELEFAX: (202) 628-8844

INFORMATION FOR SEQ ID NO: 50:

SEQUENCE CHARACTERISTICS:

LENGTH: 562 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-560-098A-50

Query Match 39.2%; Score 328.5; DB 2; Length 562;
Best Local Similarity 46.3%; Pred. No. 9.5e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

QY 3 ELHOVP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGQHCIDKSKTCYEGNGHFY 58

Db 77 QCHSVPVKSCSEPRCFNGGTCQALYFSDP-VQCPEGFAGKCEIDTRATCYEQGISY 135

QY 59 RGKASTDTMGRCLPWN SATVLQOYTHAHRSDALQLGLGKHNYCRNPNRRPWCYVQVG 118

Db 136 RGTWSTAESGAECTNWNSSALAKPYSGRRPDALRLGLGNHNYCRNPNDRDSKPCWYVKA 195

QY 119 LKPLVQECMVHDCADG 134

Db 196 GKYSSEFCSTPACSEG 211

RESULT 34
US-08-883-795A-38

Sequence 38, Application US/06883795A

Patent No. 5985607

GENERAL INFORMATION:

APPLICANT: Delcuve, Genevieve

APPLICANT: Awang, Gregor

TITLE OF INVENTION: Recombinant DNA Molecules and Expression

Vectors for Tissue Plasminogen Activator

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: BERESKIN & PARR

STREET: 40 King Street West

CITY: Toronto

STATE: Ontario

COUNTRY: Canada

ZIP: M5H 3Y2

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/883,795A

FILING DATE: 27-JUN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Gravelle, Micheline

REGISTRATION NUMBER: 40,261

REFERENCE/DOCKET NUMBER: 7841-062

TELECOMMUNICATION INFORMATION:

TELEPHONE: (416) 364-7311


```

/ TELEFAX: (416) 361-1398
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 562 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein (LPA)
/ US-08-883-795A-38
/
/ Query Match 39.2%; Score 328.5; DB 2; Length 562;
/ Best Local Similarity 46.3%; Pred. No. 9.5e-25;
/ Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;
/
QY 3 ELHQVP-SNCD--CLNGGTCVSNKYFNSNIHMCNCPKFGQGHCEIDKSKTCYEGNGHFY 58
Db 77 QCHSVFVKSCSEPRCFNGGTCQQALYFSDF-VCOCPGPGAGKCCETDTRATCYEDQGISY 135
QY 59 RGKASDTMTGRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPDNRERPWCYQVG 118
Db 136 RGWTSAESGAECTWNWSALAQKPYSGRRPDALRLGLGNHNYCRNPDNRDSDKPCYVFK 195
QY 119 LKPLVQECMVHDCADG 134
Db 196 GKYSEFCSTPACSEG 211
/
RESULT 35
US-09-703-695A-4
/ Sequence 4, Application US/09703695A
/ Patent No. 6593097
/ GENERAL INFORMATION:
/ APPLICANT: Xu, Yuan
/ TITLE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS
/ FILE REFERENCE: PI788RI
/ CURRENT APPLICATION NUMBER: US/09/703,695A
/ CURRENT FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: US 60/163,607
/ PRIOR FILING DATE: 1999-11-04
/ NUMBER OF SEQ ID NOS: 4
/ SEQ ID NO 4
/ LENGTH: 562
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-703-695A-4
/
/ Query Match 39.2%; Score 328.5; DB 4; Length 562;
/ Best Local Similarity 46.3%; Pred. No. 9.5e-25;
/ Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3
/
QY 3 ELHQVP-SNCD--CLNGGTCVSNKYFNSNIHMCNCPKFGQGHCEIDKSKTCYEGNGHFY 58
Db 77 QCHSVFVKSCSEPRCFNGGTCQQALYFSDF-VCOCPGPGAGKCCETDTRATCYEDQGISY 135
QY 59 RGKASDTMTGRCLPWN SATVLQOTYHAHRSDALQLGLGKHNYCRNPDNRERPWCYQVG 118
Db 136 RGWTSAESGAECTWNWSALAQKPYSGRRPDALRLGLGNHNYCRNPDNRDSDKPCYVFK 195
QY 119 LKPLVQECMVHDCADG 134
Db 196 GKYSEFCSTPACSEG 211
/
RESULT 36
US-09-703-695A-3
/ Patent No. 5185259
/ APPLICANT: GOEDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
/ VEHAR, GORDON A.
/ TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
/ ACTIVATOR
/ NUMBER OF SEQUENCES: 15
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/489,855

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; APPLICATION NUMBER: US/07/782,686
; FILING DATE: 01-OCT-1985
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 656,770
; FILING DATE: 01-OCT-1984
; SEQ ID NO:2:
; LENGTH: 562
; 5344773-2

Query Match      39.2%; Score 328.5; DB 6; Length 562;
Best Local Similarity 46.3%; Pred. No. 9.5e-25;
Matches 63; Conservative 14; Mismatches 54; Indels 5; Gaps 3;

QY 3 ELHQP-SNCD----CLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYF 58
DB 77 QCHSVPVKSCSEPCFNGGTCQQAIFYSDP-VQCPEGFAGKCEIDTATCYEDOGISY 135
QY 59 RGAASDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRRPWCYVQVG 118
DB 136 RGTWSTAESCAECTWNSSALAKPYSGRPDAIRLGLGNHNYCRPNDRDRSKFWCVFKA 195
QY 119 LKPLVQECMVHDCADG 134
DB 196 GKYSSSEFCSTPACSEG 211

RESULT 39
5244676-5
; Patent No. 5244676
; APPLICANT: BELL, LESLIE D.; MAYER, ERNEST J.; PALMIER, MARK O.
; TOLUNAY, H.ESER; WARREN, THOMAS G.; WUN, TZE-CHIN
; TITLE OF INVENTION: MODIFIED TISSUE PLASMINOGEN ACTIVATOR
; WITH MODIFIED GLYCOSYLATION SITE
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/203,047
; FILING DATE: 06-JUN-1988
; SEQ ID NO:5:
; LENGTH: 562
; 5244676-5

Query Match      38.4%; Score 321.5; DB 6; Length 562;
Best Local Similarity 44.9%; Pred. No. 4.8e-24;
Matches 61; Conservative 16; Mismatches 54; Indels 5; Gaps 3;

QY 3 ELHQP-SNCD---CLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYF 58
DB 77 QCHSVPVKSCSEPCFNGGTCQQAIFYSDP-VQCPEGFAGKCEIDGNSDCYFGSGAY 135
QY 59 RGAASDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRPNDRRRPWCYVQVG 118
DB 136 RGTWSTAESCAECTWNSSALAKPYSGRPDAIRLGLGNHNYCRPNDRDRSKFWCVFKA 195
QY 119 LKPLVQECMVHDCADG 134
DB 196 RRLTWECVDPVSCSEG 211

RESULT 40
US-08-438-745-15
; Sequence 15, Application US/08438745
; Patent No. 6248715
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Steven
; APPLICANT: Stratton-Thomas, Jennifer
; TITLE OF INVENTION: Expression of Urokinase Plasminogen
; TITLE OF INVENTION: Activator Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,745
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/070,153
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.

Query Match      35.8%; Score 300; DB 3; Length 233;
Best Local Similarity 77.9%; Pred. No. 2.4e-22;
Matches 53; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 SNELHQPVSNCDCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKTCYEGNGHYF 60
DB 29 SNELHQPVSNCDCCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIEDKSKQGGSGDFDYE 88
QY 61 KASDTMG 68
DB 89 KMANANKG 96

RESULT 41
US-08-438-745-17
; Sequence 17, Application US/08438745
; Patent No. 6248715
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Steven
; APPLICANT: Stratton-Thomas, Jennifer
; TITLE OF INVENTION: Expression of Urokinase Plasminogen
; TITLE OF INVENTION: Activator Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,745
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/070,153
; FILING DATE: 01-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
```

REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0939.001
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-438-745-17

Query Match 35.8%; Score 300; DB 3; Length 233;
Best Local Similarity 77.9%; Pred. No. 2.4e-22;
Matches 53; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKPGGQHCIDKSKTCYEGNGHFYRG 60
DB 29 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKPGGQHCIDKSKTCYEGNGHFYRG 88
QY 61 KASTDTMG 68
DB 89 KWANANKG 96

RESULT 42
US-09-219-019-15
Sequence 15, Application US/09219019
Patent No. 6268341
GENERAL INFORMATION:
APPLICANT: ROSENBERG, STEVEN
TITLE OF INVENTION: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR
TITLE OF INVENTION: INHIBITORS
FILE REFERENCE: 23533-0005
CURRENT APPLICATION NUMBER: US/09/219,019
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 08/438,263
PRIOR FILING DATE: 1995-05-10
PRIOR APPLICATION NUMBER: 08/280,288
PRIOR FILING DATE: 1994-07-26
PRIOR APPLICATION NUMBER: 08/070,153
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
US-09-219-019-15

Query Match 35.8%; Score 300; DB 3; Length 233;
Best Local Similarity 77.9%; Pred. No. 2.4e-22;
Matches 53; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKPGGQHCIDKSKTCYEGNGHFYRG 60
DB 29 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKPGGQHCIDKSKTCYEGNGHFYRG 88
QY 61 KASTDTMG 68
DB 89 KWANANKG 96

RESULT 43
US-09-219-019-17
Sequence 17, Application US/09219019
Patent No. 6268341
GENERAL INFORMATION:
APPLICANT: ROSENBERG, STEVEN
APPLICANT: STRATTON-THOMAS, JENNIFER R.
TITLE OF INVENTION: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR

TITLE OF INVENTION: INHIBITORS
FILE REFERENCE: 23533-0005
CURRENT APPLICATION NUMBER: US/09/219,019
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 08/438,263
PRIOR FILING DATE: 1995-05-10
PRIOR APPLICATION NUMBER: 08/280,288
PRIOR FILING DATE: 1994-07-26
PRIOR APPLICATION NUMBER: 08/070,153
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 17
LENGTH: 233
TYPE: PRT
ORGANISM: Homo sapiens
US-09-219-019-17

Query Match 35.8%; Score 300; DB 3; Length 233;
Best Local Similarity 77.9%; Pred. No. 2.4e-22;
Matches 53; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKPGGQHCIDKSKTCYEGNGHFYRG 60
DB 29 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKPGGQHCIDKSKTCYEGNGHFYRG 88
QY 61 KASTDTMG 68
DB 89 KWANANKG 96

RESULT 44
PCT-US94-05669A-15
Sequence 15, Application PC/TUS9405669A
GENERAL INFORMATION:
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Expression of Urokinase Plasminogen
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05669A
FILING DATE: 19-MAY-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0939.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-05669A-15

Query Match 35.8%; Score 300; DB 5; Length 233;
Best Local Similarity 77.9%; Pred. No. 2.4e-22;
Matches 53; Conservative 2; Mismatches 13; Indels 0; Gaps 0;

Qy	1	SNELHOVPNCDC	LANGT	CVSNKYPSNIHWCNCPKFKGGCHCEIDKSKTCTYECNGHFYRG	60
				:	
Db	29	SNELHOVPNCDC	LANGT	CVSNKYPSNIHWCNCPKFKGGCHCEIDKSKOGGSGGDFDYE	88
Qy	61	KAS	TD	TMG	68
				:	
Db	89	KWAN	N	KG	96

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RESULT 46
US-08-438-745-13
; Sequence 13, Application US/08438745
; Patent No. 6248715
; GENERAL INFORMATION:
; APPLICANT: Rosenberg, Steven
; APPLICANT: Stratton-Thomas, Jennifer
; TITLE OF INVENTION: Expression of Urokinase Plasminogen
; TITLE OF INVENTION: Activator Inhibitors
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:

```

; ADDRESS: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0,
; CURRENT APPLICATION DATA:
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; Version #1.25

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RESULT 47
US-09-219-019-13
; Sequence 13, Application US/09219019
; Patent No. 6268341
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, STEVEN
; APPLICANT: STRATTON-THOMAS, JENNIFER R.
; TITLE OF INVENTION: EXPRESSION OF UROKINASE PLASMINOGEN ACTIVATOR
; TITLE OF INVENTION: INHIBITORS
; FILE REFERENCE: 23533-0005
; CURRENT APPLICATION NUMBER: US/09/219,019
; CURRENT FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 08/438,263
; PRIOR FILING DATE: 1995-05-10
; PRIOR APPLICATION NUMBER: 08/280,288
; PRIOR FILING DATE: 1994-07-26
; PRIOR APPLICATION NUMBER: 08/070,153
; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-219-019-13

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Query Match 35.8%; Score 300; DB 3; Length 235;

Best Local Similarity 77.9%; Pred. No. 2.5e-22;
Matches 53; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
Db 31 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 90
QY 61 KASTDTWG 68
Db 91 KMANANKG 98

RESULT 48
PCT-US94-05669A-13
; Sequence 13, Application PC/TUS9405669A
; GENERAL INFORMATION:
; APPLICANT: Chiron Corporation
; TITLE OF INVENTION: Expression of Urokinase Plasminogen
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/05669A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 0939.100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2706
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-05669A-13

Query Match 35.8%; Score 300; DB 5; Length 235;
Best Local Similarity 77.9%; Pred. No. 2.5e-22;
Matches 53; Conservative 2; Mismatches 13; Indels 0; Gaps 0;
QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 60
Db 31 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKTCYEGNGHYRG 90
QY 61 KASTDTWG 68
Db 91 KMANANKG 98

RESULT 49
US-08-747-915-5
; Sequence 5, Application US/08747915
; Patent No. 5942492
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.
; APPLICANT: Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO

; TITLE OF INVENTION: UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE, NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/747,915
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 32904-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: group(11..19, 13..31, 33..42)
US-08-747-915-5

Query Match 35.0%; Score 293; DB 2; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKT 49
Db 1 SNELHQPNSCDCLNGGTCVSNKYFSNIHWCNCPKFGGQHCIDKSKT 49

RESULT 50
US-09-285-783-5
; Sequence 5, Application US/09285783
; Patent No. 6514710
; GENERAL INFORMATION:
; APPLICANT: Jones, Terence R.
; APPLICANT: Haney, David N.
; APPLICANT: Varga, Janos
; TITLE OF INVENTION: CYCLIC PEPTIDES THAT BIND TO
; UROKINASE-TYPE PLASMINOGEN ACTIVATOR RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RADER, FISMAN & GRAUER
; STREET: 1233 20TH STREET NW, SUITE 501
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,783
; FILING DATE: 05-Apr-1999
; CLASSIFICATION: <Unknown>

```

; ATTORNEY/AGENT INFORMATION:
; NAME: LIVNAT, SHMUEL
; REGISTRATION NUMBER: 33,949
; REFERENCE/DOCKET NUMBER: ANG-001/DIV (80144-0007)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 955-8787
; TELEFAX: (202) 955-3751
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Disulfide-bond
; LOCATION: group(11..19, 13..31, 33..42)
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-285-783-5

Query Match      35.0%; Score 293; DB 4; Length 49;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNCPKPKFGGQCHCEIDKSKT 49
Db      1 SNELHQVPSNCDCLNGGTCVSNKYFSNIHWNCNCPKPKFGGQCHCEIDKSKT 49

Search completed: May 25, 2004, 15:00:08
Job time : 11.901.secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2004, 14:47:10 ; Search time 5.55302 Seconds
(without alignments)
1662.947 Million cell updates/sec

Title: US-09-880-503-9
Perfect score: 554
Sequence: 1 KTCYEGNGHFRGKASTDTM.....QECVHDCADGKKPSPPEE 96

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : PIR 78.*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	100.0	431	1 UKHU	u-plasminogen acti
2	519	93.7	433	1 UKBAY	u-plasminogen acti
3	437.5	79.0	442	1 UKPG	u-plasminogen acti
4	427	77.1	432	1 SI8932	u-plasminogen acti
5	422	76.2	433	1 JN0560	u-plasminogen acti
6	408	73.6	433	1 UKMS	u-plasminogen acti
7	241	43.5	431	2 JS0599	t-plasminogen acti
8	241	43.5	477	1 A34369	t-plasminogen acti
9	241	43.5	477	2 JS0598	t-plasminogen acti
10	228.5	41.2	559	1 A35029	t-plasminogen acti
11	226	40.8	291	2 I38098	t-plasminogen acti
12	226	40.8	562	1 UKHUT	t-plasminogen acti
13	220	39.7	394	2 JS0600	t-plasminogen acti
14	219	39.5	559	1 A29941	t-plasminogen acti
15	213	38.4	477	2 JS0597	t-plasminogen acti
16	210	37.9	558	2 JC5878	plasma hyaluronan-
17	199.5	36.0	560	1 JC4795	plasma hyaluronan-
18	198.5	35.8	434	1 A35005	u-plasminogen acti
19	194.5	35.1	655	1 A46888	hepatocyte growth
20	191.5	34.6	603	2 S28941	coagulation factor
21	170.5	30.8	615	1 KFHU12	coagulation factor
22	161	29.1	1420	2 A32869	apolipoprotein(a)
23	157	28.3	4548	1 S00657	apolipoprotein(a)
24	156	28.2	120	2 E61545	plasmin (EC 3.4.21
25	155.5	28.1	593	2 S45281	coagulation factor
26	153	27.6	89	2 A60140	plasmin (EC 3.4.21
27	153	27.6	460	2 B61545	plasmin (EC 3.4.21
28	152	27.4	812	1 PLBO	plasmin (EC 3.4.21
29	150	27.1	123	2 C61545	plasmin (EC 3.4.21

ALIGNMENTS

RESULT 1

UKHU

u-plasminogen activator (EC 3.4.21.73) precursor [validated] - human

N:Alternate names: cellular plasminogen activator; urokinase, urokinase-type plasminoge
N:Contains: urokinase-type plasminogen activator chain A; urokinase-type plasminogen ac
in form

C:Species: Homo sapiens (man)

C>Date: 17-Dec-1982 #sequence revision 04-Dec-1986 #text change 15-Sep-2000

C:Accession: A00931; I52209; J0102; A37561; I38102; S65783; A37562; A37563; A37564; A3

R:Riccio, A.; Grimaldi, G.; Verde, P.; Sebastio, G.; Boast, S.; Blasi, F.

Nucleic Acids Res. 13, 2759-2771, 1985

A:Title: The human urokinase-plasminogen activator gene and its promoter.

A:Reference number: A00931; PMID:85215647; PMID:2987867

A:Accession: A00931

A:Molecule type: DNA

A:Residues: 1-431 <RIC>

A:Cross-references: GB:X02419; NID:G37601; PIDN:CA26268.1; PID:q1834524

A:Note: The authors translated the codon ATG for residue 214 as Ile

R:Nagamine, Y.; Pearson, D.; Grattan, M.

Biochem. Biophys. Res. Commun. 132, 563-569, 1985

A:Title: Exon-intron boundary sliding in the generation of two mRNAs coding for porcine

A:Reference number: I52209; MUID:86050639; PMID:3933505

30	150	27.1	169	2	A40522
31	149	26.9	810	2	B30848
32	148.5	26.8	711	1	A47136
33	148.5	26.8	810	2	I46260
34	148	26.7	790	1	PLPG
35	147.5	26.6	716	1	A40332
36	147.5	26.6	943	2	B45082
37	146.5	26.4	810	1	PLHU
38	146	26.4	937	2	A45082
39	145	26.2	805	2	I18840
40	144.5	26.1	812	1	PLMS
41	143	25.8	2869	2	T18518
42	141.5	25.5	455	2	A61545
43	139	25.1	685	1	A48289
44	137.5	24.8	716	1	JC5061
45	137.5	24.8	728	1	A60185
46	135.5	24.5	728	1	A35644
47	133.5	24.1	411	2	I51285
48	133.5	24.1	728	1	JH0579
49	131	23.6	336	2	S33879
50	127.5	23.0	710	1	I51283
51	125.5	22.7	618	2	A35827
52	124	22.4	622	1	TBHU
53	121	21.8	946	1	A47299
54	113	20.4	617	2	SI0511
55	112	20.2	625	1	TBBO
56	89	16.1	761	2	JC5759
57	87.5	15.8	558	2	T15448
58	75	13.5	253	2	JC5014
59	74	13.4	559	2	A57474
60	73.5	13.3	651	2	AF2493
61	70	12.6	323	2	T25094
62	69.5	12.5	790	2	T15709
63	68.5	12.4	364	2	T30723
64	68	12.3	161	2	SI2246
65	67	12.1	612	2	T13616
66	66.5	12.0	294	2	T23916
67	66	11.9	5762	2	A41819
68	65.5	11.8	483	2	T47974
69	65.5	11.8	1278	2	T30188
70	65.5	11.8	1426	2	B64780
71	65	11.7	542	2	B81662
72	65	11.7	951	2	T00260
73	64	11.6	481	2	A84130
74	63.5	11.5	542	2	E71502
75	63	11.4	419	1	WJFPH2

A;Accession: I52209
A;Status: preliminary; translated from GB/EMBL/DBD
A;Molecule type: DNA
A;Residues: 145-161 <NAG1>
A;Cross-references: GB:K03027; NID:G340174; PIDN:AAA61257.1; PID:G340175
R;Nagai, M.; Hiramatsu, R.; Kaneda, T.; Hayasuke, N.; Arimura, H.; Nishida, M.; Suyama, Gene 36, 183-188, 1985
A;Title: Molecular cloning of cDNA coding for human preprourokinase.
A;Reference number: J70102; MUID:86056954; PMID:2415429
A;Accession: J70102
A;Molecule type: mRNA
A;Residues: 1-213, 'I', 215-431 <NAG2>
A;Cross-references: GB:K03226; NID:G340155; PIDN:AACT97138.1; PID:G340158; GB:D00244; NID:Vardé, P.; Stoppelli, M.P.; Galeffi, P.; Di Nocera, P.; Biasi, F.
Proc. Natl. Acad. Sci. U.S.A. 81, 4727-4731, 1984
A;Title: Identification and primary sequence of an unspliced human urokinase poly(A) + RN
A;Reference number: A37561; MUID:84272706; PMID:6589620
A;Accession: A37561
A;Molecule type: mRNA
A;Residues: 66-431 <VER>
A;Cross-references: GB:D00244; NID:G220138
R;Jacobs, P.; Cravador, A.; Loriau, R.; Brockly, P.; Colau, B.; Chuchana, P.; van Elsen, DNA 4, 139-146, 1985
A;Title: Molecular cloning, sequencing, and expression in Escherichia coli of human prep
A;Reference number: I38102; MUID:85203359; PMID:3888571
A;Accession: I38102
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-150, 'W', 152-213, 'I', 215-385, 'C', 387-429, 'V', 431 <JAC>
A;Cross-references: EMBL:X02760; NID:G35297; PIDN:CAA26535.1; PID:G35298
R;Yoshimoto, M.; Ushiyama, Y.; Sakai, M.; Tamaki, S.; Hara, H.; Takahashi, K.; Sawasaki, Biochim. Biophys. Acta 1293, 83-89, 1996
A;Title: Characterization of single chain urokinase-type plasminogen activator with a no
A;Reference number: S65783; MUID:96186279; PMID:8652631
A;Accession: S65783
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 21-140, 'L', 142-213, 'I', 215-431 <YOS>
A;Cross-references: EMBL:D11143; NID:G1311467; PIDN:BA01919.1; PID:G1199928
R;Gunzler, W.A.; Steffens, G.J.; Otting, F.; Kim, S.M.A.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1155-1165, 1982
A;Title: The primary structure of high molecular mass urokinase from human urine.
A;Reference number: A37562; MUID:83055084; PMID:6754569
A;Accession: A37562
A;Molecule type: protein
A;Residues: 21-177 <GUN>
R;Schaller, J.; Nick, H.; Rickli, E.E.; Gillesse, D.; Lergier, W.; Studer, R.O.
Eur. J. Biochem. 125, 251-257, 1982
A;Title: Human low-molecular-weight urinary urokinase. Partial characterization and prel
A;Reference number: A37563; MUID:83003608; PMID:6749491
A;Accession: A37563
A;Molecule type: protein
A;Residues: 156-176, 179-193, 'T', 195, 'T', 197-224 <SCH>
R;Steffens, G.J.; Gunzler, W.A.; Otting, F.; Frankus, E.; Flohe, L.
Hoppe-Seyler's Z. Physiol. Chem. 363, 1043-1058, 1982
A;Title: The complete amino acid sequence of low molecular mass urokinase from human uri
A;Reference number: A37564; MUID:83055099; PMID:6754572
A;Accession: A37564
A;Molecule type: protein
A;Residues: 156-410 <STE>
R;Kentzer, E.J.; Buko, A.; Menon, G.; Sarin, V.K.
Biochem. Biophys. Res. Commun. 171, 401-406, 1990
A;Title: Carbohydrate composition and presence of a fucose-protein linkage in recombinan
A;Reference number: A35689; MUID:90365737; PMID:2393398
A;Accession: A35689
A;Molecule type: protein
A;Residues: 21-30, 'X', 32, 'X', 34-38, 'X', 40-43 <KEN>
A;Note: Identification of a fucose and attempt to determine its attachment site
R;Rabbani, S.A.; Desjardins, J.; Bell, A.W.; Banville, D.; Mazar, A.; Henkin, J.; Goltzm
Biochem. Biophys. Res. Commun. 173, 1058-1064, 1990
A;Title: An amino-terminal fragment of urokinase isolated from a prostate cancer cell li
A;Reference number: A36697; MUID:91097529; PMID:2125213
A;Accession: A36697

A;Molecule type: protein
A;Residues: 21-34 <RAB>
R;Li, X.; Bokman, A.M.; Llinas, M.; Smith, R.A.G.; Dobson, C.M.
submitted to the Brookhaven Protein Data Bank, July 1993
A;Cross-references: A51255; PDB:1KDU
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R;Li, X.; Smith, R.A.G.; Dobson, C.M.
Biochemistry 31, 9562-9571, 1992
A;Title: Sequential (1)H NMR assignments and secondary structure of the kringle domain f
A;Reference number: A44375; MUID:93003110; PMID:1327118
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR
R;Hansen, A.P.; Petros, A.M.; Meadows, R.F.; Netteheim, D.G.; Mazar, A.P.; Olejniczak, S.
submitted to the Brookhaven Protein Data Bank, January 1994
A;Reference number: A68822; PDB:1URK
A;Contents: annotation; conformation and disulfide bond assignments by (1)H-NMR, residue
R;Spraggon, G.S.; Phillips, C.; Nowak, U.K.; Ponting, C.P.; Saunders, D.; Dobson, C.M.;
submitted to the Brookhaven Protein Data Bank, July 1995
A;Reference number: A66058; PDB:1LMW
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 168-175; 179-426
C;Comment: This enzyme is found in urine in a high molecular mass form, consisting of A
C;Comment: Urokinase-type plasminogen activator proteolytically activates plasminogen, a
C;Genetics:
A;Gene: GDB:PLAU
A;Cross-references: GDB:119497; OMIM:191840
A;Map position: 10q24-10q24
A;Introns: 19/3; 29/1; 65/1; 123/2; 154/1; 227/2; 277/1; 324/1; 373/3
C;Function:
A;Description: proteolytically activates plasminogen
A;Pathway: fibrinolysis
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C;Keywords: fibrinolysis; glycoprotein; heterodimer; hydrolase; kringle; serine proteina
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-431/Product: urokinase-type plasminogen activator, single chain form #status predic
F;21-177/Product: urokinase-type plasminogen activator chain A #status experimental <MPA
F;31-62/Domain: EGF homology <EGF>
F;70-151/Domain: kringle homology <KRG>
F;156-177/Product: urokinase-type plasminogen activator chain A1 #status experimental <M
F;179-431/Product: urokinase-type plasminogen activator chain B #status experimental <MP
F;179-419/Domain: trypsin homology <TRY>
F;31-39 33-51 53-62 70-151 91-133 122-146 168-259 209-225 217-288 313-382 345-361 372-40
F;38/Binding site: carbohydrate (thr) (covalent) #status predicted
F;178-179/Cleavage site: Lys-Ile (plasma) #status experimental
F;224/275,376/Active site: His, Asp, Ser #status experimental
F;322/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 100.0%; Score 554; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. No. 1.3e-51;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHYRGKASTDTMGRCPLPWN SATVLQOQTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 68 KTCYEGNGHYRGKASTDTMGRCPLPWN SATVLQOQTYHAHRSDALQLGLGKHNYCRNPDN 127
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSPPEE 163
RESULT 2
UKBAY
u-plasminogen activator (EC 3.4.21.73) precursor - yellow baboon
C;Species: Papio cynocephalus, Papio hamadryas cynocephalus (yellow baboon)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C;Accession: S14687; S08651
R;Au, Y.P.T.; Wang, T.W.; Clowes, A.W.
Nucleic Acids Res. 18, 3411, 1990
A;Title: Nucleotide and deduced amino acid sequences of baboon urokinase-type plasminoge
A;Reference number: S14687; MUID:90287734; PMID:2113276
A;Accession: S14687
A;Molecule type: mRNA
A;Residues: 1-433 <AUY>
A;Cross-references: EMBL:X51935; NID:G38130; PIDN:CAA36200.1; PID:G38131
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try

C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-176/Product: plasminogen activator chain A #status predicted <ACH>
F;30-61/Domain: EGF homology <EGF>
F;59-150/Domain: kringle homology <KRG>
F;178-433/Product: plasminogen activator chain B #status predicted <BCH>
F;178-421/Domain: trypsin homology <TRY>
F;167-298,208-224,216-287,315-384,347-363,374-402/Disulfide bonds: #status predicted
F;223,274,378/Active site: His, Asp, Ser #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.7%; Score 519; DB 1; Length 433;
Best Local Similarity 94.8%; Pred. No. 7.4e-48; Indels 0; Gaps 0;
Matches 91; Conservative 1; Mismatches 4;

Qy 1 KTCYEGNGHFYRGKASTDTMGRCPLPWNATVLQOQTYHAHRS DALQLGLGKHYCRNPDN 60
Db 67 KTCYEGNGHFYRGKASTDTMGRCPLPWNATVLQOQTYHAHRS DALQLGLGKHYCRNPDN 126

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPE 96
Db 127 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPE 162

RESULT 3
UKPG
u-plasminogen activator (EC 3.4.21.73) precursor - pig
N;Alternate names: uPA
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 04-Dec-1986 #sequence_revision 17-Mar-1987 #text_change 07-Aug-1998
C;Accession: A00932
R;Nagamine, Y.; Pearson, D.; Altus, M.S.; Reich, E.
Nucleic Acids Res. 12, 952S-954I, 1984
A;Title: cDNA and gene nucleotide sequence of porcine plasminogen activator.
A;Reference number: A00932; MUID:85087954; PMID:6096832
A;Accession: A00932
A;Molecule type: DNA
A;Residues: 1-240, 'H', 242-442 <NAGI>
A;Experimental source: kidney cell line LLC-PK1
R;Nagamine, Y.
submitted to the Protein Sequence Database, December 1986
A;Reference number: A37566
A;Contents: annotation; correction to residue 241
C;Genetics:
A;Introns: 19/3; 31/1; 125/2; 165/1; 238/1; 335/1; 384/3
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-188/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F;33-64/Domain: EGF homology <EGF>
F;72-153/Domain: kringle homology <KRG>
F;190-442/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
F;153/Binding site: trypsin homology <TRY>
F;179-310,220-236,228-299,324-393,356-372,383-411/Disulfide bonds: #status predicted
F;235,286,387/Active site: His, Asp, Ser #status predicted

Query Match 79.0%; Score 437.5; DB 1; Length 442;
Best Local Similarity 74.3%; Pred. No. 4e-39;
Matches 78; Conservative 8; Mismatches 10; Indels 9; Gaps 1;

Qy 1 KTCYEGNGHFYRGKASTDTMGRCPLPWNATVLQOQTYHAHRS DALQLGLGKHYCRNPDN 60
Db 70 QTCFEGNGSHYRGKANTDTMGRCPLPWNATVLNTYHAHRS DALQLGLGKHYCRNPDN 129

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPE 96
Db 130 QRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPE 174

RESULT 4
S18932
u-plasminogen activator (EC 3.4.21.73) precursor - rat

N;Alternate names: plasminogen activator, urokinase-type; urinary plasminogen activator
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 10-Feb-1995 #text_change 18-Jun-1999
C;Accession: S24604; MUID:160186; I53472; S18932
R;Rabbani, S.A.
submitted to the EMBL Data Library, April 1992
A;Reference number: S24604
A;Accession: S24604
A;Molecule type: mRNA
A;Residues: 1-15, 'H', 17-23, 'G', 25-331, 'N', 333-432 <RAB>
A;Cross-references: EMBL:X65651; NID:G57456; PIDN:CAA46601.1; PID:G57457
A;Experimental source: tissue kidney
R;Henderson, B.R.; Tansey, W.P.; Phillips, S.M.; Ramshaw, I.A.; Kefford, R.F.
Cancer Res. 52, 2489-2496, 1992
A;Title: Transcriptional and posttranscriptional activation of urokinase plasminogen ac
A;Reference number: 160186; MUID:92233409; PMID:1568219
A;Accession: I60186
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-432 <RES>
A;Cross-references: EMBL:X63434; NID:G57465; PIDN:CAA45028.1; PID:G57466
A;Experimental source: strain Fischer 344; tissue mammary
R;Ragno, P.; Cassano, S.; Degen, J.; Kessler, C.; Blasi, F.; Rossi, G.
FEBS Lett. 306, 193-198, 1992
A;Title: The receptor for the plasminogen activator of urokinase type is up-regulated i
A;Reference number: I53472; MUID:92339549; PMID:1321734
A;Accession: I53472
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 31-62 <RE2>
A;Cross-references: EMBL:X66907; NID:G396200; PIDN:CAA47386.1; PID:G938279
C;Genetics:
A;Gene: uPA
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; tr
C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-177/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F;31-62/Domain: EGF homology <EGF>
F;70-151/Domain: kringle homology <KRG>
F;179-432/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
F;179-420/Domain: trypsin homology <TRY>
F;168-300,210-226,218-289,314-383,346-362,373-401/Disulfide bonds: #status predicted
F;225,276,377/Active site: His, Asp, Ser #status predicted

Query Match 77.1%; Score 427; DB 1; Length 432;
Best Local Similarity 77.1%; Pred. No. 5.1e-38;
Matches 74; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGRCPLPWNATVLQOQTYHAHRS DALQLGLGKHYCRNPDN 60
Db 68 KTCYEGNGSHYRGKANTDTMGRCPLPWNATVLQOQTYHAHRS DALQLGLGKHYCRNPDN 127

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPE 96
Db 128 QRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPE 163

RESULT 5
UN0560
u-plasminogen activator (EC 3.4.21.73) precursor - bovine
N;Alternate names: uPA
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: JN0560
R;Kraatzschmar, J.; Haendler, B.; Kojima, S.; Rifkin, D.B.; Schleuning, W.D.
Gene 125, 177-183, 1993
A;Title: Bovine urokinase-type plasminogen activator and its receptor: cloning and indu
A;Reference number: JN0560; MUID:93216119; PMID:8385052
A;Accession: JN0560
A;Molecule type: mRNA
A;Residues: 1-433 <KRA>
A;Cross-references: GB:I03546; NID:G163900; PIDN:AAA51419.1; PID:G163801
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; tr

C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-179/Product: plasminogen activator chain A #status predicted <MA1>
F;21-179/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F;33-64/Domain: EGF homology <EGF>
F;72-153/Domain: kringle homology <KRG>
F;181-433/Product: plasminogen activator chain B #status predicted <MA2>
F;181-421/Domain: trypsin homology <TRY>
F;170-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
F;226,277,378/Active site: His, Asp, Ser #status predicted

Query Match 76.2%; Score 422; DB 1; Length 433;
Best Local Similarity 75.0%; Pred. No. 1.8e-37;
Matches 72; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Oy 1 KTCYEGNGHYRGKASTDTMGRCPLPWNSTVLOQTYHAHRSDALQLGLGKHNCRPN 60
Db 70 KTCYGNHGSYRGKANDLSGRCLANDSPVLLKLYHAHRSDAQLGLGKHNCRPN 129

Oy 61 RRRPWCYVQGLKPLVQECWHDCAQKPKSSPPEE 96
Db 130 QRRPWCYVQGLKPLVQECWHDCAQKPKSSPPEE 165

RESULT 6

UAMS

C;Keywords: plasminogen activator (EC 3.4.21.73) precursor - mouse
C;Species: Mus.musculus (house mouse)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C;Accession: A29420; A24615
R;Degen, S.J.F.; Heckel, J.L.; Reich, E.; Degen, J.L.
Biochemistry 26, 8270-8279, 1987
A;Title: The murine urokinase-type plasminogen activator gene.
A;Reference number: A29420; MUID:85163489; PMID:281940
A;Accession: A29420
A;Molecule type: DNA
A;Residues: 1-433 <DEG>
A;Cross-references: GB:M17922; NID:G202296; PIDN:AAA40539.1; PID:G202297
R;Belin, D.; Vassalli, J.D.; Combepine, C.; Godeau, F.; Nagamine, Y.; Reich, E.; Kocher, Eur. J. Biochem. 148, 225-232, 1985
A;Title: Cloning, nucleotide sequencing and expression of cDNAs encoding mouse urokinase
A;Reference number: A24615; MUID:85179474; PMID:2985383
A;Accession: A24615
A;Molecule type: mRNA
A;Residues: 1-433 <BEL>
A;Cross-references: GB:X02389; NID:G55127; PIDN:CAA26231.1; PID:G55128
C;Genetics:
A;Introns: 19/3; 30/1; 66/1; 124/2; 155/1; 229/2; 279/1; 326/1; 375/3
C;Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; try
C;Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-178/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>
F;32-63/Domain: EGF homology <EGF>
F;71-152/Domain: kringle homology <KRG>
F;180-433/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>
F;180-421/Domain: trypsin homology <TRY>
F;169-301,211-227,219-290,315-384,347-363,374-402/Disulfide bonds: #status predicted
F;226,277,378/Active site: His, Asp, Ser #status predicted

Query Match 73.6%; Score 408; DB 1; Length 433;
Best Local Similarity 70.8%; Pred. No. 5.6e-36;
Matches 68; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

Oy 1 KTCYEGNGHYRGKASTDTMGRCPLPWNSTVLOQTYHAHRSDALQLGLGKHNCRPN 60
Db 69 KTCYGNHGSYRGKANTDKGRCLANNAFVLPQKPYNAHRSDAQLGLGKHNCRPN 128

Oy 61 RRRPWCYVQGLKPLVQECWHDCAQKPKSSPPEE 96
Db 129 QRRPWCYVQGLKPLVQECWHDCAQKPKSSPPEE 164

RESULT 7

J80599

C;Keywords: plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
N;Alternate names: tissue plasminogen activator
C;Species: Desmodus rotundus (common vampire bat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C;Accession: J80599
R;Kraetzschmar, J.; Haendler, B.; Langer, G.; Boisdol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A;Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A;Reference number: J80597; MUID:92039036; PMID:1937019
A;Accession: J80599
A;Molecule type: mRNA
A;Residues: 1-431 <KRA>
A;Cross-references: GB:M63989; NID:G166076; PIDN:AAA31594.1; PID:G166077
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-36/Domain: propeptide #status predicted <PRO>
F;37-431/Product: plasminogen activator beta #status predicted <PLA>
F;41-74/Domain: EGF homology <EGF>
F;82-163/Domain: kringle homology <KRG>
F;180-425/Domain: trypsin homology <TRY>
F;141-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide bon
F;139,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;179-180/Cleavage site: His-Ser (plasmin) #status predicted
F;226,275,382/Active site: His, Asp, Ser #status predicted
F;345-361,378-406/Disulfide bonds: #status predicted

Query Match 43.5%; Score 241; DB 2; Length 431;
Best Local Similarity 50.0%; Pred. No. 4.1e-18;
Matches 42; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

Oy 2 TCYEGNGHYRGKASTDTMGRCPLPWNSTVLOQTYHAHRSDALQLGLGKHNCRPN 61
Db 81 TCYKQGVYTRGTWSTSSGACINWNSNLTTRTYNGRSDATLGLGKHNCRPN 140

Oy 62 RRPWCYVQGLKPLVQECWHDCA 85
Db 141 SKPCYVIVKASKFILEPCSPVCS 164

RESULT 8

A34369

C;Keywords: plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C;Species: Megaderma lyra
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A34369
R;Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.E.; Jacob
J. Biol. Chem. 264, 17947-17952, 1989
A;Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin
A;Reference number: A34369; MUID:90036867; PMID:2509450
A;Accession: A34369
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-477 <GAR>
A;Cross-references: GB:J05082; NID:G166080; PIDN:AAA31596.1; PID:G166081
C;Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C;Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-36/Domain: propeptide #status predicted <PRO>
F;37-477/Product: plasminogen activator #status predicted <PLA>
F;42-79/Domain: fibronectin type I repeat homology <IFA>
F;87-120/Domain: EGF homology <EGF>
F;128-209/Domain: kringle homology <KRG>
F;226-471/Domain: trypsin homology <TRY>
F;42-72,70-79,87-98,92-105,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F;272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 43.5%; Score 241; DB 1; Length 477;
Best Local Similarity 50.0%; Pred. No. 4.5e-18;
Matches 42; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

Oy 2 TCYEGNGHYRGKASTDTMGRCPLPWNSTVLOQTYHAHRSDALQLGLGKHNCRPN 61

```
Db      127 TCYKQGVYRGKSTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 186
      127 TCYKQGVYRGKSTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 186
QY      62 RRPWCYVQVGLKPLVQECMVHDCADG 85
      62 RRPWCYVQVGLKPLVQECMVHDCADG 85
Db      187 SKPCYVYKAKFILEFCSPVCS 210
      187 SKPCYVYKAKFILEFCSPVCS 210

RESULT 9
JS0598
t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat
N:Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: JS0598
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0598
A:Molecule type: mRNA
A:Residues: 1-477 <RA>
A:Cross-references: GB:M63988; NID:GL6074; PIDN:AAA1593.1; PID:GL6075
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-477/Domain: plasminogen activator alpha-2 #status predicted <PLA>
F:42-79/Domain: fibronectin type I repeat homology <1FA>
F:87-120/Domain: EGF homology <EGF>
F:128-209/Domain: kringle homology <KRG>
F:226-471/Domain: trypsin homology <TRY>
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F:185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:225-226/Cleavage site: His-Ser (plasmin) #status predicted
F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match      43.5%; Score 241; DB 2; Length 477;
Best Local Similarity 50.0%; Pred. No. 4.5e-18;
Matches 42; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

QY      2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 61
      2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 61
Db      127 TCYKQGVYRGKSTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 186
      127 TCYKQGVYRGKSTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 186

QY      62 RRPWCYVQVGLKPLVQECMVHDCADG 85
      62 RRPWCYVQVGLKPLVQECMVHDCADG 85
Db      187 SKPCYVYKAKFILEFCSPVCS 210
      187 SKPCYVYKAKFILEFCSPVCS 210

RESULT 10
A35029
t-plasminogen activator (EC 3.4.21.68) precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A35029; A31597
R:Feng, P.; Ohlsson, M.; Ny, T.
J. Biol. Chem. 265, 2022-2027, 1990
A:Title: The structure of the TARA-less rat tissue-type plasminogen activator gene. Spec
A:Reference number: A35029; MUID:90130448; PMID:2105315
A:Accession: A35029
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-559 <PBN>
A:Cross-references: GB:M31197; NID:G207429; PIDN:AAA42261.1; PID:G207431; GB:J05226
R:Ny, T.; Leonardson, G.; Hsueh, A.O.W.
DNA 7, 671-677, 1988
A:Title: Cloning and characterization of a cDNA for rat tissue-type plasminogen activato
A:Reference number: A31597; MUID:89170114; PMID:3148445
A:Accession: A31597
A:Molecule type: mRNA
A:Residues: 1-379, 'K', 381-559 <NYT>
A:Cross-references: GB:M23697; NID:G530159; PIDN:AAA1812.1; PID:G530160
```

```
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat ho
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-29/Domain: propeptide #status predicted <PRO>
F:30-559/Domain: t-plasminogen activator #status predicted <MAT>
F:30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
F:38-75/Domain: fibronectin type I repeat homology <1F1>
F:83-116/Domain: EGF homology <EGF>
F:124-205/Domain: kringle homology <KR1>
F:124-294/Domain: kringle homology <KR2>
F:309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
F:309-553/Domain: trypsin homology <TRY>
F:38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-
F:149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
F:355,404,510/Active site: His, Asp, Ser #status predicted

Query Match      41.2%; Score 228.5; DB 1; Length 559;
Best Local Similarity 45.3%; Pred. No. 1.1e-16;
Matches 43; Conservative 11; Mismatches 36; Indels 5; Gaps 1;

QY      2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 61
      2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 61
Db      123 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 182
      123 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 182

QY      62 RRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
      62 RRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
Db      183 VKPCYVYKAKGYTTEFCSTPAC-----PKGPTED 212
      183 VKPCYVYKAKGYTTEFCSTPAC-----PKGPTED 212

RESULT 11
I38098
t-plasminogen activator precursor, inactive endothelial splice form - human
N:Alternate names: tissue plasminogen activator
C:Species: Homo sapiens (man)
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 22-Jun-1999
C:Accession: I38098; S01678
R:Siebert, P.D.; Fong, K.
Nucleic Acids Res. 18, 1086, 1990
A:Title: Variant tissue type plasminogen activator (PLAT) cDNA obtained from human endo
A:Reference number: I38098; MUID:90192128; PMID:1969145
A:Accession: I38098
A:Status: translated from GB/ENBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-291 <SIR>
A:Cross-references: EMBL:X13097; NID:G35282; PIDN:CAA1489.1; PID:G35283
C:Comment: For the main splice form, see PIR:UKHUT. This form probably does not have pr
C:Genetics:
A:Gene: GDB:PLAT
A:Cross-references: GDB:119496; OMIM:173370
A:Map position: 8p12.8p12
A:Introns: 24/3; 39/1; 85/1; 122/1; 180/2; 211/1; 268/2
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat ho
C:Keywords: alternative splicing; fibrinolysis; glycoprotein; kringle
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-32/Domain: propeptide #status predicted <PRO>
F:33-291/Product: t-plasminogen activator, inactive endothelial splice form #status pre
F:41-78/Domain: fibronectin type I repeat homology <1FA>
F:86-119/Domain: EGF homology <EGF>
F:127-208/Domain: kringle homology <KR1>
F:215-291/Domain: kringle homology #status atypical <KR2>
F:41-71,69-78,86-97,91-108,110-119,127-208,148-190,179-203/Disulfide bonds: #status pre

Query Match      40.8%; Score 226; DB 2; Length 291;
Best Local Similarity 47.7%; Pred. No. 1.1e-16;
Matches 41; Conservative 8; Mismatches 37; Indels 0; Gaps 0;

QY      2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 61
      2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 61
Db      126 TCYEDQGISYRGKSTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 185
      126 TCYEDQGISYRGKSTDTMGRPCLPWNSATVLQOQTYHAHRSALQGLGKHNYCRNPNN 185

QY      62 RRPWCYVQVGLKPLVQECMVHDCADG 87
      62 RRPWCYVQVGLKPLVQECMVHDCADG 87
```

Db 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 12

UKHUT

t-plasminogen activator (EC 3.4.21.68) precursor [validated] - human

N/Alternate names: t-PA; tissue plasminogen activator

C/Species: Homo sapiens (man)

C/Date: 14-Nov-1983 #sequence revision 14-Nov-1983 #text change 08-Dec-2000

C/Accession: A94004; A23529; A93293; S02125; A91343; A93951; A91322; A54645; 160

R/NC, Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984

Proc. Natl. Acad. Sci. U.S.A. 81, 5355-5359, 1984

A/Title: The structure of the human tissue-type plasminogen activator gene: correlation

A/Reference number: A94004; NUID:84298137; PMID:6089198

A/Accession: A94004

A/Molecule type: DNA

A/Residues: 1-562 <NVT>

A/Cross-references: GB:L00141

A/Note: the codon given for residue 93 (ACC) is inconsistent with the authors' translation

R/Friezner Degen, S.J.; Rajput, B.; Reich, E.

J. Biol. Chem. 261, 6972-6985, 1986

A/Title: The human tissue plasminogen activator gene.

A/Reference number: A23529; NUID:86196143; PMID:3009482

A/Accession: A23529

A/Molecule type: DNA

A/Residues: 1-562 <DEG>

A/Cross-references: GB:K03021; NUID:9339817; PIDN:AA98809.1; PID:G339818

R/Itagaki, Y.; Yasuda, H.; Morinaga, T.; Mitsuoka, S.; Higashio, K.

Agric. Biol. Chem. 55, 1225-1232, 1991

A/Title: Purification and characterization of tissue plasminogen activator secreted by h

A/Reference number: JT0562; NUID:91291340; PMID:1368681

A/Accession: JT0562

A/Molecule type: mRNA

A/Residues: 31-562 <LTA>

A/Cross-references: DBJL:D01096; NUID:9220128; PIDN:BAA00881.1; PID:G441174

A/Experimental source: embryonic lung fibroblast IMR-90 cells

R/Pennica, D.; Holmes, W.E.; Kohr, W.J.; Harkins, R.N.; Vehar, G.A.; Ward, C.A.; Bennett

Nature 301, 214-221, 1983

A/Title: Cloning and expression of human tissue-type plasminogen activator cDNA in Esche

A/Reference number: A93293; NUID:83115262; PMID:6337343

A/Accession: A93293

A/Molecule type: mRNA

A/Residues: 1-562 <PEN>

A/Cross-references: GB:L00141

A/Experimental source: melanoma cells

R/Sasaki, H.; Saito, Y.; Hayashi, M.; Otsuka, K.; Niwa, M.

Nucleic Acids Res. 15, 5695, 1988

A/Title: Nucleotide sequence of the tissue-type plasminogen activator cDNA from human fe

A/Reference number: S02125; NUID:85285279; PMID:3133640

A/Accession: S02125

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-562 <SAS>

A/Cross-references: EMBL:X07393; NUID:937243; PIDN:CAA30302.1; PID:G37244

A/Experimental source: fetal lung cells

R/Kagitani, H.; Tagawa, M.; Hatanaka, K.; Ikari, T.; Saito, A.; Bando, H.; Okada, K.; Ma

FEBS Lett. 189, 145-149, 1985

A/Title: Expression in Escherichia coli of finger-domain lacking tissue-type plasminogen

A/Reference number: A91343; NUID:85285620; PMID:3896853

A/Accession: A91343

A/Molecule type: mRNA

A/Residues: 1-38, 'G', 86-433, 'E', 435-562 <KAG>

A/Experimental source: Detroit 562 cells; ATCC 138

R/Edlund, T.; Ny, T.; Ranby, M.; Heden, L.O.; Palm, G.; Holmgren, E.; Josephson, S.

Proc. Natl. Acad. Sci. U.S.A. 80, 349-352, 1983

A/Title: Isolation of cDNA sequences coding for a part of human tissue plasminogen activ

A/Reference number: A93951; NUID:83169656; PMID:6572897

A/Accession: A93951

A/Molecule type: mRNA

A/Residues: 251-358 <BDL>

A/Experimental source: melanoma cells

R/Polh, G.; Kallstrom, M.; Bergsdorf, N.; Wallen, P.; Jornvall, H.

Biochemistry 23, 3701-3707, 1984

A/Title: Tissue plasminogen activator: peptide analyses confirm an indirectly derived am differences.

A/Reference number: A90488; NUID:85000468; PMID:6433976

A/Contents: annotation; melanoma cells, partial sequence of residues 36-562, active and I

R/Polh, G.; Kaplan, L.; Einarsson, M.; Wallen, P.; Jornvall, H.

FEBS Lett. 168, 29-32, 1984

A/Title: Differences between uterine and melanoma forms of tissue plasminogen activator.

A/Reference number: A91322; NUID:84158956; PMID:6538514

A/Accession: A91322

A/Molecule type: protein

A/Residues: 33-45; 311-320 <POH>

A/Experimental source: uterus

R/Van Zonneveld, A.J.; Veerman, H.; Pannekoek, H.

J. Biol. Chem. 261, 14214-14218, 1986

A/Reference number: A37567; NUID:87033611; PMID:3021732

A/Contents: annotation; fibrin binding site

R/Verheijen, J.H.; Caspers, M.P.M.; Chang, G.T.G.; de Munk, G.A.W.; Pouwels, P.H.; Enger

EXBO J. 5, 3525-3530, 1986

A/Title: Involvement of finger domain and kringle 2 domain of tissue-type plasminogen ac

A/Reference number: A37568; NUID:87161761; PMID:3030730

A/Contents: annotation; fibrin binding site

R/Dodd, I.; Nunn, B.; Robinson, J.H.

Thromb. Haemost. 59, 523-528, 1988

A/Title: Isolation, identification and pharmacokinetic properties of human tissue-type p

A/Reference number: A60902; NUID:89044681; PMID:3142086

A/Contents: annotation; novel forms of expressed recombinant t-PA

R/Harris, T.J.R.; Patel, T.; Maston, F.A.O.; Lattle, S.; Emtage, J.S.; Opdenakker, G.;

Mol. Biol. Med. 3, 279-292, 1986

A/Title: Cloning of cDNA coding for human tissue-type plasminogen activator and its expr

A/Reference number: A54645; NUID:86284200; PMID:3090401

A/Accession: A54645

A/Molecule type: mRNA

A/Residues: 1-562 <HAR>

A/Cross-references: GB:M5518; NUID:9190031; PIDN:AAA60111.1; PID:G190032

R/Reddy, V.B.; Garramone, A.J.; Sasaki, H.; Wei, C.

DNA 6, 461-472, 1987

A/Title: Expression of human uterine tissue-type plasminogen activator in mouse cells us

A/Reference number: I60110; NUID:88054470; PMID:2824147

A/Accession: I60110

A/Status: translated from GB/EMBL/DBDJ

A/Molecule type: mRNA

A/Residues: 1-562 <RES>

A/Cross-references: GB:M18182; NUID:9340176; PIDN:AAA36800.1; PID:G340177

R/Fisher, R.; Waller, E.K.; Grossi, G.; Thompson, D.; Tizard, R.; Schleuning, W.D.

J. Biol. Chem. 260, 11223-11230, 1985

A/Title: Isolation and characterization of the human tissue-type plasminogen activator s

A/Reference number: I55232; NUID:85289338; PMID:3161893

A/Accession: I55232

A/Status: preliminary; translated from GB/EMBL/DBDJ

A/Molecule type: DNA

A/Residues: 1-36 <RE2>

A/Cross-references: GB:M1890; NUID:9339837; PIDN:AAA61213.1; PID:G339839

C/Comment: Cleavage by plasmin or trypsin produces two chains held together by a single

F/1-23/Domain: signal sequence #status predicted <SIG>

F/24-32/Domain: propeptide #status predicted <PRO>

F/33-562/Product: t-plasminogen activator #status experimental <MAT>

F/31-310/Product: t-plasminogen activator chain A #status experimental <ACH>

F/41-78/Domain: fibronectin type I repeat homology <IFI>

F/86-119/Domain: EGF homology <EGF>

F/127-208/Domain: kringle homology <KR1>

F/215-296/Domain: kringle homology <KR2>

F:311-562/Product: t-plasminogen activator chain B #status experimental <BCH>
 F:311-556/Domain: trypsin homology <TRY>
 F:41-71,69-78,86-97,91-108,119-127-208,148-190,179-203,215-286,236-278,267-291,299-4
 F:152,483/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:219/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:310-311/Cleavage site: Arg-Ile (plasmin, trypsin) #status experimental
 F:357,405/Active site: His, Asp #status predicted
 F:513/Active site: Ser #status experimental

Query Match 40.8%; Score 226; DB 1; Length 562;
 Best Local Similarity 47.7%; Pred. No. 2.1e-16;
 Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCVEGNHFRYKASTDTMGRLCPWNSATVLQOYTHAHRSDALQGLGKHNCRPNDR 61
 126 TCYEQGISYRGTWTSTASGAECTWNSALAAQKPSRRPDATRLGLGNHNYCENPDRD 185

Db

QY 62 RRPWCYVQGLKPLVQECMVHDCADG 87
 186 SRPWCYVFKAGKYSFECSTPACSEG 211

Db

RESULT 13

JS0600
 t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
 N:Alternate names: tissue plasminogen activator
 C:Species: Desmodus rotundus (common vampire bat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: JS0600
 R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
 Gene 105, 229-237, 1991
 A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
 A:Reference number: JS0597; MUID:92039036; PMID:1937019
 A:Accession: JS0600
 A:Molecule type: mRNA
 A:Residues: 1-394 <KRA>
 A:Cross-references: GB:M63990; NID:q166078; PIDN:AAA31595.1; PID:G166079
 A>Note: the authors translated the codon ATC for residue 75 as Thr
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-394/Product: plasminogen activator gamma #status predicted <PLA>
 F:45-126/Domain: kringle homology <KEG>
 F:143-388/Domain: trypsin homology <TRY>
 F:45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bonds:
 F:142-143/Cleavage site: His-Ser (plasmin) #status predicted
 F:189,238,345/Active site: His, Asp, Ser #status predicted
 F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.7%; Score 220; DB 2; Length 394;
 Best Local Similarity 45.2%; Pred. No. 6.6e-16;
 Matches 38; Conservative 13; Mismatches 33; Indels 0; Gaps 0;

QY 2 TCVEGNHFRYKASTDTMGRLCPWNSATVLQOYTHAHRSDALQGLGKHNCRPNDR 61
 44 TCYEQGISYRGTWTSTASGAECTWNSALAAQKPSRRPDATRLGLGNHNYCENPDRD 103

Db

QY 62 RRPWCYVQGLKPLVQECMVHDCA 85
 104 SRPWCYVFKARKFTSESCVPVCS 127

Db

RESULT 14

A29941
 t-plasminogen activator (EC 3.4.21.68) precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A29941; S48205; S48207; S48206
 R:Rickles, R.J.; Darrow, A.L.; Strickland, S.
 J. Biol. Chem. 263, 1563-1569, 1988
 A:Title: Molecular cloning of complementary DNA to mouse tissue plasminogen activator m
 A:Reference number: A29941; MUID:88087303; PMID:2826484

A:Accession: A29941
 A:Molecule type: mRNA
 A:Residues: 1-559 <RIC>
 A:Cross-references: GB:J09520; NID:g202109; PIDN:AAA40470.1; PID:g202110
 R:Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
 Eur. J. Biochem. 224, 863-871, 1994
 A:Title: Characterization of the murine plasma fibrinolytic system.
 A:Reference number: S48202; MUID:95010076; PMID:7523120
 A:Accession: S48205
 A:Molecule type: protein
 A:Residues: 33-37, 'X', 39-40 <LIJ>
 A:Accession: S48207
 A:Molecule type: protein
 A:Residues: 309-316 <LI2>
 A:Accession: S48206
 A:Molecule type: protein
 A:Residues: 33-37, 'X', 39-40 <LIW>
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-17/Domain: signal sequence #status predicted <SIG>
 F:18-29/Domain: propeptide #status predicted <PRO>
 F:30-559/Product: t-plasminogen activator #status predicted <MAT>
 F:30-308/Product: t-plasminogen activator chain A #status predicted <ACH>
 F:38-75/Domain: fibronectin type I repeat homology <IFI>
 F:83-116/Domain: EGF homology <EGF>
 F:124-205/Domain: kringle homology <KR1>
 F:213-294/Domain: kringle homology <KR2>
 F:309-559/Product: t-plasminogen activator chain B #status predicted <BCH>
 F:309-553/Domain: trypsin homology <TRY>
 F:38-68,66-75,83-94,88-105,107-116,124-205,145-187,176-200,213-294,234-276,265-289,297-
 F:149,481/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:308-309/Cleavage site: Arg-Ile (plasmin, trypsin) #status predicted
 F:355,404,510/Active site: His, Asp, Ser #status predicted

Query Match 39.5%; Score 219; DB 1; Length 559;
 Best Local Similarity 46.0%; Pred. No. 1.2e-15;
 Matches 40; Conservative 11; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCVEGNHFRYKASTDTMGRLCPWNSATVLQOYTHAHRSDALQGLGKHNCRPNDR 61
 123 TCVEQGISYRGTWTSTASGAECTWNSALAAQKPSRRPDATRLGLGNHNYCENPDRD 182

Db

QY 62 RRPWCYVQGLKPLVQECMVHDCADGK 88
 183 LRWCYVFKAGKTTFCSTPACPKK 209

Db

RESULT 15

JS0597
 t-plasminogen activator (EC 3.4.21.68) alpha-1 precursor - common vampire bat
 N:Alternate names: tissue plasminogen activator
 C:Species: Desmodus rotundus (common vampire bat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: JS0597
 R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Do
 Gene 105, 229-237, 1991
 A:Title: The plasminogen activator family from the salivary gland of the vampire bat De
 A:Reference number: JS0597; MUID:92039036; PMID:1937019
 A:Accession: JS0597
 A:Molecule type: mRNA
 A:Residues: 1-477 <KRA>
 A:Cross-references: GB:M63987; NID:G166070; PIDN:AAA31591.1; PID:G166071
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:23-36/Domain: propeptide #status predicted <PRO>
 F:37-477/Product: plasminogen activator alpha-1 #status predicted <PLA>
 F:42-79/Domain: fibronectin type I repeat homology <IFA>
 F:87-120/Domain: EGF homology <EGF>
 F:128-209/Domain: kringle homology <KRG>
 F:226-471/Domain: trypsin homology <TRY>
 F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-
 F:153,398/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:225-226/Cleavage site: His, Ser (plasmin) #status predicted
F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 38.4%; Score 213; DB 2; Length 477;
Best Local Similarity 46.4%; Pred. No. 4.4e-15;
Matches 39; Conservative 10; Mismatches 35; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGPRCLPWNSTVLTQTYHAHRSDALQGLGKHNCRPNRR 61
DB 127 TCYEGGQVTVRGTWSTAESRVEICINWNSLLTRTYNGRMPDAFNGLGNHNYCRPNRGA 186

QY 62 RRPWCYVQGLKPLVQECMVHDC 85

DB 187 RRPWCYVVIKAGKPTSSCSFVCS 210

RESULT 16

JC5878

Plasma hyaluronan-binding protein precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 16-Jul-1999

C:Accession: JC5878

R:Hashimoto, K.; Tobe, T.; Sumiya, J.; Saguchi, K.; Sano, Y.; Nakano, Y.; Choi-Miura, N.

Biolog. Pharm. Bull. 20, 1127-1130, 1997

A:Title: Cloning of the cDNA for a mouse homologue of human PHBP: A novel hyaluronan-binding protein

A:Reference number: JC5878; MUID:98045239; PMID:9401717

A:Accession: JC5878

A:Molecule type: mRNA

A:Residues: 1-558 <HAS>

C:Comment: This protein acts as serine protease.

C:Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsin

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-311/Product: plasma hyaluronan-binding protein large chain #status predicted <MATL>

F:75-106/Domain: EGF homology <EG1>

F:113-145/Domain: EGF homology <EG2>

F:152-185/Domain: EGF homology <EG3>

F:192-274/Domain: kringle homology <KRI>

F:312-558/Product: plasma hyaluronan-binding protein small chain #status predicted <MATL>

F:312-548/Domain: trypsin homology <TRY>

Query Match 37.9%; Score 210; DB 2; Length 558;

Best Local Similarity 43.5%; Pred. No. 1.1e-14;

Matches 40; Conservative 14; Mismatches 34; Indels 4; Gaps 2;

QY 3 CYEGNGHFYRGKASTDTMGPRCLPWNSTVLTQTYHAHRSDALQGLGKHNCRPNRR 62
DB 192 CYVGDGYSYRGKSKVTNQNPCLYWNHLLQETYNMFEDAEHTGIAEHFNCRNPDGDH 251

QY 63 RRPWCYVQGLKPLVQECMVHDCADGKPS 93

DB 252 KPWCFVKVNSEKVKWEYCDVTVC---PVPDTP 280

RESULT 17

JC4795

Plasma hyaluronan-binding protein precursor - human

N:Alternate names: hepatocyte growth factor activator-like protein; PHBP

N:Contains: serine proteinase (EC 3.4.21.-)

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1995 #sequence_revision 16-Aug-1996 #text_change 19-Jul-2002

C:Accession: JC4795

R:Choi-Miura, N.H.; Tobe, T.; Sumiya, J.; Nakano, Y.; Sano, Y.; Mazda, T.; Tomita, M.

J. Biochem. 119, 1157-1165, 1996

A:Title: Purification and characterization of a novel hyaluronan-binding protein (PHBP)

x activator.

A:Reference number: JC4795; MUID:96425001; PMID:8827452

A:Accession: JC4795

A:Molecule type: mRNA

A:Residues: 1-560 <CHO>

A:Cross-references: GB:S83182; NID:g1836158; PIDN:AAB46909.1; PID:g1836159

A:Experimental source: plasma

A>Note: parts of this sequence, including the amino ends of the mature chains, were detected

C:Genetics:

A:Gene: GDB:HABP2; HABP; PHBP; HGFAL

A:Cross-references: GDB:4573962

C:Complex: a disulfide-bonded heterodimer of chains produced from the same precursor; the

C:Superfamily: plasma hyaluronan-binding protein; EGF homology; kringle homology; trypsin

C:Keywords: Chondroitin sulfate proteoglycan; glycoprotein; hyaluronic acid; hydrolase; }

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-311/Product: plasma hyaluronan-binding protein, 50K chain #status predicted <50K>

F:77-108/Domain: EGF homology <EG1>

F:115-147/Domain: EGF homology <EG2>

F:154-187/Domain: EGF homology <EG3>

F:194-276/Domain: kringle homology <KRI>

F:314-550/Domain: trypsin homology <TRY>

F:314-516/Product: plasma hyaluronan-binding protein, catalytic chain #status predicted

F:54, 207/Binding site: carboxylate (Asn) (covalent) #status predicted

F:77-88,82-97,99-108,115-125,120-136,138-147,154-165,159-176,178-187,194-276,215-257,246

F:77-82,405,509/Active site: His, Asp, Ser #status predicted

Query Match 36.0%; Score 199.5; DB 1; Length 560;

Best Local Similarity 40.2%; Pred. No. 1.4e-13;

Matches 39; Conservative 15; Mismatches 40; Indels 3; Gaps 2;

QY 3 CYEGNGHFYRGKASTDTMGPRCLPWNSTVLTQTYHAHRSDALQGLGKHNCRPNRR 62

DB 194 CYVGDGYSYRGKSKVTNQNPCLYWNHLLQETYNMFEDAEHTGIAEHFNCRNPD 253

QY 63 RRPWCYVQGLKPLVQECMVHDC--DGKKPSSPPEE 96

DB 254 KPWCFIKVTNDKVKWEYCDVSACSQAQVAYPEESPT 290

RESULT 18

A35005

N:Plasminogen activator (EC 3.4.21.73) precursor - chicken

N:Alternate names: uPA

C:Species: Gallus gallus (chicken)

C>Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 16-Jul-1999

C:Accession: A35005

J. Biol. Chem. 265, 1339-1344, 1990

A:Title: The chicken urokinase-type plasminogen activator gene.

A:Reference number: A35005; MUID:90110185; PMID:2295632

A:Accession: A35005

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-434 <LES>

A:Cross-references: GB:J05187; NID:g212858; PIDN:AAA49131.1; PID:g212859

C:Superfamily: urokinase-type plasminogen activator; EGF homology; kringle homology; trypsin

C:Keywords: glycoprotein; heterodimer; hydrolase; kringle; serine proteinase

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-171/Product: urokinase-type plasminogen activator chain A #status predicted <ACH>

F:40-71/Domain: EGF homology <EGF>

F:79-158/Domain: kringle homology <KRG>

F:173-428/Product: urokinase-type plasminogen activator chain B #status predicted <BCH>

F:173-416/Domain: trypsin homology <TRY>

F:162-296,202-218,210-285,310-379,342-358,369-397/Disulfide bonds: #status predicted

F:217,272,373/Active site: His, Asp, Ser #status predicted

Query Match 35.8%; Score 198.5; DB 1; Length 434;

Best Local Similarity 54.4%; Pred. No. 1.4e-13;

Matches 37; Conservative 7; Mismatches 19; Indels 5; Gaps 2;

QY 3 CYEGNGHFYRGKASTDTMGPRCLPWNSTVLTQTYHAHRSDALQGLGKHNCRPNRR 61

DB 79 CYSGNGDYRGNAEDP---GCLYWDHPSVIRMGDYHADLNKALQGLGKHNCRPNR 134

QY 62 RRPWCYVQ 69

DB 135 SRPWCYVK 142

RESULT 19

A4688

hepatocyte growth factor activator (EC 3.4.21.-) precursor [validated] - human

C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 25-Aug-1995 #text_change 08-Dec-2000
C;Accession: A46688
R;Wiyazawa, K.; Shimomura, T.; Kitamura, A.; Kondo, J.; Morimoto, Y.; Kitamura, N.
J. Biol. Chem. 268, 10024-10028, 1993
A;Title: Molecular cloning and sequence analysis of the cDNA for a human serine protease d coagulation factor XII.
A;Reference number: A46688; MUID:93252878; PMID:7683665
A;Accession: A46688
A;Molecule type: mRNA
A;Residues: 1-655 <NIV>
A;Cross-references: DDBJ:DL4012; NID:g219680; PID:BAA03113.1; PID:g219681
A;Experimental source: Liver (mRNA); serum (protein)
A;Note: sequence extracted from NCBI backbone (NCBIN:131227, NCBIIP:131228)
A;Note: parts of the sequence, including the amino ends of the heavy and light chains, c C;Genetics:
A;Gene: GDB:HGFAC; HGFA; HGFAP
A;Cross-references: GDB:9954514
A;Map position: 4p16-4p16
C;Function:
A;Description: activates hepatocyte growth factor by specific proteolytic cleavage
A;Pathway: tissue repair and regeneration
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Keywords: glycoprotein; hydrolase; kringles; liver; plasma; serine proteinase
F;1-34/Domain: signal sequence #status predicted <SIG>
F;108-148/Domain: fibronectin type II repeat homology <IF2>
F;164-197/Domain: EGF homology <EG1>
F;202-237/Domain: fibronectin type I repeat homology <IF1>
F;245-278/Domain: EGF homology <EG2>
F;286-367/Domain: kringles homology <KRG>
F;373-407/Product: hepatocyte growth factor activator light chain #status experimental
F;408-555/Product: hepatocyte growth factor activator heavy chain #status experimental
F;408-541/Domain: trypsin homology <TRY>
F;40-48,290,488,492,546/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;164-175,169-186,188-197,202-230,228-237,245-256,250-267,269-278,286-367,307-349,338-36 F;447,497,598/Active site: His, Asp, Ser #status predicted
Query Match 35.1%; Score 194.5; DB 1; Length 655;
Best Local Similarity 40.4%; Pred. No. 5.7e-13;
Matches 42; Conservative 8; Mismatches 41; Indels 13; Gaps 1;
QY 3 CYEGNGHFYRGKASTDMGRCLPWN SATVLOQTYHAHRS DALQGLGKHNYCRNPDRR 62
DB 286 CFLGNGTGYRGVASTASGLSCLAWNSDLLYQELHVDVSGAALLGLGPHAYCRNPDRNDE 345
QY 63 RPKCYVQVGLKPLVQSCVHDC-----ADGKKPSPP 93
DB 346 RPKCYVVKDSALSWECRIEACSLTRVQLSPDLLATLPEPASP 389
RESULT 20
coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)
N;Alternate names: Hageman factor
C;Species: Cavia porcellus (guinea pig)
C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C;Accession: S28941
R;Semba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambata, T.; Okabe, H. Biochim. Biophys. Acta 1159, 113-121, 1992
A;Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage si A;Reference number: S28941; MUID:93003367; PMID:1390917
A;Accession: S28941
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-603 <SEM>
A;Cross-references: EMBL:X68615; NID:g49578; PIDN:CAA48600.1; PID:g49579
C;Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology;
C;Keywords: hydrolase; serine proteinase
F;46-87/Domain: fibronectin type II repeat homology <IF2>
F;134-169/Domain: fibronectin type I repeat homology <FBI>
F;177-208/Domain: EGF homology <EGF>
F;216-294/Domain: kringles homology <KRG>
F;359-597/Domain: trypsin homology <TRY>

Query Match 34.6%; Score 191.5; DB 2; Length 603;
Best Local Similarity 39.6%; Pred. No. 1.1e-12;
Matches 38; Conservative 15; Mismatches 38; Indels 5; Gaps 2;
QY 2 TCYEGNGHFYRGKASTDMGRCLPWN SATVLOQTYHAHRS DALQGLGKHNYCRNPDRN 60
DB 215 SCYEGRGVSYRGWARTVSGAKQCRWAS----BATYRNMTAEQALRRGLGHTFCRNPDRN 270
QY 61 RRPWCYVQVGLKPLVQSCVHDCADGKKPSPP 96
DB 271 DTRWCYVWGNRLSWECYDLAQCCQYPPQPTATPHD 306
RESULT 21
coagulation factor XIIa (EC 3.4.21.38) precursor [validated] - human
N;Alternate names: Hageman factor (activated)
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1985 #sequence_revision 30-Jun-1991 #text_change 08-Dec-2000
C;Accession: A29411; A26814; A00930; A25191; A22248; A21037
R;Cool, D.E.; MacGillivray, R.T.A.
J. Biol. Chem. 262, 13662-13673, 1987
A;Title: Characterization of the human blood coagulation factor XII gene. Intron/exon 9 A;Reference number: A29411; MUID:88007593; PMID:2888762
A;Accession: A29411
A;Molecule type: DNA
A;Residues: 1-615 <COO>
A;Cross-references: GB:M17466; GB:J02807; NID:gl80355; PIDN:AAB59490.1; PID:gl80357
R;Tripodis, M.; Citarella, F.; Guida, S.; Galeffi, P.; Fantoni, A.; Cortese, R. Nucleic Acids Res. 14, 3146, 1986
A;Title: cDNA sequence coding for human coagulation factor XII (Hageman).
A;Reference number: A26814; MUID:86176794; PMID:3754331
A;Accession: A26814
A;Molecule type: mRNA
A;Residues: 4-615 <TRI>
A;Cross-references: GB:M31315; NID:gl82291; PIDN:AAA70225.1; PID:gl82292
R;Cool, D.E.; Edgell, C.J.S.; Louie, G.V.; Zoller, M.J.; Brayer, G.D.; MacGillivray, R. J. Biol. Chem. 260, 13666-13675, 1985
A;Title: Characterization of human blood coagulation factor XII cDNA. Prediction of the A;Reference number: A00930; MUID:86033830; PMID:3877053
A;Accession: A00930
A;Molecule type: mRNA
A;Residues: 14-332, 'S', 334-615 <CO2>
R;Que, B.G.; Davis, E.W. Biochemistry 25, 1523-1528, 1986
A;Title: Characterization of a cDNA coding for human factor XII (Hageman factor).
A;Reference number: A25191; MUID:86216049; PMID:3011063
A;Accession: A25191
A;Molecule type: mRNA
A;Residues: 146-378, 'G', 380-615 <QUE>
A;Cross-references: GB:M3147; NID:gl80360; PIDN:AAA70224.1; PID:gl80361
R;McMullen, B.A.; Fujikawa, K. J. Biol. Chem. 260, 5328-5341, 1985
A;Title: Amino acid sequence of the heavy chain of human alpha-factor XIIa (activated H A;Reference number: A22248; MUID:85182674; PMID:3886654
A;Accession: A22248
A;Molecule type: protein
A;Residues: 20-379 <WCM>
R;Fujikawa, K.; McMullen, B.A. J. Biol. Chem. 258, 10924-10933, 1983
A;Title: Amino acid sequence of human beta-factor XIIa.
A;Reference number: A21037; MUID:83291041; PMID:6604055
A;Accession: A21037
A;Molecule type: protein
A;Residues: 354-362; 373-615 <FUJ>
R;Harris, R.J.; Lang, V.T.; Spellman, M.W. J. Biol. Chem. 267, 5102-5107, 1992
A;Title: O-linked fucose is present in the first epidermal growth factor domain of fact A;Reference number: A44606; MUID:92184750; PMID:1544894
A;Contents: annotation; carbohydrate binding site
C;Genetics:

A>Status: preliminary

A:Molecule type: protein
A:Residues: 1-120 <SCH>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog
C:Keywords: hydrolase; serine proteinase
F:37-114/Domain: kringle homology <KR4>

Query Match 28.2%; Score 156; DB 2; Length 120;
Best Local Similarity 39.6%; Pred. No. 1.5e-09;
Matches 36; Conservative 7; Mismatches 30; Indels 18; Gaps 5;

Qy 3 CYEGNGHFYRGKASTDGMGRPCLPWNSATVLQQTYHAHRSDAL-----QLGLGKHNYCRN 57
 ||||| :||||
Db 37 CYHENGGSYRGTSTTITGRKCQSWSMT-----PHRHEKTPEHPPEAGL-TNNYCEN 88
 ||||| :||||

Qy 58 PDNRPRWCYVQGKLPLV--QCWVHDCA 86
 ||||| :||||
Db 89 PDADSKPCYT---TDPSVRWEFCNLRLCKLD 116
 ||||| :||||

RESULT 25

S45281
coagulation factor XIIa (EC 3.4.21.38) precursor - bovine (fragment)
N/Alternate names: Hageman factor (activated)
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Apr-1995 #sequence_revision 22-Apr-1995 #text_change 21-Jan-2000
C/Accession: S45281; A61329
R/Shibuya, Y.; Senba, U.; Okabe, H.; Kambara, T.; Yamamoto, T.
Biochim. Biophys. Acta 1206, 63-70, 1994
A>Title: Primary structure of bovine Hageman factor (blood coagulation factor XII): comparison with human factor XII
A:Reference number: S45281; MUID:94242782; PMID:8186251
A:Accession: S45281
A:Molecule type: mRNA
A:Residues: 1-593 <SHT>
A/Cross-references: CB:S70164
A/Note: The authors translated the codon GAG for residue 23 as Val, GAG for residue 70 as Phe, and ATC for residue 203 as Phe, GTG for residue 247 as Leu, CCG for residue 286 as Gly.
R/Fujikawa, K.; Walsh, K.A.; Davie, E.W.
Biochemistry 16, 2270-2278, 1977
A>Title: Isolation and characterization of bovine factor XII (Hageman factor).
A:Reference number: A61329; MUID:77182112; PMID:861210
A:Accession: A61329
A:Molecule type: protein
A:Residues: 10-16,'X',18-19;525-550 <FUJ>
C/Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homology
C:Keywords: blood coagulation; fibrinolysis; glycoprotein; hydrolyase; monomer; plasma;
F:37-78/Domain: fibronectin type II repeat homology <IIF2>
F:88-120/Domain: EGF homology <EGF>
F:125-160/Domain: fibronectin type I repeat homology <FB1>
F:207-287/Domain: kringle homology <KR>
F:350-587/Domain: trypsin homology <TRY>
F:541/Active site: Ser #status predicted

Query Match 28.1%; Score 155.5; DB 2; Length 593;
Best Local Similarity 38.4%; Pred. No. 7.7e-09;
Matches 33; Conservative 9; Mismatches 37; Indels 7; Gaps 3;

Qy 2 TCYE-GNGHYFRGKASDTDMGRPCLPWNSATVLQQTY-HAIRSDALQLGKHKNYCRNP 58
 ||||| :||||
Db 206 SCYDDRORGLSYRGWGAGTTLSGAQCQSWAS----EATYWNVTAEQVLNKGLEDHAFCRNP 261
 ||||| :||||

Qy 59 DNRPRWCYVQGKLPLVQCWVHDCA 84
 ||||| :||||
Db 262 DNDRPWCFIWKGDRLSNMYCRLAPC 287
 ||||| :||||

RESULT 26

A60140
plasmin (EC 3.4.21.7) precursor - chicken (fragment)
N/Alternate names: plasminogen
C/Species: Gallus gallus (chicken)
C/Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text change 16-Jul-1999


```
QY 60 NRREPWCYVQVGLKPLV--QECMVHDCADGKK--PSSP 93
Db 438 ADKSPWCYT---TDPVRWFEFNLKCKSETPQVPAAP 472

RESULT 29
C61545
Plasmin (EC 3.4.21.7) precursor - goat (fragments)
N/Alternate names: plasminogen
C/Species: Capra aegagrus hircus (domestic goat)
C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 12-May-1995
C/Accession: C61545
R/Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A/Title: Structural aspects of the plasminogen of various species.
A/Reference number: A61545; MUID:89005015; PMID:3168975
A/Accession: C61545
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-123<SCH>
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: hydrolase; serine proteinase
F;4-118/Domain: kringle homology <KR4>

Query Match 27.1%; Score 150; DB 2; Length 123;
Best Local Similarity 37.5%; Pred. No. 6.7e-09;
Matches 33; Conservative 12; Mismatches 31; Indels 12; Gaps 4;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWSATV--LQOYTHAHRSDALQGLGKKNYCRNPD 60
Db 41 CYHNGQSTYGTSTTTGKQCSWSSMPHRRHQKTPESYNAGLTM-----NYCRNPD 95

QY 61 RREPWCYVQVGLKPLV--QECMVHDCAD 86
Db 96 DKSEWCYT---TDPVRWFEFNLKCKSE 120

RESULT 30
A40522
Plasmin (EC 3.4.21.7) precursor - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Feb-1992 #sequence_revision 17-Apr-1993 #text_change 16-Jul-1999
C/Accession: A40522
R/Kanalias J.J.; Makker, S.P.
J. Biol. Chem. 266, 10825-10829, 1991
A/Title: Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor
A/Reference number: A40522; MUID:91250378; PMID:1645711
A/Accession: A40522
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-169<KAN>
A/Cross-references: GB:M62832; NID:G206215; PIDN:AAA1884.1; PID:9554488
A/Note: the authors translated the codon TCT for residue 76 as Ala
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: fibrinolysis; kringle homology; hydrolase; kringle; serine proteinase
F;34-112,55-95,83-107/Disulfide bonds: #status predicted

Query Match 27.1%; Score 150; DB 2; Length 169;
Best Local Similarity 34.3%; Pred. No. 9.1e-09;
Matches 37; Conservative 14; Mismatches 31; Indels 26; Gaps 7;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQL---GLGKKNYCRNPD 59
Db 34 CYOENGKSYRGTSITNTGKCSWSS-----VSNTPSHSKTPTANFPDSSL-ENNYCRNPD 87

QY 60 NRRPWCYVQVGLKPLV--QECMVHDCAD-----GKKPSP 93
Db 88 NDORGPMCF---TDPVRWFEFNLKRCSETGGVAESAIVPOVPSAP 132

RESULT 31
```

```
B30848
Plasmin (EC 3.4.21.7) precursor - rhesus macaque
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 22-Jun-1999
C/Accession: B32869; B30848
R/Tomlinson, J.E.; McLean, J.W.; Lawn, R.M.
J. Biol. Chem. 264, 5957-5965, 1989
A/Title: Rhesus monkey apolipoprotein(a). Sequence, evolution, and sites of synthesis.
A/Reference number: A32869; MUID:89174660; PMID:2925643
A/Accession: B32869
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-810<TOM>
A/Cross-references: GB:J04697; NID:G342272; PIDN:AAA36901.1; PID:G342273
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-9/Domain: signal sequence #status predicted <SIG>
F;103-181/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;581-803/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,3
bonds: #status predicted
F;622,665,760/Active site: His, Asp, Ser #status predicted

Query Match 26.9%; Score 149; DB 2; Length 810;
Best Local Similarity 36.4%; Pred. No. 5.2e-08;
Matches 36; Conservative 12; Mismatches 35; Indels 16; Gaps 6;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHR---SDALQGLGKKNYCRNPD 59
Db 377 CYHGDGQSYRGTSITTTGKQCSWSS-----MTPWHKTEPTENFNAGL-TWNYCRNPD 430

QY 60 NRREPWCYVQVGLKPLV--QECMVHDCAD--DGKKPSP 94
Db 431 ADKGPWCFT---TDPVRWFEFNLKCKSETGSGVAAPPP 466

RESULT 32
A47136
macrophage-stimulating protein 1 precursor - human
C/Species: Homo sapiens (man)
C/Date: 03-May-1994 #sequence_revision 14-Nov-1997 #text_change 18-Jun-1999
C/Accession: A40331; B40331; A47136; A61395
R/Han, S.; Stuart, L.A.; Degen, S.J.F.
Biochemistry 30, 9768-9780, 1991
A/Title: Characterization of the DNFI5S2 locus on human chromosome 3: identification of
A/Reference number: A40331; MUID:92002016; PMID:1655021
A/Accession: A40331
A/Molecule type: DNA
A/Residues: 1-711<HAL>
A/Cross-references: GB:M74179
A/Accession: B40331
A/Molecule type: mRNA
A/Residues: 1-711<HA2>
A/Cross-references: GB:M74178; NID:G183976; PIDN:AAA50165.1; PID:G183977
R/Yoshimura, T.; Tuhki, N.; Wang, M.H.; Skeel, A.; Leonard, E.J.
J. Biol. Chem. 268, 15461-15468, 1993
A/Title: Cloning, sequencing, and expression of human macrophage stimulating protein (M
A/Reference number: A47136; MUID:93340141; PMID:8393443
A/Accession: A47136
A/Molecule type: mRNA
A/Residues: 1-12, 'C', 14-622, 'F', 624-711<YOS>
A/Cross-references: GB:J11924; NID:G9398037; PIDN:AAA59872.1; PID:G9398039
A/Note: authors translated the codon TTT for residue 623 as leu; parts of this sequence
R/Skeel, A.; Yoshimura, T.; Showalter, S.D.; Tanaka, S.; Appella, E.; Leonard, E.J.
J. Exp. Med. 173, 1227-1234, 1991
A/Title: Macrophage stimulating protein: purification, partial amino acid sequence, and
A/Reference number: A61395; MUID:91217635; PMID:1827141
A/Accession: A61395
```

```

RESULT 34
PLPG
plasmin (EC 3.4.21.7) precursor - pig (fragment)
N/Alternate names: plasminogen
N/Contains: miniplasminogen
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 07-Sep-1990 #sequence revision 01-Nov-1996 #text_change 18-Jul-1997
C/Accession: S03733; S03737; A25834
R/Schaller, J.; Marti, T.; Roeseleat, S.J.; Kaempfer, U.; Rickli, E.E.
Fibrinolysis 1, 91-102, 1987
A/Rittle: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the ca
A/Reference number: S03733
A/Accession: S03733
A/Molecule type: Protein
A/Residues: 1-560 <SCH>
R/Brunisholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.;
Eur. J. Biochem. 114, 465-470, 1981
A/Rittle: Comparison of the primary structure of the N-terminal CNBR fragments of human, i
A/Reference number: S03735; MUID:81212097; PMID:7238497
A/Accession: S03737
A/Molecule type: Protein
A/Residues: 1-57 <BRU>
R/Marti, T.; Schaller, J.; Rickli, E.E.
Eur. J. Biochem. 149, 279-285, 1985
A/Rittle: Determination of the complete amino-acid sequence of porcine miniplasminogen.
A/Reference number: A25834; MUID:85203907; PMID:3846533
A/Accession: A25834
A/Molecule type: Protein
A/Residues: 450-790 <MAR>
C/Function:
A/Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the walls of the Graafian follicle; also activates the urokinase-type plasminogen act
A/Pathway: fibrinolysis
C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C/Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma; serine prote
F/1-790/Product: plasminogen #status predicted <PRO>
F/1-77/Domain: plasminogen-related protein precursor homology (fragment) <PLPH>
F/78-560/Product: plasmin chain A #status predicted <APT>
F/84-162/Domain: kringle homology <KR1>
F/166-243/Domain: kringle homology <KR2>
F/256-333/Domain: kringle homology <KR3>
F/358-435/Domain: kringle homology <KR4>
F/450-790/Product: miniplasminogen #status experimental <MIN>
F/461-540/Domain: kringle homology <KR5>
F/561-790/Product: plasmin chain B #status experimental <BCH>
F/561-783/Domain: trypsin homology <TRY>
F/30-54, 34-42, 84-162, 105-145, 133-157, 166-243, 169-297, 187-226, 215-238, 256-333, 277-316, 305
bonds: #status predicted
F/602,645,740/Active site: His, Asp, Ser #status predicted

Query Match 26.7%; Score 148; DB 1; Length 790;
Best Local Similarity 38.2%; Pred. No. 6.4e-08;
Matches 34; Conservative 8; Mismatches 33; Indels 14; Gaps 5;

QY 3 CYEGNGHFVRGKASDTWGPPCLPWN SATVLOOTYHAHR---SDALQLGLGKHNYCRNPD 59
Db 358 CYRNGESYRGSSSTITGRKQSW-----VSMTPHRHKTPGNFPNAGL-TMNYCRNPD 411
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
QY 60 NRRRPWCYVQVGLKPLV--QECWHDCA 86
Db 412 ADKSPWCYT---TDRVRWEYCNLKKCE 437
: ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||

RESULT 35
A40332
N/Alternate names: hepatocyte growth factor-like protein
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1999
C/Accession: A40332; B40332
R/Begen, S.J.F.; Stuart, L.A.; Han, S.; Jamison, C.S.
Biochemistry 30, 9781-9791, 1991

```

A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth factor
A;Reference number: A40332; MUID:92002017; PMID:1832957
A;Accession: A40332
A;Molecule type: DNA
A;Residues: 1-716 <DEG>
A;Cross-references: GB:M74180; NID:gl93831; PIDN:AAA50166.1; PID:gl93832
A;Accession: B40332
A;Molecule type: mRNA
A;Residues: 1-18,'P',20-716 <DEG2>
A;Cross-references: GB:M74181; NID:gl93833; PIDN:AAA50167.1; PID:gl93834
C;Genetics:
A;Introns: 18/1; 67/2; 105/1; 143/2; 189/1; 229/2; 269/1; 334/2; 378/1; 412/2; 458/1; 47
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: duplication; glycoprotein; growth factor; kringle
F;1-31/Domain: signal sequence #status predicted <SIG>
F;19-488,489-716/Product: macrophage-stimulating protein 1 #status experimental <MAT>
F;19-483/Domain: alpha chain #status experimental <ACH>
F;110-186/Domain: kringle homology <XR1>
F;121-268/Domain: kringle homology <XR2>
F;292-370/Domain: kringle homology <XR3>
F;379-457/Domain: kringle homology <XR4>
F;484-711/Domain: beta chain #status experimental <BCH>
F;489-709/Domain: trypsin homology <TRY>
F;72,173,305,620/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 26.6%; Score 147.5; DB 1; Length 716;
Best Local Similarity 36.5%; Pred. No. 6.6e-08;
Matches 38; Conservative 11; Mismatches 34; Indels 21; Gaps 7;
CY 3 CYEGNGHFYRGKASTDTMGRPCLPWN SATVLOQTYHAHRSDALQLGLGKKNYCRN 57
DB 379 CYHSGSEQYRGVSVKTRKGVCQCHWSET-----PHKPPQPTTSAPQAGL-EANFCRN 430
CY 58 PD-NRRPWCYVQVGLKP--LVQECMVHDCADGKKPS--SPPEE 96
DB 431 PDGDSHGPPWCYT---LDPDILFYCALQRCDDQDPESILDPDPQ 471
RESULT 36
B45082
neurotrophic receptor ror2 precursor - human
N;Contents: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C;Accession: B45082
R;Maslakowski, P.; Carroll, R.D.
J. Biol. Chem. 267, 26181-26190, 1992
A;Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
A;Reference number: A45082; MUID:93100347; PMID:1334494
A;Accession: B45082
A;Molecule type: mRNA
A;Residues: 1-943 <MAS>
A;Cross-references: GB:M97639; NID:G337466; PIDN:AAA60276.1; PID:G337467
A;Note: sequence extracted from NCBI backbone (NCBIP:120918)
C;Genetics:
A;Gene: GDB:NTRK2
A;Cross-references: GDB:I136454
A;Map position: 6p21-6p21
C;Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringle homology; pro
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-937/Product: neurotrophic receptor ror2 #status predicted <MAT>
F;76-137/Domain: immunoglobulin homology <INM>
F;316-394/Domain: kringle homology <KRG>
F;412-428/Domain: transmembrane #status predicted <TMN>
F;471-753/Domain: protein kinase homology <KIN>
F;479-487/Region: protein kinase ATP-binding motif
F;70,188,318/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 26.6%; Score 147.5; DB 2; Length 943;
Best Local Similarity 39.3%; Pred. No. 8.6e-08;
Matches 33; Conservative 10; Mismatches 36; Indels 5; Gaps 4;

QY 3 CYEGNGHFYRGKASTDTMGRPCLPWN SATVLOQTYHAHRSDALQLGLGKKNYCRNPNRR 62
DB 316 CYNGSGVDYRGTAATTSKSGHCQCPW--ALQPHSHLSSTDFELG--GGHAYCENPGQOM 372
QY 63 R-PWCYVQVGLKPLVQECMVHDC 85
DB 373 EGPMCFCTQ-NKNVAMELCDFVSCS 395
RESULT 37
PLHU
plasmin (EC 3.4.21.7) precursor [validated] - human
N;Alternate names: plasminogen precursor [misnomer]
N;Contents: angiotatin; microplasmin; plasminogen
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1994 #sequence_revision 02-Dec-1994 #text_change 15-Sep-2000
C;Accession: A35229; ID:2242; K26646; I62738; I84609; S03735; A00929; A04627; A04625; A0
R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.
J. Biol. Chem. 265, 6104-6111, 1990
A;Title: Characterization of the gene for human plasminogen, a key proenzyme in the fib
A;Reference number: A35229; MUID:90202879; PMID:2318848
A;Accession: A35229
A;Molecule type: DNA
A;Residues: 1-810 <PET>
A;Cross-references: GB:J05286; GB:M34276; NID:gl90064; PIDN:AAA60113.1; PID:G387026
A;Experimental source: leukocyte; lung fibroblast
R;Margaretta, N.; Bruno, L.; Pontoglio, M.; Candiani, G.; Meroni, G.; Ottolenghi, S.; T
Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990
A;Title: Definition of the transcription initiation site of human plasminogen gene in 1
A;Reference number: I52242; MUID:91097523; PMID:2268308
A;Accession: I52242
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-16 <MAL1>
A;Cross-references: GB:M62890; NID:gl90092; PIDN:AAA36454.1; PID:G553613
R;Forsgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.
FEBS Lett. 213, 254-260, 1987
A;Title: Molecular cloning and characterization of a full-length cDNA clone for human p
A;Reference number: A26646; MUID:87162490; PMID:3030813
A;Accession: A26646
A;Molecule type: mRNA
A;Residues: 1-471,'D',473-810 <FOR>
A;Cross-references: GB:X05199; NID:G35530; PIDN:CAA28831.1; PID:G35531
A;Experimental source: liver
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:85023311; PMID:6148961
A;Accession: I62738
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 292-471,'D',473-810 <MAL2>
A;Cross-references: GB:K02922; NID:gl90112; PIDN:AAA60124.1; PID:G387031
A;Accession: I84609
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 367-419 <MAL3>
A;Cross-references: GB:K02921; NID:gl90110; PIDN:AAA60123.1; PID:gl90111
R;Brühnholz, R.A.; Lerch, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.
Eur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBR fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
A;Molecule type: protein
A;Residues: 20-71,'E',73-76 <BRU>
R;Søtrup-Jensen, L.; Petersen, T.E.; Magnusson, S.
submitted to the Atlas, July 1977
A;Reference number: A00929
A;Accession: A00929
A;Molecule type: Protein
A;Residues: 20-71,'E',73-85,87-106,'D',108-360,'E',362-810 <SOT>
R;Wiman, B.

Eur. J. Biochem. 76, 129-137, 1977
 A>Title: Primary structure of the B-chain of human plasmin.
 A:Reference number: A04627; PMID:7722545; PMID:142009
 A:Accession: A04627
 A:Molecule type: protein
 A:Residues: 581-810 <W11>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 50, 489-494, 1975
 A>Title: Structural relationship between "glutamic acid" and "lysine" forms of human plasminogen fragment from human plasminogen the
 A:Reference number: A04625; PMID:75093329; PMID:122932
 A:Accession: A04625
 A:Molecule type: protein
 A:Residues: 20-50,'Q',51-71,'E',73-85,87-100 <W12>
 R:Wiman, B.; Wallen, P.
 Eur. J. Biochem. 58, 539-547, 1975
 A>Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen the
 A:Reference number: A04626; PMID:76043692; PMID:126853
 A:Accession: A04626
 A:Molecule type: protein
 A:Residues: 483-507,'E',509-604 <W13>
 R:Robbins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
 J. Biol. Chem. 248, 1631-1633, 1973
 A>Title: The primary structure of human plasminogen. II. The histidine loop of human plasminogen
 A:Reference number: A92125; PMID:73149248; PMID:4694729
 A:Contents: annotation, active site
 R:Groskopf, W.R.; Summaria, L.; Robbins, K.C.
 J. Biol. Chem. 244, 3530-3597, 1969
 A>Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
 A:Reference number: A93048; PMID:69234739; PMID:4240117
 A:Contents: annotation, active site
 R:Trexler, M.; Vally, Z.; Pattach, L.
 J. Biol. Chem. 257, 7401-7406, 1982
 A>Title: Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen.
 A:Reference number: A93382; PMID:82213905; PMID:6919539
 A:Contents: annotation; omega-aminocarboxylic acid binding sites
 R:Vally, Z.; Pattach, L.
 J. Biol. Chem. 259, 13690-13694, 1984
 A>Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
 A:Reference number: A93458; PMID:85054794; PMID:6094526
 A:Contents: annotation; fibrin binding site; omega-aminocarboxylic acid binding site
 R:Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehndel, S.; McCance, S.G.;
 J. Biol. Chem. 271, 29461-29467, 1996
 A>Title: Kringle domains of human angiostatin. Characterization of the anti-proliferative
 A:Reference number: A58811; PMID:97067211; PMID:8910613
 A:Contents: annotation
 R:Liijnen, H.R.; Ugwu, F.; Bini, A.; Collen, D.
 Biochemistry 37, 4699-4702, 1998
 A>Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1 (M)
 A:Reference number: A58812; PMID:9548733; PMID:9548733
 A:Contents: annotation
 R:Tulinsky, A.; Mulichak, A.M.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51341; PDB:1PK4
 A:Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
 R:Tulinsky, A.; Wu, T.P.
 submitted to the Brookhaven Protein Data Bank, July 1991
 A:Reference number: A51488; PDB:3PK4
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
 R:Wu, T.P.; Tulinsky, A.
 submitted to the Brookhaven Protein Data Bank, August 1993
 A:Reference number: A51911; PDB:1PKR
 A:Contents: annotation; X-ray crystallography, 2.48 angstroms, residues 102-181
 R:Padmanabhan, K.; Tulinsky, A.
 submitted to the Brookhaven Protein Data Bank, April 1994
 A:Reference number: A52408; PDB:1PMK
 A:Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
 R:Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995
 A:Reference number: A63244; PDB:1CEA
 A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
 R:Tulinsky, A.; Mathews, I.I.
 submitted to the Brookhaven Protein Data Bank, December 1995

A:Reference number: A65245; PDB:1L2B
A:Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R:Mulichak, A.M.; Tulinsky, A.; Ravichandran, K.G.
A:Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 Å
A:Reference number: A58819; MUID:92031502; PMID:1657148
A:Contents: annotation
R:Wu, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
A:Title: The refined structure of the epsilon-aminocaproic acid complex of human plasminogen kringle 4
A:Reference number: A58818; MUID:92031503; PMID:1657149
A:Contents: annotation
R:De Vos, A.M.; Utsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrock, M.J.
A:Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.4 Å
A:Reference number: A39463; MUID:92111803; PMID:1310033
A:Contents: annotation; X-ray crystallography, 2.4 angstroms
R:Stec, B.; Teser, M.M.; Whitlow, W.; Yamano, A.
A:Title: Submitted to the Brookhaven Protein Data Bank, June 1995
A:Reference number: A65980; PDB:1KRN
R:Rejante, M.; Llinas, M.
A:Title: Submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65803; PDB:1HPJ
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejante, M.; Llinas, M.
A:Title: Submitted to the Brookhaven Protein Data Bank, August 1996
A:Reference number: A65804; PDB:1HPK
A:Contents: annotation; conformation by (1)H-NMR, residues 103-181
R:Rejante, M.R.; Llinas, M.
A:Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A:Reference number: S43645; MUID:94237157; PMID:8181475
A:Contents: annotation; conformation by (1)H-NMR, residues 96-184
R:Rejante, M.R.; Llinas, M.
A:Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasminogen kringle 1.
A:Reference number: A58817; MUID:94237158; PMID:8181476
A:Contents: annotation; conformation by (1)H-NMR
C:Comment: Plasminogen is synthesized by the kidney and is present in plasma and many other body fluids.
C:Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU and PIR:FGUHG).
C:Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately after release from fibrin clots.
C:Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial conditions.
C:Comment: Streptolysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. Toxic solid tumors.
C:Genetics:
A:Gene: GDB:PLG
A:Cross-references: GDB:119498; OMIM:173350
A:Map position: 6q26-q27
A:Introns: 17/1; 62/2; 98/1; 136/2; 193/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529/1
C:function:
A:description: dissolves the fibrin of blood clots; acts as a proteolytic factor in various tissues; also activates the urokinase-type plasminogen activator.
A:pathway: fibrinolysis
A:superfamily: plasmin;
C:keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hydrolysis; plasminogen-related protein precursor homology <PLPH>
F1-19/Domain: signal sequence #status predicted <SIG>
F20-810/Product: plasminogen #status experimental <PRO>
F20-96/Domain: activation peptide #status experimental <APT>
F179-466/Product: angiostatin #status experimental <AST>
F197-550,581-810/Product: plasmin #status experimental <MAT>
F197-580/Domain: plasmin chain A #status experimental <CHA>
F103-181/Domain: kringle homology <KR1>
F185-262/Domain: kringle homology <KR2>
F275-352/Domain: kringle homology <KR3>
F377-454/Domain: kringle homology <KR4>
F481-560/Domain: kringle homology <KR5>
F550-580,581-810/Product: microplasmin #status experimental <MMT>

Query Match 26.4%; Score 146.5; DB 1; Length 810;

Query Match 26.4%; Score 146.5; D3 1; Length 810;

Best Local Similarity 37.4%; Pred. No. 9.5e-08;
Matches 37; Conservative 13; Mismatches 32; Indels 17; Gaps 7;
QY 3 CYEENGHFRYRGKASTDTMGRCPLPWSATVLOQTYHAHRS--SDALQLGLGKHNYCRNPD 59
Db 377 CYHGDSQSYRGTSSTTTTCKKQSHSS-----WTPRHQKTPENYNAGL-TMNYCRNPD 430
QY 60 NRRRPWCYVQVGLKPLV--QECVHDCADGKKPS--SPP 94
Db 431 ADKGPWCFT---TDPVRWEYCNLKCS-GTEASVVAPP 465
RESULT 38
A45082
neurotrophic receptor ror1 precursor - human
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 19-May-2000
C;Accession: A45082
R;Maslakowski, P.; Carroll, R.D.
J. Biol. Chem. 267, 26181-26190, 1992
A;Title: A novel family of cell surface receptors with tyrosine kinase-like domain.
A;Reference number: A45082; MUID:93100347; PMID:1334494
A;Accession: A45082
A;Molecule type: mRNA
A;Residues: 1-937 <MAS>
A;Cross-references: GB:M97675; NID:G337464; PIDN:AAA50275.1; PID:G337465
A;Note: sequence extracted from NCBI backbone (NCBIP:120916)
C;Genetics:
A;Gene: GDB:NTRKX1
A;Cross-references: GDB:136453
A;Map position: 6p21-6p21
C;Superfamily: neurotrophic receptor ror; immunoglobulin homology; kringle homology; pro
C;Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyros
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-937/Product: neurotrophic receptor ror1 #status predicted <MAT>
F;72-133/Domain: immunoglobulin homology <IMM>
F;313-391/Domain: kringle homology <KRG>
F;404-425/Domain: transmembrane #status predicted <TM1>
F;471-753/Domain: protein kinase homology <KIN>
F;47,66,184,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 26.4%; Score 146; DB 2; Length 937;
Best Local Similarity 44.1%; Pred. No. 1.2e-07;
Matches 30; Conservative 5; Mismatches 25; Indels 8; Gaps 3;
QY 3 CYEENGHFRYRGKASTDTMGRCPLPWSATVLOQTYHAHRS--SDALQLG--LGKHNYCRNPD 60
Db 313 CYNSTGVDYRGTVSVTKSGRCQCPWNS-----QYPHTHTFTALRPPELNGHSHYCNPCN 367
QY 61 RRR-PMCY 67
Db 368 QKEAPWCF 375
RESULT 39
T18840
hypothetical protein CO1G6.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T18840
R;Barks, M.
submitted to the EMBL Data Library, August 1994
A;Reference number: Z19029
A;Accession: T18840
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-806 <WIL>
A;Cross-references: EMBL:Z35595; PIDN:CAA84639.1; GSPDB:GN00020; CESP:CO1G6.8
A;Experimental source: clone CO1G6
C;Genetics:
A;Gene: CESP:CO1G6.8
A;Map position: 2

A;Introns: 36/3; 170/3; 217/3; 636/3; 760/1
Query Match 26.2%; Score 145; DB 2; Length 806;
Best Local Similarity 35.2%; Pred. No. 1.4e-07;
Matches 32; Conservative 12; Mismatches 35; Indels 12; Gaps 5;
QY 3 CYEENGHFRYRGKASTDTMGRCPLPWSATVLOQTYHAHRS--SDALQLGGLGKHNYCRNPD 62
Db 232 CYNSTGTYEGTVAQTSSGKQCAPWIDST--SRDENVHRRPEL---MNSKNYCRNPGGKK 286
QY 63 -RPMCYVQVGLKPLVQE--CMVHDCADGKKP 90
Db 287 SRPCY----SKPMGQEYCDVPCCPSDMYP 313
RESULT 40
PLMS
plasmin (EC 3.4.21.7) precursor - mouse
N;Contains: angiotatin; plasminogen
C;Species: Mus musculus (house mouse)
C;Date: 20-Sep-1991 #sequence_revision 01-Nov-1996 #text_change 18-Jun-1999
C;Accession: A38514; S48202; S48203
R;Deegen, S.J.F.; Bell, S.M.; Schaefer, L.A.; Elliott, R.W.
Genomics 8, 49-61, 1990
A;Title: Characterization of the cDNA coding for mouse plasminogen and localization of
A;Reference number: A38514; MUID:91184812; PMID:2081600
A;Accession: A38514
A;Molecule type: mRNA
A;Residues: 1-812 <DEG>
A;Cross-references: GB:J04766; NID:G200402; PIDN:AAA50168.1; PID:G200403
R;Lijnen, H.R.; van Hoef, B.; Beelen, V.; Collen, D.
Eur. J. Biochem. 224, 863-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIJ>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 22-27 <LIJ>
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many o
C;Comment: Plasminogen is converted into plasmin by plasminogen activators, both plasm
e inhibitor, the activation involves also removal of the activation peptide.
C;Comment: Stremelysin 1 (see PIR:KCMSS1) acts on plasminogen to produce angiotatin. I
eul in treating solid tumors.
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ac
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog
C;Keywords: angiotatin inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-812/Product: plasminogen #status predicted <PRO>
F;20-96/Domain: activation peptide #status predicted <APT>
F;79-466/Product: angiotatin #status predicted <AST>
F;97-581,582-812/Product: plasmin #status predicted <MAT>
F;103-181/Domain: chain A #status predicted <ACH>
F;185-262/Domain: kringle homology <KR1>
F;185-262/Domain: kringle homology <KR2>
F;275-352/Domain: kringle homology <KR3>
F;377-454/Domain: kringle homology <KR4>
F;481-560/Domain: kringle homology <KR5>
F;582-812/Domain: chain B #status predicted <BCH>
F;582-805/Domain: trypsin homology <TRY>
F;49-73,53-61,103-181,124-164,152-176,185-262,188-316,206-245,234-257,275-352,296-335,3
bonds: #status predicted
F;78-79/Cleavage site: Glu-Asn (stromelysin 1) #status predicted
F;136,308/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;466-467/Cleavage site: Thr-Val (stromelysin 1) #status predicted
F;581-582/Cleavage site: Arg-Val (plasminogen activator) #status experimental
F;624,667,762/Active site: His, Asp, Ser #status predicted


```
Query Match      26.1%; Score 144.5; DB 1; Length 812;
Best Local Similarity 32.7%; Pred. No. 1.6e-07;
Matches 33; Conservative 8; Mismatches 47; Indels 13; Gaps 4;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWNASATVLTQTYHAHRSDALQLGLG--KKNYCRNPDN 60
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 275 CLRGRNGYRGTVSVTVSGTKQKRW-----EQTPHRNRTPTENFFCKNLENYCRNPDG 329
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 RRRPWCYVQGLKPLVQECMVHDCADGKKP-----SSPPEE 96
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 330 ETAPWCYT-TDSQLRWEYCEIPSCSSASPDQSDSSVPPEE 369
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 41
T18518
apolipoprotein(a) - western European hedgehog (fragment)
C:Species: Erinaceus europaeus (western European hedgehog)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 07-Dec-1999
C:Accession: T18518
R:Lawn, R.N.; Boonmark, N.W.; Schwartz, K.; Lindahl, G.E.; Wade, D.P.; Byrne, C.D.; Fong
J. Biol. Chem. 270, 24004-24009, 1995
A>Title: The recurring evolution of lp(a): Insights from cloning of hedgehog apolipoprotein
A:Reference number: I46259; MUID:96025778; PMID:7592597
A:Accession: T18518
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-2869 <LAW>
A:Cross-references: EMBL:U33170; NID:G1046358; PID:G1046359; PIDN:AAC48522.1
A:Experimental source: liver
C:Comment: The lipoprotein lp(a), a major inherited risk factor for atherosclerosis, contains apolipoprotein(a).
```

```
Query Match      25.8%; Score 143; DB 2; Length 2869;
Best Local Similarity 35.18; Pred. No. 7.5e-07;
Matches 33; Conservative 8; Mismatches 45; Indels 8; Gaps 4;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWNASATVLTQTYHAHRSDALQLGLGKKNYCRNPDNR 62
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2591 CLENGENYQGNMAITVSGQCQGRKQTPHREYTPENYPSKNL-FG--NYCRNPDGBI 2647
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 63 RPMCYYVQGLKPLVQECMVHDCADGKKPSPPEE 96
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 2648 APWCYT-TNSAVRWEYCSITC-----ESSPPIE 2676
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

```
RESULT 42
A61545
plasmin (EC 3.4.21.7) precursor - horse (fragments)
N:Alternate names: plasminogen
N:Contains: miniplasminogen
C:Species: Equus caballus (domestic horse)
C>Date: 28-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 18-Jul-1997
C:Accession: A61545; S17527
R:Schaller, J.; Rickli, E.E.
Enzyme 40, 63-69, 1988
A>Title: Structural aspects of the plasminogen of various species.
A:Reference number: A61545; MUID:8905015; PMID:3168975
A:Accession: A61545
A:Molecule type: protein
A:Residues: 1-33;34-117 <SCH>
R:Schaller, J.; Straub, C.; Kaempfer, U.; Rickli, E.E.
Protein Seq. Data Anal. 4, 69-74, 1991
A>Title: Complete amino acid sequence of equine miniplasminogen.
A:Reference number: S17527; MUID:92052077; PMID:1946332
A:Accession: S17527
A:Molecule type: protein
A:Residues: 118-455 <SC2>
C:Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; plasma; serine proteinase; 2
F:1-33-34-117.118-455/Product: plasminogen (fragments) #status experimental <PRO>
F:1-33/Domain: activation peptide (fragment) #status experimental <APT>
F:34-117,118-225,226-455/Product: plasmin (fragments) #status experimental <MAT>
```

```
F:37-114/Domain: kringle homology <KR4>
F:118-455/Product: miniplasminogen #status experimental <MIN>
F:126-205/Domain: kringle homology <KR5>
F:226-455/Domain: plasmin chain B #status experimental <BCH>
F:226-448/Domain: trypsin homology <TRY>
F:267,310,405/Active site: His, Asp, Ser #status predicted

Query Match      25.5%; Score 141.5; DB 2; Length 455;
Best Local Similarity 34.4%; Pred. No. 1.9e-07;
Matches 33; Conservative 15; Mismatches 35; Indels 13; Gaps 5;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWNASATV--LQOTYHAHRSDALQLGLGKKNYCRNPDN 60
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 37 CYQKGESYRGTSITVTGKKCSWSNTPHWQKPEKYPNADLTW-----NYCRNPDG 91
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 RRRPWCYVQGLKPLV--QECMVHDCADG-KKPSSP 93
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 92 DKGPWCYT---TDSVRWEFCNLRKCKSETVQEPSEP 124
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 43
A48289
neurotrophic receptor for precursor - fruit fly (Drosophila melanogaster)
N:Alternate names: trk-related receptor
N:Contains: protein-tyrosine kinase (BC 2.7.1.112)
C:Species: Drosophila melanogaster
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 17-Nov-2000
C:Accession: A48289
R:Wilson, C.; Goeberdhan, D.C.I.; Steller, H.
Proc. Natl. Acad. Sci. U.S.A. 90, 7109-7113, 1993
A>Title: Dror, a potential neurotrophic receptor gene, encodes a Drosophila homolog of t
A:Reference number: A48289; MUID:93348222; PMID:8394009
A:Accession: A48289
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-885 <WIL>
A:Cross-references: GB:L20297; NID:G348103; PIDN:AAA28860.1; PID:G348104
C:Genetics:
A:Gene: FlyBase:bsk
A:Cross-references: FlyBase:FBgn0010407
C:Superfamily: Drosophila neurotrophic receptor for; kringle homology; protein kinase ho
C:Keywords: ATP; glycoprotein; kringle; phosphotransferase; transmembrane protein; tyros.
F:237-310/Domain: kringle homology <KRG>
F:314-338/Domain: transmembrane #status predicted <TML>
F:408-677/Domain: protein kinase homology <KIN>
F:416-424/Region: protein kinase ATP-binding motif
F:45,63,129,144,250/Binding site: carbohydrate (Asn) (covalent) #status predicted
```

```
Query Match      25.1%; Score 139; DB 1; Length 685;
Best Local Similarity 34.5%; Pred. No. 5.2e-07;
Matches 30; Conservative 19; Mismatches 28; Indels 10; Gaps 5;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWNASATVLTQTYHAHRSDALQLGLGKKNYCRNPDN 60
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 235 ENCYWEDGSTYRGVANVSASGKPLRW--SWLMKEI-----SDFPEL-IGQ-NYCRNPGS 285
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 -RRPWCYVQGLKPLVQECMVHDCAD 86
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 286 VENSPWCFVDSRRRIELCDIPKCAD 312
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 44
JC5061
macrophage-stimulating protein 1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 16-Jun-2000
C:Accession: JC5061
R:Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu, N.
Biochem. Biophys. Res. Commun. 227, 273-280, 1996
A>Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in
A:Reference number: JC5061; MUID:97011126; PMID:8858136
A:Accession: JC5061
A:Molecule type: mRNA
```


R;Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
Biochem. J. 278, 35-41, 1991
A;Title: Purification and characterization of biologically active scatter factor from r
A;Reference number: S17173; MUID:91354223; PMID:1831975
A;Accession: S17173
A;Molecule type: protein
A;Residues: 436-517,'T',519 <COP>
R;Gherardi, E.; Stoker, M.
Nature 346, 228, 1990
A;Title: Hepatocytes and scatter factor.
A;Reference number: S10966; MUID:90326152; PMID:2142751
A;Accession: S10966
A;Status: preliminary
A;Molecule type: Protein
A;Residues: 496-507,'X',509-512,'L',514-516,'X',518-519 <NAT>
R;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Birchmeier, W.
J. Biol. Chem. 270, 830-836, 1995
A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
A;Reference number: I48758; MUID:95122532; PMID:7822318
A;Accession: I48758
A;Status: preliminary; translated from GB/EMBL/DBDBJ
A;Molecule type: DNA
A;Residues: 1-30 <RES>
A;Cross-references: EMBL:X81630; NID:G673451; PIDN:CAA57286.1; PID:G673452
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; py
F;1-32/Domain: signal sequence #status predicted <SIG>
F;56-495,'X',496-728/Product: hepatocyte growth factor #status predicted <MAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;129-207/Domain: kringle homology <K1>
F;112-289/Domain: kringle homology <K2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor
F;436-719/Domain: trypsin homology <TRY>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;438-607/Disulfide bonds: #status predicted

Query Match 24.8%; Score 137.5; DB 1; Length 728;
Best Local Similarity 32.0%; Pred. No. 7.9e-07;
Matches 31; Conservative 12; Mismatches 35; Indels 19; Gaps 4;

QY 3 CYEGNGHFYRGKASTDTMBPCLPWNISATVLQTYTHARRSDALQLGLG-----KHNYCRNP 58
DB 306 CIGQCGEGYRGTSITWNGIPQGRWDS-----QVPHKHDTIPENFKCXDLRENYCRNP 358
QY 59 DNRRRRWYCVY-----VOVGLKPLVQECMV---HDCADG 87
DB 359 DGAESPWCFTTDNIRVGYCQIPKCDVSSGQDCYRG 395

RESULT 46
A35644
hepatocyte growth factor precursor - rat
N;Alternate names: hepatoin A; scatter factor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 21-Jul-2000
C;Accession: A35644; S13211
R;Tashiro, K.; Hagiya, M.; Nishikawa, T.; Seki, T.; Shimonishi, M.; Shimizu, S.; Nakamu
Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990
A;Title: Deduced primary structure of rat hepatocyte growth factor and expression of th
A;Reference number: A35644; MUID:90222197; PMID:2139229
A;Accession: A35644
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <TAS>
A;Cross-references: GB:D90102; GB:M32987; NID:9220766; PIDN:BAAL4133.1; PID:G220767
A;Note: the authors translated the codon GAG for residue 70 as Gln. GAC for residue 417

100

R;Okajima, A.; Miyazawa, K.; Kitamura, N.
Eur. J. Biochem. 193, 375-381, 1990
A;Title: Primary structure of rat hepatocyte growth factor and induction of its mRNA during
A;Reference number: S13211; MUID:91031482; PMID:2146117
A;Accession: S13211
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-728 <OKA>
A;Cross-references: EMBL:X54400; NID:G56353; PIDN:CAA38266.1; PID:G4539554
C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
C;Function:
A;Description: stimulates mitosis of hepatocytes and other cells
A;Note: does not have proteinase activity
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyH
F;1-32/Domain: signal sequence #status predicted <SIG>
F;56-495/Product: hepatocyte growth factor #status predicted <WAT>
F;56-495/Domain: hepatocyte growth factor alpha chain #status predicted <ACH>
F;123-207/Domain: kringle homology <KR1>
F;212-289/Domain: kringle homology <KR2>
F;306-384/Domain: kringle homology <KR3>
F;392-470/Domain: kringle homology <KR4>
F;496-728/Domain: hepatocyte growth factor beta chain #status predicted <BCH>
F;496-719/Domain: trypsin homology <TRY>
F;33/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;295,403,569,656/Binding site: carboxylate (Asn) (covalent) #status predicted
F;488-607/Disulfide bonds: #status predicted

Query Match 24.5%; Score 135.5; DB 1; Length 728;
Best Local Similarity 32.0%; Pred. No. 1.3e-06;
Matches 31; Conservative 11; Mismatches 36; Indels 19; Gaps 4;
Qy 3 CYEGNGHYFGKASTDTMGPRCLPWSATVLQTYHAHRSALQLGLG----KHNYCRNP 58
Db 306 CIRKQGGYGRGTTNINWNGIPQCRWDS-----QYPKHDTIPENFKCKDLRENYCRNP 358
Qy 59 DNRRRPCY-----VOVGLKPLVQECMV---HDCADG 87
Db 359 DGASPCWCTTDPNIRVGYCSQIPKCDVSSQDCYRG 395

RESULT 47
151285
hepatocyte growth factor/scatter factor - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Jul-1999
C;Accession: I51285
R;Steit, A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard
Development 121, 813-824, 1995
A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node during
A;Reference number: I51285; MUID:95237013; PMID:7720585
A;Accession: I51285
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-411 <STR>
A;Cross-references: GB:S77480; NID:G998675; PID:G998676
C;Superfamily: hepatocyte growth factor; kringle homology; trypsin homology
F;124-197/Domain: kringle homology <KR3>
F;202-279/Domain: kringle homology <KR2>
F;296-374/Domain: kringle homology <KR3>

Query Match 24.1%; Score 133.5; DB 2; Length 411;
Best Local Similarity 32.0%; Pred. No. 1.2e-06;
Matches 32; Conservative 12; Mismatches 41; Indels 15; Gaps 4;
Qy 2 TCYEGNGHYFGKASTDTMGPRCLPWSATVLQTYHAHR--SDALQGLGKHNYCRNP 59
Db 295 TCIOQGGYGRGTVNTINWSGIQCRWDS-----QPPHQNITPENFKCKDLRENYCRNP 349
Qy 60 NRRRRCY-----VOVGLKPLVQECMV---HDCADGKPS 91
Db 350 GSSEPCWCTTDPNIRIGYCSQIPKCDVSNEDQCYRGNGKS 389

RESULT 48

JH0579
hepatocyte growth factor precursor [validated] - human
N;Alternate names: hepatopietin A; scatter factor
C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Dec-2000
C;Accession: JH0579; JH0333; A41140; B36677; A36677; A33512; A39006; PH0114; A37796; S06
R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A;Title: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JH0579; MUID:91340155; PMID:1831432
A;Accession: JH0579
A;Molecule type: DNA
A;Residues: 1-728 <SEK>
A;Cross-references: DBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
submitted to JTPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JH0333
A;Accession: JH0333
A;Molecule type: DNA
A;Residues: 1-481, RT, 484-728 <SE2>
R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991
A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth f.
A;Reference number: A41140; MUID:91334393; PMID:1831266
A;Accession: A41140
A;Molecule type: mRNA
A;Residues: 1-728 <WEI>
R;Seki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth facto.
A;Reference number: A36677; MUID:91025062; PMID:2145836
A;Accession: B36677
A;Molecule type: mRNA
A;Residues: 1-728 <SE3>
A;Cross-references: GB:M60718; NID:G184031; PIDN:AAA52648.1; PID:G184032
A;Accession: A36677
A;Molecule type: mRNA
A;Residues: 1-161, 167-728 <SE4>
A;Cross-references: EMBL:X16323
A;Experimental source: leukocyte
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, N.; Arakaki, N.; Nakaya
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth fac
A;Reference number: A33512; MUID:83992017; PMID:2528952
A;Accession: A33512
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-728 <MIY>
A;Cross-references: GB:M29145; NID:G184041; PIDN:AAA52650.1; PID:G305846
R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocy
A;Reference number: A39006; MUID:91110540; PMID:1824873
A;Accession: A39006
A;Molecule type: mRNA
A;Residues: 1-161, 167-728 <RUB>
A;Cross-references: GB:M55379
A;Experimental source: embryonic lung
R;Toshiyama, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hirono, S.; Kondo, J.; Nakayama, J
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both native and
A;Reference number: PH0114; MUID:91207365; PMID:1826837
A;Accession: PH0114
A;Molecule type: protein
A;Residues: 32-43/53-58 <YOS>
A;Experimental source: plasma
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2097-2108, 1990

[illegible]

Best Local Similarity 30.1%; Pred. No. 9.1e-06;
Matches 31; Conservative 10; Mismatches 35; Indels 27; Gaps 5;
QY 1 KTCYEGNGHFYRGKASTDTMGRECLPWSATVLQQTYYAHR-----SDALQLGLGKH 52
Db 287 KDCWKGGGEGYRGVSSTYNGIQQRWDS-----QFPHLHFTPENYKCKDL-----SE 335
QY 53 NYCENPDNRPRWCY-----VQVGLKPLVQECNV---HDCADG 87
Db 336 NYCENPDGSESPWCFTTDPNIRIGHCSQIKKCOASNOQBCYIG 378

Search completed: May 25, 2004, 14:58:37
Job time : 6.55302 secs

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OM protein - protein search, using sw model

Run on: May 25, 2004, 14:43:40 ; Search time 3.70202 Seconds

(without alignment)
1350.274 Million cell updates/sec

Title: US-09-880-503-9

Perfect score: 554

Sequence: 1 KTCYEGNGHFGKASTDTM.....QECMVHDCADGKKGSPPEE 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	554	100.0	431	1	UROK_HUMAN
2	519	93.7	433	1	P00749 papio cynoc
3	437.5	79.0	442	1	P04188 sus scrofa
4	427	77.1	432	1	P29598 rattus norv
5	422	76.2	433	1	P05589 bos taurus
6	408	73.6	433	1	P06869 mus musculu
7	241	43.5	431	1	P98121 desmodus ro
8	241	43.5	477	1	P15638 desmodus ro
9	228.5	41.2	559	1	P19637 rattus norv
10	226	40.8	562	1	TPA_HUMAN
11	220	39.7	394	1	URT2 DESRO
12	219	39.5	559	1	TPA_MOUSE
13	213	38.4	477	1	URT1 DESRO
14	209	37.7	566	1	TPA_BOVIN
15	198.5	35.8	434	1	UROK_CHICK
16	194.5	35.1	655	1	HGFA_HUMAN
17	191.5	34.6	603	1	FA12 CAVPO
18	188	33.9	653	1	HGPA_MOUSE
19	170.5	30.8	615	1	FA12_HUMAN
20	161	29.1	1420	1	AP0A_YACMU
21	159	28.7	473	1	KRM1_MOUSE
22	159	28.7	473	1	KRM1_RAT
23	158	28.5	452	1	KRM1_XENLA
24	157	28.3	4548	1	AP0A_HUMAN
25	156	28.2	475	1	KRM1_HUMAN
26	155.5	28.1	593	1	FA12_BOVIN
27	152	27.4	812	1	PLMN_BOVIN
28	150	27.1	169	1	PLMN_RAT
29	149	26.9	810	1	PLMN_YACMU
30	148.5	26.8	462	1	KRM2_HUMAN
31	148.5	26.8	711	1	HGFL_HUMAN
32	148.5	26.8	810	1	PLMN_ERIEU
33	148	26.7	333	1	PLMN_CANEA

34	148	26.7	790	1	PLMN_PIG
35	147.5	26.6	716	1	HGFL_MOUSE
36	147.5	26.6	943	1	ROR2_HUMAN
37	147.5	26.6	944	1	KRM2_MOUSE
38	146.5	26.4	461	1	KRM2_MOUSE
39	146.5	26.4	810	1	PLMN_HUMAN
40	146	26.4	937	1	ROR1_HUMAN
41	146	26.4	937	1	ROR1_MOUSE
42	144.5	26.1	812	1	PLMN_MOUSE
43	139	25.1	685	1	ROR1_DROME
44	137.5	24.8	728	1	HGF_MOUSE
45	135.5	24.5	728	1	HGF_RAT
46	133.5	24.1	728	1	HGF_HUMAN
47	131	23.6	325	1	PLMN_PETMA
48	125.5	22.7	618	1	THR3_MOUSE
49	124.5	22.5	343	1	PLMN_SHEEP
50	124	22.4	622	1	THR3_HUMAN
51	119.5	21.6	724	1	ROR2_DROME
52	113	20.4	617	1	THR3_RAT
53	112	20.2	625	1	THR3_BOVIN
54	111	20.0	338	1	PLMN_HORSE
55	96	17.3	875	1	NETR_HUMAN
56	89	16.1	761	1	NETR_MOUSE
57	73	13.2	559	1	ECM1_MOUSE
58	70.5	12.7	540	1	ECM1_HUMAN
59	69	12.5	369	1	V181_FOPPV
60	68	12.3	161	1	ASF1_HELAN
61	66	11.9	2871	1	FBN1_PIG
62	65.5	11.8	1278	1	NPC1_MOUSE
63	65.5	11.8	1426	1	RHSD_ECOLI
64	65	11.7	542	1	LNT_CHLMU
65	63.5	11.5	542	1	LNT_CHLTR
66	63.5	11.5	775	1	AD28_HUMAN
67	63	11.4	410	1	HMH2_DROME
68	63	11.4	1342	1	Z335_HUMAN
69	62	11.2	1088	1	PRH_PETCR
70	62	11.2	2871	1	FBN1_BOVIN
71	61	11.0	934	1	CLTC_HUMAN
72	60	10.8	230	1	RT07_MARPO
73	59.5	10.7	138	1	PA2A_VIPAA
74	59.5	10.7	138	1	PA2B_VIPAA
75	59.5	10.7	138	1	PA2C_VIPAA

ALIGNMENTS

RESULT 1	
UROK_HUMAN	UROK_HUMAN STANDARD; PRT; 431 AA.
ID	UROK_HUMAN Q15844; Q16618; Q969W6;
AC	P00749; Q15844; Q16618; Q969W6;
DT	21-JUL-1986 (Rel. 01, Created)
DT	20-MAR-1987 (Rel. 04, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE	(U-plasminogen activator)
GN	PLAU
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=85215647; PubMed=2987867;
RA	Riccio A., Grimaldi G., Verde P., Sebastio G., Boast S., Biasi F.,
RT	"The human urokinase-plasminogen activator gene and its promoter."
RL	Nucleic Acids Res. 13:2759-2771(1985).
RN	[2]
RP	SEQUENCE FROM N.A.
RA	Holmes W.E., Pennica D., Blaber M., Rey M.W., Guenzler W.A.,
RA	Steffens G.J., Heyneker H.L.
RT	"Cloning and expression of the gene for pro-urokinase in Escherichia coli."

RT Biotechnology 3:923-929(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86056954; PubMed=2415429;
 RA Nagai M., Hiratsutsu R., Kaneda T., Hayasuke N., Arimura H.,
 RA Nishida M., Suyama T.;
 RT "Molecular cloning of cDNA coding for human preprourokinase.";
 RL Gene 36:183-188(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85203359; PubMed=3888571;
 RA Jacobs P., Cravador A., Loriau R., Brockly F., Colau B., Chuchana P.,
 RA van Elsen A., Herzog A., Bollen A.;
 RT "Molecular cloning, sequencing, and expression in *Escherichia coli* of
 RT human preprourokinase cDNA.";
 RL DNA 4:139-146(1985).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85203359; PubMed=3888571;
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RL [6]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Lung;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young J.W., Green E.D., Dickson M.C.,
 RA Blakeley R.W., Touchman J.W., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [7]
 RP SEQUENCE OF 66-431 FROM N.A.
 RX MEDLINE=84272706; PubMed=6589620;
 RA Verde P., Stoppelli M.P., Galeffi P., di Nocera P., Blasi F.;
 RT "Identification and primary sequence of an unspliced human urokinase
 RT poly(A)+ RNA";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4727-4731(1984).
 RN [8]
 RP SEQUENCE OF 21-177.
 RX MEDLINE=83055084; PubMed=6754569;
 RA Gunzler W.A., Steffens G.J., Otting F., Kim S.-M.A., Frankus E.,
 RA Flohe L.;
 RT "The primary structure of high molecular mass urokinase from human
 RT urine. The complete amino acid sequence of the A chain";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1155-1165(1982).
 RN [9]
 RP SEQUENCE OF 156-176 AND 179-224.
 RX MEDLINE=83003608; PubMed=6749491;
 RA Schaller J., Nick H., Rickli E.E., Gillesen D., Lergier W.,
 RA Studer R.O.;
 RT "Human low-molecular-weight urinary urokinase. Partial
 RT characterization and preliminary sequence data of the two polypeptide
 RT chains";
 RL Eur. J. Biochem. 125:251-257(1982).
 RN [10]
 RP SEQUENCE OF 158-410.
 RX MEDLINE=83055099; PubMed=6754572;
 RA Steffens G.J., Gunzler W.A., Otting F., Frankus E., Flohe L.;
 RT "The complete amino acid sequence of low molecular mass urokinase
 RT from human urine";
 RL Hoppe-Seyler's Z. Physiol. Chem. 363:1043-1058(1982).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
 RX MEDLINE=96000858; PubMed=8591045;
 RA Spraggon G., Phillips C., Nowak U.K., Ponting C.P., Saunders D.,
 RA Dobson C.M., Stuart D.I., Jones E.Y.;
 RT "The crystal structure of the catalytic domain of human
 RT urokinase-type plasminogen activator";
 RL Structure 3:681-691(1995).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 159-411.
 RX MEDLINE=20266327; PubMed=10805774;
 RA Sperl S., Jacob U., Arroyo de Prada N., Sturzebecher J., Wilhelm O.G.,
 RA Bode W., Magdolen V., Huber R., Moroder L.;
 RT "(4-aminomethyl)phenylguanidine derivatives as nonpeptidic highly
 RT selective inhibitors of human urokinase";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:5113-5118(2000).
 RN [13]
 RP STRUCTURE BY NMR.
 RX MEDLINE=89127526; PubMed=2536903;
 RA Oswald R.E., Bogusky M.J., Bamberger M., Smith R.A.G., Dobson C.M.;
 RT "Dynamics of the multidomain fibrinolytic protein urokinase from two-
 RT dimensional NMR";
 RL Nature 337:579-582(1989).
 RN [14]
 RP STRUCTURE BY NMR OF 67-155.
 RX MEDLINE=93003110; PubMed=1327118;
 RA Li X., Smith R.A.G., Dobson C.M.;
 RT "Sequential 1H NMR assignments and secondary structure of the kringle
 RT domain from urokinase";
 RL Biochemistry 31:9562-9571(1992).
 RN [15]
 RP STRUCTURE BY NMR OF 67-155.
 RX MEDLINE=94149701; PubMed=8107091;
 RA Li X., Bokman A.M., Llinas M., Smith R.A.G., Dobson C.M.;
 RT "Solution structure of the kringle domain from urokinase-type
 RT plasminogen activator";
 RL J. Mol. Biol. 235:1548-1559(1994).
 RN [16]
 RP VARIANT LEU-141.
 RX MEDLINE=96186279; PubMed=8652631;
 RA Yoshimoto M., Ushiyama Y., Sakai M., Tamaki S., Hara H., Takahashi K.,
 RA Sawasaki Y., Hanada K.;
 RT "Characterization of single chain urokinase-type plasminogen
 RT activator with a novel amino-acid substitution in the kringle
 RT structure";
 RL Biochim. Biophys. Acta 1293:83-89(1996).
 RN [17]
 RP VARIANT LEU-141.
 RX MEDLINE=97218551; PubMed=9065988;
 RA Conne B., Berczy M., Belin D.;
 RT "Detection of polymorphisms in the human urokinase-type plasminogen
 RT activator gene";
 RL Thromb. Haemost. 77:434-435(1997).
 RN [18]
 RP ERRATUM.
 RA Conne B., Berczy M., Belin D.;
 RT Thromb. Haemost. 78:973-973(1997).
 RN [19]
 RP VARIANT LEU-141.
 RX MEDLINE=97337920; PubMed=9194591;
 RA Turkmen B., Schmitt M., Schmalheidt B., Trommler P., Hell W.,
 RA Kreutzburg S., Graeff H., Magdolen V.;
 RT "Mutational analysis of the genes encoding urokinase-type plasminogen
 RT activator (uPA) and its inhibitor PAI-1 in advanced ovarian cancer";
 RL Electrophoresis 18:686-689(1997).
 CC -!- FUNCTION: Potent plasminogen activator and is clinically used for
 CC therapy of thrombolytic disorders.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: Found in high and low molecular mass forms. Each consists

CC of two chains, A and B. The high molecular mass form contains a
CC long chain A. Cleavage occurs after residue 155 in the low
CC molecular mass form to yield a short A1 chain.
CC -!- PHARMACEUTICAL: Available under the name Abbokinase (Abbott). Used
CC in Pulmonary Embolism (PE) to initiate fibrinolysis.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
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CC -----
CC EMBL; X02419; CAA26268.1; -
CC EMBL; M15476; AAA61253.1; -
CC EMBL; D00244; BAA00175.1; -
CC EMBL; D11143; BAA01919.1; -
CC EMBL; X02760; CAA26535.1; -
CC EMBL; AF377330; AAK53822.1; -
CC EMBL; BC013575; AAH13575.1; -
CC EMBL; K03226; AAC97138.1; -
CC EMBL; K02286; AAA61252.1; -
CC EMBL; A21571; CAA01559.1; -
CC EMBL; A18397; CAA01390.1; -
CC PIR; A00931; UKHU.
CC PDB; 1KDU; 31-OCT-93.

Query Match 100.0%; Score 554; DB 1; Length 431;
Best Local Similarity 100.0%; Pred. NO. 8.3e-55;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLTQYTHAHSRALQLGLGKHNYCRNPDN 60
Db 68 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLTQYTHAHSRALQLGLGKHNYCRNPDN 127
Qy 61 RRRPWCYVQGLKPLVQSCVHDCADGKXPSSPPEE 96
Db 128 RRRPWCYVQGLKPLVQSCVHDCADGKXPSSPPEE 163

RESULT 2
UROK_PAPCY STANDARD; PRT; 433 AA.
AC P16227;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-plasminogen activator).
GN PLAU.
OC Papio cynocephalus (Yellow baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Papio.
OX NCBI_TaxID=9556;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thoracic aorta;
RX MEDLINE=90287734; PubMed=2113276;
RA Au Y.P.T.; Wang T.W.; Clowes A.W.;
RT "Nucleotide and deduced amino acid sequences of baboon urokinase-type
RT plasminogen activator.";
RL Nucleic Acids Res. 18:3411-3411(1990).
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -!- SUBUNIT: Found in high and low molecular mass forms. Each consists
CC of two chains, A and B. The high molecular mass form contains a
CC long chain A. Cleavage occurs after residue 155 in the low
CC molecular mass form to yield a short A1 chain (By similarity).

CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC -----
CC EMBL; X51935; CAA36200.1; -
CC PIR; S14687; UKBAY.
CC HESP; P00749; ILMW.
CC MROPS; S01231; -
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR008293; Pept_S1A_UPA.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00051; Kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PIRSF001144; Urk_plasm_act; 1.
CC PRINTS; PSC0018; KRINGLE.
CC ProDom; PDC00395; Kringle; 1.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; Tryp_SPC; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS50026; EGF_3; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS00070; KRINGLE_2; 1.
CC PROSITE; PS50240; TRYPsin_DOM; 1.
CC PROSITE; PS00134; TRYPsin_HIS; 1.
CC PROSITE; PS00135; TRYPsin_SER; 1.
KW Plasminogen activator; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 433 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 176 CHAIN A (BY SIMILARITY).
FT CHAIN 155 176 SHORT A CHAIN (A1) (BY SIMILARITY).
FT CHAIN 178 433 CHAIN B (BY SIMILARITY).
FT DOMAIN 26 62 EGF-LIKE.
FT DOMAIN 69 150 KRINGLE.
FT DOMAIN 151 177 CONNECTING PEPTIDE.
FT DOMAIN 178 433 SERINE PROTEASE.
FT DISULFID 30 38 BY SIMILARITY.
FT DISULFID 32 50 BY SIMILARITY.
FT DISULFID 52 61 BY SIMILARITY.
FT DISULFID 167 298 INTERCHAIN (BY SIMILARITY).
FT DISULFID 208 224 BY SIMILARITY.
FT DISULFID 216 287 BY SIMILARITY.
FT DISULFID 315 384 BY SIMILARITY.
FT DISULFID 347 363 BY SIMILARITY.
FT DISULFID 374 402 BY SIMILARITY.
FT ACT_SITE 223 223 CHARGE RELAY SYSTEM.
FT ACT_SITE 274 274 CHARGE RELAY SYSTEM.
FT ACT_SITE 378 378 CHARGE RELAY SYSTEM.
FT CARBOHYD 324 324 N-LINKED (GLCNAC...) (BY SIMILARITY).
SQ SEQUENCE 433 AA; 48595 MW; 816D22DFEDDC8792 CRC64;

Query Match 93.7%; Score 519; DB 1; Length 433;
Best Local Similarity 94.8%; Pred. NO. 7.1e-51;
Matches 91; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLTQYTHAHSRALQLGLGKHNYCRNPDN 60
Db 67 KTCYEGNGHYRGKASTDTMGRCLMNSATVLTQYTHAHSRALQLGLGKHNYCRNPDN 126

```
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKFSSPPE 96
| | | | | | | | | | | | | | | | | | | | | |
DB 127 RRRPWCYVQVGLKPLVQECMVHDCADGKKFSSPPE 162

RESULT 3
UROK_PIG STANDARD; PRT; 442 AA.
AC P04185;
DT 20-MAR-1987 (Rel. 04, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-plasminogen activator).
GN PLAU.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCB1_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=85087954; PubMed=6096832;
RA Nagamine Y., Pearson D., Altus M.S., Reich E.;
RT "cDNA and gene nucleotide sequence of porcine plasminogen activator.";
EL Nucleic Acids Res. 12:9525-9541(1984).
RN [2]
RP REVISION TO 241.
RA Nagamine Y.;
RL Submitted (DEC-1986) to the PIR data bank.
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
    plasminogen to form plasmin.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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    entities requires a license agreement (See http://www.isb-sib.ch/announce/
    or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01648; CAA25806.1; -.
DR EMBL; X02724; CAA26511.1; -.
DR PIR; A00932; UKPG.
DR HSSP; P00749; 1KDU.
DR MEROPS; S01.231; -.
DR InterPro; IPR009003; Cys_ser_trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR008293; Pept_S1A_uPA.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PIRSF; PIRSF001144; Urk_plasm_act; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM001130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
```

```
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 442 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 188 CHAIN A (BY SIMILARITY).
FT CHAIN 190 442 CHAIN B (BY SIMILARITY).
FT DOMAIN 29 65 EGF-LIKE.
FT DOMAIN 72 153 KRINGLE.
FT DOMAIN 154 189 CONNECTING PEPTIDE.
FT DOMAIN 190 442 SERINE PROTEASE.
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .).
FT DISULFID 33 41 BY SIMILARITY.
FT DISULFID 35 53 BY SIMILARITY.
FT DISULFID 55 64 BY SIMILARITY.
FT DISULFID 179 310 INTERCHAIN (BY SIMILARITY).
FT DISULFID 220 236 BY SIMILARITY.
FT DISULFID 228 299 BY SIMILARITY.
FT DISULFID 324 393 BY SIMILARITY.
FT DISULFID 356 372 BY SIMILARITY.
FT DISULFID 383 411 BY SIMILARITY.
FT ACT_SITE 235 235 CHARGE RELAY SYSTEM.
FT ACT_SITE 286 286 CHARGE RELAY SYSTEM.
FT ACT_SITE 387 387 CHARGE RELAY SYSTEM.
FT CONFLICT 241 241 Q -> H (IN REF. 1; CAA25806).
FT CONFLICT 242 242 Q -> H (IN REF. 1; CAA26511).
FT CONFLICT 288 288 A -> GS (IN REF. 1; CAA25806).
SQ SEQUENCE 442 AA; 49116 MW; EE32FCEP501321EE CRC64;

Query Match 79.0%; Score 437.5; DB 1; Length 442;
Best Local Similarity 74.3%; Pred. No. 1.1e-41;
Matches 78; Conservative 8; Mismatches 10; Indels 9; Gaps 1;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWNSTVLTQTYHAHRSDALQLGLGKHNYCRPN 60
| | | | | | | | | | | | | | | | | | | | | |
DB 70 QTCFEGNGHSYRGKANTNTGRCPLPWNSTVLTQTYHAHRSDALQLGLGKHNYCRPN 129
| | | | | | | | | | | | | | | | | | | | | |
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKFSSPPE 96
| | | | | | | | | | | | | | | | | | | | | |
DB 130 QRRPWCYVQVGLKPLVQECMVHDCADGKKFSSPPE 174
| | | | | | | | | | | | | | | | | | | | | |

RESULT 4
UROK_PIG STANDARD; PRT; 432 AA.
AC P29598;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-plasminogen activator).
GN PLAU.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=92233409; PubMed=1568219;
RA Henderson B.R., Tansey W.P., Phillips S.M., Ramshaw I.A.,
RA Kefford R.F.;
RT "Transcriptional and posttranscriptional activation of urokinase
    plasminogen activator gene expression in metastatic tumor cells.";
RL Cancer Res. 52:2489-2496(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Rabbani S.A.;
RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
    plasminogen to form plasmin.
CC -1- SUBUNIT: Found in high and low molecular mass forms. Each consists
    of two chains, A and B. The high molecular mass form contains a
    long chain A. Cleavage occurs after residue 156 in the low
```


molecular mass form to yield a short A1 chain (By similarity).
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 kringle domain.

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EMBL: X63434, CAA45028.1; -
EMBL: X65651, CAA46601.1; -
PIR: S24604, S18932.
HSSP: P00749, 1KDU.
MEROPS: S01.231; -
InterPro: IPR009003; Cys Ser trypsin.
InterPro: IPR006209; EGF-like.
InterPro: IPR006210; IEGF.
InterPro: IPR000001; Kringle.
InterPro: IPR008293; Pept_S1A_UA.
InterPro: IPR001254; Peptidase_S1.
InterPro: IPR001314; Peptidase_S1A.
Pfam: PF00051; kringle; 1.
Pfam: PF00089; trypsin; 1.
PIRSF: PIRSF001144; Urk plasem act; 1.
PRINTS: PR00722; CHYMOTRYPSIN.
PRINTS: PR00018; KRINGLE.
ProDom: PD000395; Kringle; 1.
SMART: SM00181; EGF; 1.
SMART: SM00130; KR; 1.
SMART: SM00020; Tryp_SPC; 1.
PROSITE: PS00022; EGF_1; 1.
PROSITE: PS01186; EGF_2; FALSE_NEG.
PROSITE: PS50026; EGF_3; 1.
PROSITE: PS00021; KRINGLE 1; 1.
PROSITE: PS00070; KRINGLE 2; 1.
PROSITE: PS02134; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
PROSITE: PS00135; TRYPSIN_SRP; 1.
Plasminogen activator; Hydrolase; Serine protease; Glycoprotein; Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 432 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 20 177 CHAIN A (BY SIMILARITY).
FT CHAIN 156 177 SHORT A CHAIN (A1) (BY SIMILARITY).
FT CHAIN 179 432 CHAIN B (BY SIMILARITY).
FT DOMAIN 27 63 EGF-LIKE.
FT DOMAIN 70 151 KRINGLE.
FT DOMAIN 152 178 CONNECTING PEPTIDE.
FT DOMAIN 179 432 SERINE PROTEASE.
FT DISULFID 31 39 BY SIMILARITY.
FT DISULFID 33 51 BY SIMILARITY.
FT DISULFID 53 62 BY SIMILARITY.
FT DISULFID 168 300 INTERCHAIN (BY SIMILARITY).
FT DISULFID 210 226 BY SIMILARITY.
FT DISULFID 218 289 BY SIMILARITY.
FT DISULFID 314 383 BY SIMILARITY.
FT DISULFID 346 362 BY SIMILARITY.
FT DISULFID 373 401 BY SIMILARITY.
FT ACT_SITE 225 225 CHARGE RELAY SYSTEM.
FT ACT_SITE 276 276 CHARGE RELAY SYSTEM.
FT ACT_SITE 377 377 CHARGE RELAY SYSTEM.
FT CONFLICT 16 16 N -> H (IN REF. 2).
FT CONFLICT 24 24 E -> G (IN REF. 2).
FT CONFLICT 332 332 D -> N (IN REF. 2).
SQ SEQUENCE 432 AA; 47957 MW; 4EB1B96C716244C8 CRC64;

Query Match 77.1%; Score 427; DB 1; Length 432;
Best Local Similarity 77.1%; Pred. No. 1.6e-40;
Matches 74; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYFGKASTDNGRPCLPWSNATVLQOTYHHRSDALQLGIGKHYCENPDN 60
Db 68 KTCYHNGOSYRGKANTDTKGRPCLANWSFVLTQOTYHHRSDALSLGIGKHYCRNPDN 127
QY 61 RRRPCYVQVGLKPLVQECWHDCAKGPSPPE 96
Db 128 QRRPCYVQVGLKPLVQECWHDCAKGPSPPE 163

RESULT 5

UROK_BOVIN STANDARD; PRT; 433 AA.
AC Q05589; Q28209;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DE (U-plasminogen activator).
GN PLAU.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aortic endothelium;
RX MEDLINE=93216119; PubMed=8385052;
RA Kraetzschmar J, Haendler B., Kojima S., Rifkin D.B.,
RA Schleuning W.-D.;
RT "Bovine urokinase-type plasminogen activator and its receptor:
RT cloning and induction by retinoic acid.";
RL Gene 125:177-183(1993).
RN [2]
RP SEQUENCE OF 12-433 FROM N.A.
RC TISSUE=Kidney;
RA Ravn P., Berglund L., Petersen T.E.;
RT "Cloning and characterization of the bovine plasminogen activators uPA
RL Int. Dairy J. 5:605-617(1995).
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -!- INDUCTION: By retinoic acid.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L03546; AAA51419.1; -
CC EMBL: X85801; CAA59796.1; -
CC PIR: JNC560; JN0560.
CC HSSP: P00749; 1LMW.
CC MEROPS: S01.231; -
CC InterPro: IPR009003; Cys Ser trypsin.
CC InterPro: IPR006209; EGF-like.
CC InterPro: IPR000001; Kringle.
CC InterPro: IPR008293; Pept_S1A_UA.
CC InterPro: IPR001254; Peptidase_S1.
CC InterPro: IPR001314; Peptidase_S1A.
CC Pfam: PF00051; kringle; 1.
CC Pfam: PF00089; trypsin; 1.
CC PIRSF: PIRSF001144; Urk plasmin act; 1.
CC PRINTS: PR00722; CHYMOTRYPSIN.
CC PRINTS: PR00018; KRINGLE.
CC ProDom: PD000395; Kringle; 1.

DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TRYD_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00026; EGF_3; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Signal; Zymogen.
FT SIGNAL 1 20
FT CHAIN 21 433 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 179 CHAIN A (BY SIMILARITY).
FT CHAIN 181 433 CHAIN B (BY SIMILARITY).
FT DOMAIN 29 65 EGF-LIKE.
FT DOMAIN 72 153 KRINGLE.
FT DOMAIN 154 180 CONNECTING PEPTIDE.
FT DOMAIN 181 433 SERINE PROTEASE.
FT DISULFID 33 41 BY SIMILARITY.
FT DISULFID 35 53 BY SIMILARITY.
FT DISULFID 55 64 BY SIMILARITY.
FT DISULFID 170 301 INTERCHAIN (BY SIMILARITY).
FT DISULFID 211 227 BY SIMILARITY.
FT DISULFID 219 290 BY SIMILARITY.
FT DISULFID 315 384 BY SIMILARITY.
FT DISULFID 347 363 BY SIMILARITY.
FT DISULFID 374 402 BY SIMILARITY.
FT ACT_SITE 226 226 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 277 277 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 378 378 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CONFLICT 189 189 A -> T (IN REF. 2).
SQ SEQUENCE 433 AA; 48730 MW; 4DE1B8D4DA47027A CRC64;
Query Match 76.2%; Score 422; DB 1; Length 433;
Best Local Similarity 75.0%; Pred. No. 5.7e-40;
Matches 72; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 KTCYEGNHPYRGKASTDTMGRLCLPWSATVLQQTVAHRSALQLGKGKNCNPDN 60
DB 70 KTYQGNHGYRGKARDLSGRCLAWDSFTVLLKWHARSDALQLGKGKNCNPDN 129
QY 61 RRPWCYVQGLKPLVQECMVHDCADKPKSPPEE 96
DB 130 QRREPCVYQGLKQFQFCMVQCSVKGKSPREK 165
RESULT 6
UROK_MOUSE STANDARD; PRT; 433 AA.
AC P06869;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (UPA)
DE (U-plasminogen activator).
GN PLAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85179474; PubMed=2985383;
RA Belin D., Vassalli J.-D., Combepine C., Godeau F., Nagamine Y.,
RA Reich E., Koehler H.P., Duvoisin R.M.;
RT "Cloning, nucleotide sequencing and expression of cDNAs encoding
RT mouse urokinase-type plasminogen activator.";
RL Eur. J. Biochem. 148:225-232 (1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88163489; PubMed=2831940;

RA Degen S.J.F., Heckel J.L., Reich E., Degen J.L.;
RT "The murine urokinase-type plasminogen activator gene.";
RL Biochemistry 26:8270-8279 (1987).
CC -1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -1- SUBUNIT: Found in high and low molecular mass forms. Each consists
CC of two chains, A and B. The high molecular mass form contains a
CC long chain A. Cleavage occurs after residue 156 in the low
CC molecular mass form to yield a short A1 chain (by similarity).
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X02389; CAA26231.1; -
CC EMBL; M17922; AAA40539.1; -
CC PIR; A29420; UKWS.
CC HSSP; P00749; 1KDU.
CC MEROPS; S01.231; -
CC MGD; MGI:97611; Plau.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR008293; Pept_S1A_upa.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00051; Kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PIRSF001144; Urokinase act; 1.
CC PRINTS; PRO0722; CHYMOTRYPSIN.
CC PROSITE; PS00018; Kringle.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; TRYD_SPC; 1.
CC PROSITE; PS00022; EGF_1; 1.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS00026; EGF_3; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS00070; KRINGLE_2; 1.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
CC PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Zymogen; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 433 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 178 CHAIN A (BY SIMILARITY).
FT CHAIN 157 178 SHORT A CHAIN (A1).
FT CHAIN 180 433 CHAIN B (BY SIMILARITY).
FT DOMAIN 28 64 EGF-LIKE.
FT DOMAIN 71 152 KRINGLE.
FT DOMAIN 153 179 CONNECTING PEPTIDE.
FT DOMAIN 180 433 SERINE PROTEASE.
FT DISULFID 32 40 BY SIMILARITY.
FT DISULFID 34 52 BY SIMILARITY.
FT DISULFID 54 63 BY SIMILARITY.
FT DISULFID 169 301 INTERCHAIN (BY SIMILARITY).
FT DISULFID 211 227 BY SIMILARITY.
FT DISULFID 219 290 BY SIMILARITY.
FT DISULFID 315 384 BY SIMILARITY.
FT DISULFID 347 363 BY SIMILARITY.
FT DISULFID 374 402 BY SIMILARITY.
FT ACT_SITE 226 226 CHARGE RELAY SYSTEM.
FT ACT_SITE 277 277 CHARGE RELAY SYSTEM.

FT	ACT SITE	378	378	CHARGE RELAY SYSTEM.
SQ	SEQUENCE	433 AA;	48268 MW;	A99C35F6250443F9 CRC64;
	Query Match		73.6%;	Score 408; DB 1; Length 433;
	Best Local Similarity		70.8%;	Pred. No. 2.1e-38;
	Matches	68;	Conservative	12; Mismatches 16; Indels 0; Gaps 0;
Qy	1	KTCYEGNGHYPGKASDTTGRCPLPNSATVLQOTYHAHRSDALQIGLGHNYCRPN	60	
Db	69	KTIHNGDSYRGKANTDTTGRCPLANNAVLQFPNAHRPDAISLGLGHNYCRPN	128	
Qy	61	RRRPFWCYVGLKPLVQECMVHDCADGKCSPPPEE	96	
Db	129	OKRFWCYVOIGLRFQVOCMVHDCSLKTSSSVDQ	164	

RESULT 7	URTB DESRO	STANDARD;	PRT; 431 AA.
ID	URTB DESRO		
AC	P98121;		
DT	01-FEB-1996 (Rel. 33, Created)		
DT	01-FEB-1996 (Rel. 33, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSPA		
DE	beta).		
OS	Desmodus rotundus (Vampire bat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;		
OC	Desmodontinae; Desmodus.		
OX	NCBI TaxID=9430;		

SEQUENCE FROM N.A.
 R1 TISSUE=Salivary gland;
 R2 MEDLINE=92039036; PubMed=1937019;
 R3 Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 R4 Alagon A., Donner P., Schleuning W.D.;
 R5 "the plasminogen activator family from the salivary gland of the
 R6 vampire bat Desmodus rotundus: cloning and expression.";
 R7 Gene 105:229-237(1991).
 R8 [2]
 R9 CHARACTERIZATION.
 R10 MEDLINE=93393059; PubMed=1309059;
 R11 Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 R12 Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 R13 Donner P.;
 R14 "Plasminogen activators from the saliva of Desmodus rotundus (common
 R15 vampire bat): unique fibrin specificity.";
 R16 Ann. N.Y. Acad. Sci. 667:395-403(1992).
 R17
 R18 -!- FUNCTION: Probably essential to support the feeding habits of this
 R19 exclusively haematophagous animal. Probable potent thrombolytic
 R20 agent.
 R21
 R22 -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 R23 plasminogen to form plasmin.
 R24
 R25 CC

```
CC CC -!- SUBUNIT: Monomer.
CC CC -!- SIMILARITY: Belongs to peptidase family S1.
CC CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC CC -!- SIMILARITY: Contains 1 kringle domain.
CC CC -----
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CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; M63989; AAA31594.1; -.
CC CC PIR; J05539; J05599.
CC CC HSRF; P98119; IA51.
CC CC -----
CC CC MEROPS: S01.239; -.
CC CC InterPro; IPR009003; Cys_Ser_trypsin.
CC CC InterPro; IPR006209; EGF-like.
CC CC InterPro; IPR006210; IEGL.
CC CC -----
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[1] SEQUENCE FROM N.A.
 RP TISSUE=Salivary gland;
 RX MEDLINE=82039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RT vampire bat *Desmodus rotundus*: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX TISSUE=Salivary gland;
 RX MEDLINE=90036867; PubMed=2509450;
 RA Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
 RA Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
 RT "Isolation, characterization, and cDNA cloning of a vampire bat
 RT salivary plasminogen activator.";
 RL J Biol. Chem. 264:17947-17952(1989).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=9339059; PubMed=1309059;
 RA Schleuning W.D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of *Desmodus rotundus* (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 657:395-403(1992).
 CC -!- FUNCTION: Probably essential to support the feeding habits of this
 CC exclusively haematophagous animal. Probable potent thrombolytic
 CC agent.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
 CC plasminogen to form plasmin.
 CC -!- ENZYME REGULATION: Activity toward plasminogen is stimulated in
 CC the presence of fibrin I.
 CC -!- SUBUNIT: Monomer.
 CC -!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
 CC and the kringle domain apparently mediates fibrin-induced
 CC stimulation of activity.
 CC -!- SIMILARITY: Belongs to peptidase family S1.
 CC -!- SIMILARITY: Contains 1 EGF-like domain.
 CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.

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 or send an email to license@isb-sib.ch).

 CC EMBL; M63988; AAA31593.1; -;
 CC EMBL; J05082; AAA31596.1; -;
 CC PIR; A34369; A34369;
 CC PIR; J05098; J05098;
 CC HSP; P98119; IAS1.
 CC MEROPS; S01.232; -;
 CC InterPro; IPR009003; Cys_Ser_trypsin.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR000083; Fibrctn1.
 CC InterPro; IPR006210; IEGF.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR001354; Peptidase_S1.
 CC InterPro; IPR001314; Peptidase_S1a.
 CC Pfam; PF00008; EGF; 1.
 CC Pfam; PF00039; fn1; 1.
 CC Pfam; PF00051; kringle; 1.
 CC Pfam; PF00089; trypsin; 1.
 CC PRINTS; PR00722; CHYMOTRYPSIN.
 CC PRINTS; PR00018; KRINGLE.
 CC ProDom; PD000395; Kringle; 1.
 CC SMART; SM00181; EGF; 1.
 CC SMART; SM00058; FN1; 1.

DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; TRYD_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS50026; EGF_3; 1.
 DR PROSITE; PS01253; FIBONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS0240; TRYPSIN_DOM; 1.
 DR PROSITE; PS0134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36 POTENTIAL
 FT CHAIN 37 477 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 2.
 FT DOMAIN 40 82 FIBONECTIN TYPE-I.
 FT DOMAIN 83 121 EGF-LIKE.
 FT DOMAIN 128 209 KRINGLE.
 FT DOMAIN 225 477 SERINE PROTEASE.
 FT ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 321 321 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 428 428 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT DISULFID 42 72 BY SIMILARITY.
 FT DISULFID 70 79 BY SIMILARITY.
 FT DISULFID 87 98 BY SIMILARITY.
 FT DISULFID 92 109 BY SIMILARITY.
 FT DISULFID 111 120 BY SIMILARITY.
 FT DISULFID 128 209 BY SIMILARITY.
 FT DISULFID 149 191 BY SIMILARITY.
 FT DISULFID 180 204 BY SIMILARITY.
 FT DISULFID 214 345 BY SIMILARITY.
 FT DISULFID 257 273 BY SIMILARITY.
 FT DISULFID 265 334 BY SIMILARITY.
 FT DISULFID 359 434 BY SIMILARITY.
 FT DISULFID 391 407 BY SIMILARITY.
 FT DISULFID 424 452 BY SIMILARITY.
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 403 403 N -> K (IN REF. 2).
 FT CONFLICT 417 417 Y -> H (IN REF. 2).
 FT CONFLICT 435 435 M -> R (IN REF. 2).
 SQ SEQUENCE 477 AA; 53719 MW; 17486555C0E5077C CRC64;
 Query Match 43.5%; Score 241; DB 1; Length 477;
 Best Local Similarity 50.0%; Pred. No. 1.4e-19;
 Matches 42; Conservative 12; Mismatches 30; Indels 0; Gaps 0;
 QY 2 TCYEGNGHYRGKASTDTMGPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRPNR 61
 Db 127 TCYKQGVYRTWTSTSSGAQCINWNSLLTRTYNGRSDAITGLGNHNYCRPNR 186
 QY 62 RRPWCYVQGLKPLVQECWHDCA 85
 Db 187 SRPWCYVTKASKFILEFCSPVCS 210
 RESULT 9
 TPA_RAT STANDARD; PRT; 559 AA.
 ID_TPA_RAT
 AC P19637;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (TPA)
 DE (t-PA) (t-plasminogen activator).
 GN PLAT.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89170114; PubMed=3148445;

GN PLAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Melanoma;
RX MEDLINE=83115262; PubMed=6337343;
RA Pennica D., Holmes W.E., Kohr W.J., Harkins R.N., Vehar G.A.,
RA Ward C.A., Bennett W.F., Yelverton E., Seeburg P.H., Heyneker H.L.,
RA Goeddel D.V., Collen D.;
RT "Cloning and expression of human tissue-type plasminogen activator
RT cDNA in *E. coli*.";
RL Nature 301:214-221(1983).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=8262579; PubMed=3133640;
RA Sasaki H., Saito Y., Hayashi M., Otsuka K., Niwa M.;
RT "Nucleotide sequence of the tissue-type plasminogen activator cDNA
RT from human fetal lung cells.";
RL Nucleic Acids Res. 16:5695-5695(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88054470; PubMed=2824147;
RA Reddy V.B., Garramone A.J., Sasak H., Wei C.-M., Watkins P., Galli J.,
RA Hsiung N.;
RT "Expression of human uterine tissue-type plasminogen activator in
RT mouse cells using BPV vectors.";
RL DNA 6:461-472(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=66196143; PubMed=3009482;
RA Frierer Desen S.J., Rajput B., Reich E.;
RT "The human tissue plasminogen activator gene";
RL J. Biol. Chem. 261:6972-6985(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=84298137; PubMed=6089198;
RA Ny T., Elgh P., Lund B.;
RT "The structure of the human tissue-type plasminogen activator gene:
RT correlation of intron and exon structures to functional and
RT structural domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5355-5359(1984).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284200; PubMed=3090401;
RA Harris T.J., Patel T., Marston F.A., Little S., Emtage J.S.,
RA Opdenakker G., Volckaert G., Rombauts W., Billiau A., Somer P.;
RT "Cloning of cDNA coding for human tissue-type plasminogen activator
RT and its expression in *Escherichia coli*.";
RL Mol. Biol. Med. 3:279-292(1986).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC TISSUE=Umbilical vein;
RX MEDLINE=90192129; PubMed=2107528;
RA Siebert P.D., Fong K.;
RT "Variant tissue-type plasminogen activator (PLAT) cDNA obtained from
RT human endothelial cells";
RL Nucleic Acids Res. 18:1086-1086(1990).
RN [8]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Tshihyuki S., Canninci F., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [9]
RP SEQUENCE OF 212-361 FROM N.A.
RX MEDLINE=83169656; PubMed=6572897;
RA Edlund T., Ny T., Raanby M., Heden L.-O., Palm G., Holmgren E.,
RA Josephson S.;
RT "Isolation of cDNA sequences coding for a part of human tissue
RT plasminogen activator";
RL Proc. Natl. Acad. Sci. U.S.A. 80:349-352(1983).
RN [10]
RP SEQUENCE OF 1-36 FROM N.A.
RX MEDLINE=85289338; PubMed=3161893;
RA Fisher R., Waller E.K., Grossi G., Thompson D., Tizard R.,
RA Schleuning W.-D.;
RT "Isolation and characterization of the human tissue-type plasminogen
RT activator structural gene including its 5' flanking region.";
RL J. Biol. Chem. 260:11223-11230(1985).
RN [11]
RP SEQUENCE OF 31-562 FROM N.A.
RX MEDLINE=91291340; PubMed=1368681;
RA Itagaki Y., Yasuda H., Morinaga T., Mitsuda S., Higashio K.;
RT "Purification and characterization of tissue plasminogen activator
RT secreted by human embryonic lung diploid fibroblasts, INR-90 cells.";
RL Agric. Biol. Chem. 55:1225-1232(1991).
RN [12]
RP SEQUENCE OF 36-562.
RC TISSUE=Melanoma;
RX MEDLINE=85000468; PubMed=6433976;
RA Pohl G., Kaelinstroem M., Bergsdorf N., Wallen P., Joernvall H.;
RT "Tissue plasminogen activator: peptide analyses confirm an indirectly
RT derived amino acid sequence, identify the active site serine residue,
RT establish glycosylation sites, and localize variant differences.";
RL Biochemistry 23:3701-3707(1984).
RN [13]
RP SEQUENCE OF 33-52 AND 311-330.
RC TISSUE=Melanoma;
RX MEDLINE=83209620; PubMed=6682760;
RA Wallen P., Pohl G., Bergsdorf N., Raanby M., Ny T., Joernvall H.;
RT "Purification and characterization of a melanoma cell plasminogen
RT activator";
RL Eur. J. Biochem. 132:681-686(1983).
RN [14]
RP STRUCTURE OF CARBOHYDRATES.
RX MEDLINE=90092112; PubMed=2513186;
RA Pfeiffer G., Schmidt M., Strube K.-H., Geyer R.;
RT "Carbohydrate structure of recombinant human uterine tissue
RT plasminogen activator expressed in mouse epithelial cells.";
RL Eur. J. Biochem. 186:273-286(1989).
RN [15]
RP CARBOHYDRATE-LINKAGE SITE THR-96.
RX MEDLINE=91159408; PubMed=1900431;
RA Harris R.J., Leonard C.K., Guzzetta A.W., Spellman M.W.;
RT "Tissue plasminogen activator has an O-linked fucose attached to
RT threonine-61 in the epidermal growth factor domain.";
RL Biochemistry 30:2311-2314(1991).
RN [16]
RP DISULFIDE BONDS IN KRINGLE 2.
RX MEDLINE=91244765; PubMed=1645336;
RA Vlahos C.J., Wilhelm O.G., Hassell T., Jaskunas S.R., Bang N.U.;
RT "Disulfide pairing of the recombinant kringle-2 domain of tissue
RT plasminogen activator produced in *Escherichia coli*.";
RL J. Biol. Chem. 266:10070-10072(1991).

[17]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=96200985; PubMed=8613982;
RA Lamba D., Bauer M., Huber R., Fischer S., Rudolph R., Kohnert U.,
Bode W.;
RT "The 2.3 A crystal structure of the catalytic domain of recombinant
two-chain human tissue-type plasminogen activator.";
RL J. Mol. Biol. 258:117-135(1996).
[18]
RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF CATALYTIC DOMAIN.
RX MEDLINE=97449126; PubMed=9305622;
RA Renatus M., Engh R.A., Stubbs M.T., Huber R., Fischer S., Kohnert U.,
Bode W.;
RT "Lysine 156 promotes the anomalous proenzyme activity of tPA: X-ray
crystal structure of single-chain human tPA.";
RL EMBO J. 16:4797-4805(1999).
[19]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF KRINGLE 2.
RX MEDLINE=92118803; PubMed=1310033;
RA de Vos A., Ultsch M.H., Kelley R.F., Padmanabhan K., Tulinsky A.,
Westbrook M.L., Kossiakof A.A.;
RT "Crystal structure of the kringle 2 domain of tissue plasminogen
activator at 2.4-A resolution.";
RL Biochemistry 31:270-279(1992).
[20]
RP STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=90122799; PubMed=2558718;
RA Byeon I.-J.L., Kelley R.F., Llinas M.;
RT "1H NMR structural characterization of a recombinant kringle 2 domain
from human tissue-type plasminogen activator.";
RL Biochemistry 28:9350-9360(1989).
[21]
RP STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=91200042; PubMed=1901789;
RA Byeon I.-J.L., Kelley R.F., Llinas M.;
RT "Kringle-2 domain of the tissue-type plasminogen activator. 1H-NMR
assignments and secondary structure.";
RL Eur. J. Biochem. 197:155-165(1991).
[22]
RP STRUCTURE BY NMR OF KRINGLE 2.
RX MEDLINE=92106329; PubMed=1762144;
RA Byeon I.-J.L., Llinas M.;
RT "Solution structure of the tissue-type plasminogen activator kringle
2 domain complexed to 6-aminohexanoic acid an antifibrinolytic
drug.";
RL J. Mol. Biol. 222:1035-1051(1991).
[23]
Query Match 40.8%; Score 226; DB 1; Length 562;
Best Local Similarity 47.7%; Pred. No. 8.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
QY 2 TCYEGNGHYRGKASTDTWGRDCLPWSATVLOQTHAHSALQGLGKHNYCRNPDNR 61
DB 126 TCYEDQGISYRGTWSTAESGAECTNWNSSALAKPKYSGRPRPAIRLGLGNHNYCRNPD 185
QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
DB 186 SKWCYVFKAGKYSSSEFCSTPACSEG 211
RESULT 11
URTG_DESGO
ID URTG_DESGO STANDARD; PRT; 394 AA.
AC P49150;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSFA
gamma).
DE Desmodus rotundus (Vampire bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;

Desmodontinae; Desmodus.
NCBI_TaxID=9430;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=92039036; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
Alagon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
vampire bat Desmodus rotundus: cloning and expression.";
RL Gene 105:229-237(1991).
[2]
RP CHARACTERIZATION.
RX MEDLINE=93391059; PubMed=1309059;
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
Donner P.;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common
vampire bat): unique fibrin specificity.";
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
CC -!- FUNCTION: Probably essential to support the feeding habits of this
exclusively haematophagous animal. Probable potent thrombolytic
agent.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 kringle domain.
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or send an email to license@sib-sib.ch).
EMBL; M63990; AAA31595.1; -.
PIR; J50600; JS0600.
DR HSSP; P98119; IAS1.
DR MEROPS; S01.239; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle_
InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
PFam; PF00051; kring1; 1.
PFam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1; Spc; 1.
SMART; SM00020; Tryp_Spc; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS00240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
Kring1e; Signal; Multigene family.
KW SIGNAL 1 36 POTENTIAL.
FT CHAIN 37 394 SALIVARY PLASMINOGEN ACTIVATOR GAMMA.
FT DOMAIN 45 126 KRINGLE.
FT DOMAIN 142 394 SERINE PROTEASE.
FT ACT_SITE 189 189 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 345 345 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT DISULFID 45 126 BY SIMILARITY.
FT DISULFID 66 108 BY SIMILARITY.
FT DISULFID 97 121 BY SIMILARITY.
FT DISULFID 131 262 BY SIMILARITY.
FT DISULFID 174 190 BY SIMILARITY.
FT DISULFID 182 251 BY SIMILARITY.
FT DISULFID 276 351 BY SIMILARITY.


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FT DISULFID 308 324 BY SIMILARITY.
FT DISULFID 341 369 BY SIMILARITY.
FT CARBOHYD 315 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 394 AA; 44105 MW; 9CCD6F52F3D81FCD CRC64;

Query Match 39.7%; Score 220; DB 1; Length 394;
Best Local Similarity 45.2%; Pred. No. 2.6e-17;
Matches 38; Conservative 13; Mismatches 33; Indels 0; Gaps 0;

QY 2 TCVEGNHFRGKASTDTRGCPPLWNSATVLOOTVHAHRSALQGLGKKNYCRPNR 61
DB 44 TCYKDGQVTVRGTSWSESQAQCNINLLIRTYNGRMPFAVKLGLGNHNYCRNPDGA 103
QY 62 RRPWCYVQGLKPLVQECMVHDC 85
DB 104 SKWCYVYKARKKTSSECSVEPCS 127

RESULT 12
TPA_MOUSE STANDARD; PRT; 559 AA.
AC P11214; Q91VP2;
DT 01-JUL-1989 (Rel. 11, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tissue-type plasminogen activator precursor (EC 3.4.21.68) (LPA)
GN PLAT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8807303; PubMed=2826484;
RA Rickles R.J., Darrow A.L., Strickland S.;
RT "Molecular cloning of complementary DNA to mouse tissue plasminogen
RT activator mRNA and its expression during F9 teratocarcinoma cell
RT differentiation";
RL J. Biol. Chem. 263:1563-1569(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Mammary gland;
RA Straube R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.L., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
RA Buterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Warra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Converts the abundant, but inactive, zymogen plasminogen
CC to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By
CC controlling plasmin-mediated proteolysis, it plays an important
CC role in tissue remodeling and degradation, in cell migration and
CC many other physiopathological events.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
CC plasminogen to form plasmin.
CC -!- SUBUNIT: Heterodimer of chain A and chain B held by a disulfide
CC bond.
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CC -!- SUBCELLULAR LOCATION: Secreted; extracellular.
CC -!- PM: THE SINGLE CHAIN, ALMOST FULLY ACTIVE ENZYME, CAN BE FURTHER
CC PROCESSED INTO A TWO-CHAIN FULLY ACTIVE FORM BY A CLEAVAGE AFTER
CC ARG-308 CATALYZED BY PLASMIN, TISSUE KALLIKREIN OR FACTOR XA.
CC -!- MISCELLANEOUS: Binds to the kringle structure of the fibrin A
CC chain. Binding to fibrin enhances its catalytic activity.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 2 kringle domains.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J03520; AAA04070.1; --
CC EMBL; BC011256; AAH11256.1; --
CC PIR; A29941; A29941.
CC HSSP; P00750; IASH.
CC MEROPS; S01.232; --
CC MGD; MGI:97610; Plat.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR006209; EGF-like.
CC InterPro; IPR000083; Fibrinctn1.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00008; EGF; 1.
CC Pfam; PF00039; fn1; 1.
CC Pfam; PF00051; Kringle; 2.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 2.
CC SMART; SM00181; EGF; 1.
CC SMART; SM00058; FN1; 1.
CC SMART; SM00130; KR; 2.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00022; EGF 1; 1.
CC PROSITE; PS01186; EGF 2; 1.
CC PROSITE; PS00026; EGF 3; 1.
CC PROSITE; PS01253; FIBRONECTIN 1; 1.
CC PROSITE; PS00021; KRINGLE 1; 2.
CC PROSITE; PS00070; KRINGLE 2; 2.
CC PROSITE; PS00240; TRYPsin DOM; 1.
CC PROSITE; PS00134; TRYPsin HIS; 1.
CC PROSITE; PS00135; TRYPsin SER; 1.
CC Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
CC Plasma; Kringle; EGF-like domain; Repeat; Signal.
CC SIGNAL; 1 17 PROBABLE.
CC PROPEP; 18 28
CC CHAIN; 30 559
CC CHAIN; 30 308
CC
CC CHAIN; 309 559
CC
CC DOMAIN; 36 78 FIBRONECTIN TYPE-I.
CC DOMAIN; 79 117 EGF-LIKE.
CC DOMAIN; 124 205 KRINGLE 1.
CC DOMAIN; 213 294 KRINGLE 2.
CC DOMAIN; 309 359 SERINE PROTEASE.
CC ACT_SITE; 355 355 CHARGE RELAY SYSTEM.
CC ACT_SITE; 404 404 CHARGE RELAY SYSTEM.
CC ACT_SITE; 510 510 CHARGE RELAY SYSTEM.
CC DISULFID; 38 68 BY SIMILARITY.
CC DISULFID; 66 75 BY SIMILARITY.
CC DISULFID; 83 94 BY SIMILARITY.
CC DISULFID; 88 105 BY SIMILARITY.
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-!- FUNCTION: Probably essential to support the feeding habits of this
-!- exclusively haematophagous animal. Potent thrombolytic agent.
-!- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
-!- plasminogen to form plasmin.
-!- ENZYME REGULATION: Activity toward plasminogen is stimulated in
-!- the presence of fibrin I.
-!- SUBUNIT: Monomer.
-!- DOMAIN: The fibronectin type-I domain mediates binding to fibrin,
-!- and the kringle domain apparently mediates fibrin-induced
-!- stimulation of activity.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 1 fibronectin type I domain.
-!- SIMILARITY: Contains 1 kringle domain.
-!- SIMILARITY: Contains 1 kringle domain.

-----
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EMBL; M63987; AAA31591.1; -.
EMBL; M63986; AAA31592.1; -.
PIR; JS0597; JS0597.
PDB; 1A5I; 23-MAR-99.
MEROPS; S01.232; -.
GlycoSuiteDB; P98119; -.
InterPro; IPR009003; Cys_Ser_trypsin.
InterPro; IPR006209; EGF_like.
InterPro; IPR000083; Fibrctnctn1.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; K-kringle.
InterPro; IPR001254; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00008; EGF; 1.
Pfam; PF00039; fn1; 1.
Pfam; PF00051; kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CRYMOTRYPsin.
PRODOM; PD000395; Kringle; 1.
SMART; SM00181; EGF; 1.
SMART; SM00058; FN1; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00267; EGF_3; 1.
PROSITE; PS01253; FIBRONECTIN_1; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPsin_DOM; 1.
PROSITE; PS00134; TRYPsin_HIS; 1.
PROSITE; PS00135; TRYPsin_SER; 1.
Plasminogen activation; Hydrolase, Serine protease; Glycoprotein;
kringle; EGF-like domain; Signal; Multigene family; 3D-structure.
SIGNAL
CHAIN 1 36
DOMAIN 37 477 SALIVARY PLASMINOGEN ACTIVATOR ALPHA 1.
DOMAIN 40 82 FIBRONECTIN TYPE-I.
DOMAIN 83 121 EGF-LIKE.
DOMAIN 128 209 KRINGLE.
DOMAIN 225 477 SERINE PROTEASE.
ACT SITE 272 272 CHARGE RELAY SYSTEM.
ACT SITE 321 321 CHARGE RELAY SYSTEM.
ACT SITE 428 428 CHARGE RELAY SYSTEM.
DISULFID 42 72 BY SIMILARITY.
DISULFID 70 79 BY SIMILARITY.
DISULFID 87 98 BY SIMILARITY.
DISULFID 92 109 BY SIMILARITY.
DISULFID 111 120 BY SIMILARITY.
DISULFID 128 209 BY SIMILARITY.

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FT	DISULFID	149	191	BY SIMILARITY.
FT	DISULFID	180	204	BY SIMILARITY.
FT	DISULFID	214	345	
FT	DISULFID	257	273	
FT	DISULFID	265	334	
FT	DISULFID	359	434	
FT	DISULFID	391	407	
FT	DISULFID	424	452	
FT	CARBOHYD	153	153	
FT	CARBOHYD	398	398	N-LINKED (GLCNAC. . .).
FT				/FTid=CAR_000027.
FT				N-LINKED (GLCNAC. . .).
FT				/FTid=CAR_000028.
FT	TURN	214	215	
FT	STRAND	223	224	
FT	TURN	226	227	
FT	STRAND	230	231	
FT	HELIX	234	236	
FT	TURN	238	239	
FT	STRAND	240	245	
FT	STRAND	254	263	
FT	TURN	264	265	
FT	STRAND	266	269	
FT	HELIX	271	273	
FT	TURN	280	282	
FT	STRAND	284	287	
FT	TURN	297	298	
FT	STRAND	300	309	
FT	TURN	311	312	
FT	TURN	315	317	
FT	TURN	319	320	
FT	STRAND	323	328	
FT	STRAND	338	338	
FT	TURN	339	340	
FT	STRAND	341	341	
FT	STRAND	345	345	
FT	TURN	349	350	
FT	TURN	355	356	
FT	STRAND	358	363	
FT	STRAND	366	366	
FT	STRAND	374	374	
FT	STRAND	379	385	
FT	STRAND	388	390	
FT	HELIX	393	398	
FT	TURN	403	404	
FT	STRAND	405	409	
FT	TURN	425	426	
FT	TURN	428	429	
FT	STRAND	431	436	
FT	TURN	437	438	
FT	STRAND	439	448	
FT	TURN	455	456	
FT	STRAND	459	463	
FT	HELIX	464	467	
FT	HELIX	468	474	
FT	SEQUENCE	477 AA; 53616 MW; AA06FD1739C10B5E CRC64;		
Query Match		38.4%; Score 213; DB 1; Length 477;		
Best Local Similarity		46.4%; Pred. No. 2e-16;		
Matches	39; Conservative	10; Mismatches 35; Indels 0; Gaps 0;		
Qy	2	TCVGGNGHGYRKGASTDTMGREFCLPWN SATVLOQTVHAHRS DALQLGLGKHNYCRNP NR 61		
Db	127	TCVGGGVYRGTWNTAERSRVECIWNSSLLTRRTYNGRMPDAFNLGLGNHNYCRNPNGA 186		
Qy	62	RRPCWYVQGLKPLVQECMVDCA 85		
Db	187	KPFCWYVIRAKGFTSGSCGVPVCS 210		
RESULT 14				
TPA_BOVIN				
ID_TPA_BOVIN		STANDARD;	PRT:	566 AA.
AC_Q28198;				

DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Plasma; Kringle; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 21
FT PROPEP 22 33
FT CHAIN 34 566
FT CHAIN 34 334
FT CHAIN 315 566
FT CHAIN 40 82
FT DOMAIN 83 121
FT DOMAIN 128 209
FT DOMAIN 219 300
FT DOMAIN 315 566
FT ACT_SITE 361 361
FT ACT_SITE 410 410
FT ACT_SITE 517 517
FT DISULFID 42 72
FT DISULFID 70 79
FT DISULFID 87 98
FT DISULFID 92 109
FT DISULFID 111 120
FT DISULFID 128 209
FT DISULFID 149 191
FT DISULFID 180 204
FT DISULFID 219 300
FT DISULFID 240 282
FT DISULFID 271 295
FT DISULFID 303 434
FT DISULFID 346 362
FT DISULFID 354 423
FT DISULFID 448 523
FT DISULFID 480 496
FT DISULFID 513 541
FT DISULFID 513 541
FT CARBOHYD 153 153
FT CARBOHYD 487 487
SQ SEQUENCE 566 AA; 63701 MW; 2EB6EB4E32276C3 CRC64;
Query Match 37.7%; Score 209; DB 1; Length 566;
Best Local Similarity 47.6%; Pred. No. 6.6e-16;
Matches 39; Conservative 9; Mismatches 34; Indels 0; Gaps 0;
QY 3 CYEGNGHFRGKASTDTGRCPLPWNASVLOQTTHAHRSDALQLGLGHVCRNPDRR 62
DB 219 CYTGNGLAYRGTRSHRTKSGASCLPWNVSFLTSKIYTAWKSNAPALGLGHVCRNPDRR 278
QY 63 RPWCYVQVGLKPLVQECVHDC 84
DB 279 QPWCYVQVGLKPLVQECVHDC 300
RESULT 15
ID UROK_CHICK STANDARD; PRT; 434 AA.
AC P5120;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urokinase-type plasminogen activator precursor (EC 3.4.21.73) (uPA)
DS (U-plasminogen activator).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90110185; PubMed=2295632;
RA Leslie N.D., Kessler C.A., Bell S.M., Degen J.L.;
RT "The chicken urokinase-type plasminogen activator gene."

J. Biol. Chem. 265:1339-1344(1990).
-1- CATALYTIC ACTIVITY: Specific cleavage of Arg-|-Val bond in
plasminogen to form plasmin.
-1- SIMILARITY: Belongs to peptidase family S1.
-1- SIMILARITY: Contains 1 EGF-like domain.
-1- SIMILARITY: Contains 1 kringle domain.
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EMBL; J05187; AAA49131.1; -
EMBL; J05188; AAA49130.1; -
PIR; A35005; A35005.
HSP; P00763; IDPO.
MEROPS; S01.231; -
InterPro; IPR009003; Cys Ser trypsin.
InterPro; IPR006209; EGF-like.
InterPro; IPR006210; IEGF.
InterPro; IPR000001; Kringle.
InterPro; IPR008293; Pept_S1A_uPA.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
PIRSF; PIRSF001144; Urokinase; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00181; EGF; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp_SPC; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00026; EGF_3; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
KW Kringle; EGF-like domain; Signal; Zymogen.
FT SIGNAL 1 20
FT CHAIN 21 434 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
FT CHAIN 21 171 CHAIN A (BY SIMILARITY).
FT CHAIN 173 434 CHAIN B (BY SIMILARITY).
FT DOMAIN 36 72 EGF-LIKE.
FT DOMAIN 79 158 KRINGLE.
FT DOMAIN 159 172 CONNECTING PEPTIDE.
FT DOMAIN 173 434 SERINE PROTEASE.
FT DISULFID 40 48 BY SIMILARITY.
FT DISULFID 42 60 BY SIMILARITY.
FT DISULFID 62 71 BY SIMILARITY.
FT DISULFID 162 296 INTERCHAIN (BY SIMILARITY).
FT DISULFID 202 218 BY SIMILARITY.
FT DISULFID 210 285 BY SIMILARITY.
FT DISULFID 310 379 BY SIMILARITY.
FT DISULFID 342 358 BY SIMILARITY.
FT DISULFID 369 397 BY SIMILARITY.
FT ACT_SITE 217 217 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 272 272 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 373 373 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 228 228 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 434 AA; 49400 MW; BD81048DD666A55 CRC64;
Query Match 35.8%; Score 198.5; DB 1; Length 434;
Best Local Similarity 54.4%; Pred. No. 7.6e-15;
Matches 37; Conservative 7; Mismatches 19; Indels 5; Gaps 2;

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QY 3 CYGNGHYRGKASTDMGRPCLPMSATVLO-QTVHAHRSALQGLGKHYCRNPDR 61
Db 79 CYSGNEDYRGMAEDP---GCLYWDHPSVIRNGDYHADLKHALQGLGKHYCRNPGR 134
QY 62 RRPWCYVQ 69
Db 135 SRPWCYTK 142

RESULT 16
HGFA_HUMAN STANDARD; PRT; 655 AA.
AC Q04756; Q14726;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor activator precursor (EC 3.4.21.-) (HGF
DE activator) (HGFA).
GN HGFA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Liver, and Serum;
RX MEDLINE=93252878; PubMed=7693665;
RA Miyazawa K., Shimomura T., Kitamura A., Kondo J., Morimoto Y.,
RA Kitamura N.;
RT "Molecular cloning and sequence analysis of the cDNA for a human
RT serine protease responsible for activation of hepatocyte growth
RT factor. Structural similarity of the protease precursor to blood
RT coagulation factor XII.";
RL J. Biol. Chem. 268:10024-10028(1993).
RN [2]
SEQUENCE OF 40-655 FROM N.A.
RA Zhao S., Odell C.;
RL Submitted (PEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Activates hepatocyte growth factor (HGF) by
CC converting it from a single chain to a heterodimeric form.
CC -!- SUBUNIT: Dimer of a short chain and a long chain linked by a
CC disulfide bond.
CC -!- SUBCELLULAR LOCATION: Secreted as an inactive single-chain
CC precursor and is then activated to a heterodimeric form.
CC -!- TISSUE SPECIFICITY: Liver.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -!- CAUTION: It is uncertain whether Met-1 is the initiator.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC
CC -----
CC EMBL; D14012; BAA03113.1; -
CC EMBL; Z69923; -; NOT_ANNOTATED_CDS.
CC PIR; A46688; A46688.
CC DR MEROPS; S01.228; -.
CC DR Genew; HGNC:4894; HGFA.
CC MIM; 604552; -.
CC DR GO; GO:0005576; C:extracellular; TAS.
CC DR GO; GO:0004252; F:serine-type endopeptidase activity; TAS.
CC DR GO; GO:0006508; F:proteolysis and peptidolysis; TAS.
CC DR InterPro; IPR009003; Cys_Ser_trypsin.
CC DR InterPro; IPR000742; EGF_2.
CC DR InterPro; IPR006209; EGF_like.
```

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DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00083; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000995; FN_Type_II; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Glycoprotein; Plasma; Serine protease; Kringle; Signal;
KW EGF-like domain; Repeat; Zymogen.
FT SIGNAL 1 30
FT PROPEP 31 372
FT CHAIN 373 407
FT
FT CHAIN 408 655
FT DOMAIN 108 148
FT DOMAIN 160 198
FT DOMAIN 200 240
FT DOMAIN 241 279
FT DOMAIN 286 367
FT DOMAIN 408 655
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FT ACT_SITE 598 598
FT DISULFID 108 133
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FT DISULFID 188 197
FT DISULFID 202 230
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FT DISULFID 338 362
FT DISULFID 394 521
FT DISULFID 432 448
FT DISULFID 440 510
FT DISULFID 535 604
FT DISULFID 567 593
FT DISULFID 594 622
FT CARBOHYD 48 48
FT CARBOHYD 290 290
FT CARBOHYD 468 468
FT CARBOHYD 492 492
FT CARBOHYD 546 546
FT CARBOHYD 644 644
FT CONFLICT 644 644
FT
FT CHAIN 408 655
FT FIBRONECTIN TYPE-II.
FT EGF-LIKE 1.
FT FIBRONECTIN TYPE-I.
FT EGF-LIKE 2.
FT KRINGLE.
FT SERINE PROTEASE.
FT CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CHARGE RELAY SYSTEM (BY SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT INTERCHAIN (BY SIMILARITY).
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT BY SIMILARITY.
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT R -> Q (IN REF. 2).
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```

SQ SEQUENCE 655 AA; 70681 MW; 2CF72F1E1B962ED7 CRC64;
Query Match 35.1%; Score 194.5; DB 1; Length 655;
Best Local Similarity 40.4%; Pred. No. 3.3e-14;
Matches 42; Conservative 8; Mismatches 41; Indels 13; Gaps 1;

QY 3 CYEGNGHFYGKASTDTMGRCPLPWNATVLQOTVHAHRSDALOLGKGKNYCRRPNR 62
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 286 CFLNGGTGYRGVAGTSASGSCLAWNSDLLIQELHVDVSVAALLGLGPHAYCRRPNDE 345
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

QY 63 RPWCYVQVGLKPLVQECWHDC-----ADGKKPSP 93
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 346 RPWCYVVKDSALSWEYCRLEACESLTRVQLSPDLLLATLPEPASP 389
   :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 17
FAI2 CAVPO STANDARD; PRT; 603 AA.
ID _FAI2 CAVPO
AC Q04952;
DT 01-FEB-1996 (Rel. 33, Created)
DI 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
DE (HAF) (Fragment).
GN F12.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 19-37; 318-332 AND 359-373.
RC TISSUE=Liver;
RX MEDLINE=93003367; PubMed=1390917;
RA Senba U., Yamamoto T., Kunisada T., Shibuya Y., Tanase S.,
RA Kambara T., Okabe H.;
RT "Primary structure of guinea-pig Hageman factor: sequence around the
RT cleavage site differs from the human molecule.";
RL Biochim. Biophys. Acta 1159:113-121(1992).
CC -! FUNCTION: Factor XII is a serum glycoprotein that participates in
CC the initiation of blood coagulation, fibrinolysis, and the
CC generation of bradykinin and angiotensin.
CC -! CATALYTIC ACTIVITY: Cleaves selectively Arg--|-tle bonds in factor
CC VII to form factor VIIIa and factor XI to form factor Xla.
CC -! MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor Xlla and then to beta-factor Xlila. Alpha-factor
CC Xlila activates factor XI to factor Xla.
CC -! SIMILARITY: Belongs to peptidase family S1.
CC -! SIMILARITY: Contains 2 EGF-like domains.
CC -! SIMILARITY: Contains 1 fibronectin type I domain.
CC -! SIMILARITY: Contains 1 fibronectin type II domain.
CC -! SIMILARITY: Contains 1 kringle domain.
CC -----
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CC -----
DR EMBL; X68615; CAA48600.1; -.
DR FIR; S28941; S28941.
DR HSSP; P00763; IDPO.
DR MEROPS; S01.211; -.
DR InterPro; IPRO009003; Cys_ser_trypsin.
DR InterPro; IPRO00742; EGF-2.
DR InterPro; IPRO01881; EGF_Ca.
DR InterPro; IPRO06209; EGF_Like.
DR InterPro; IPRO00083; Fibrctncl.
DR InterPro; IPRO00562; FN type_II.
DR InterPro; IPRO06210; IEGF.

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[illegible]

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Db      283 CFLGNTGTRGVASTRAASGLSCLAWNSDLLYOELHVDVAAAVLLGLGPHAYCRNPKDE 342
Qy      63 RWCYV 68
Db      343 RWCYV 348

RESULT 19
FA12_HUMAN
ID FA12_HUMAN STANDARD; PRT; 615 AA.
AC P00748; P78339;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
DE (HAFT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88007593; PubMed=2888762;
RA Cool D.E., McGillivray R.T.A.;
RT "Characterization of the human blood coagulation factor XII gene.
RT Intron/exon gene organization and analysis of the 5'-flanking
RT region.";
RL J. Biol. Chem. 262:13662-13673 (1987).
RN [2]
RP SEQUENCE FROM N.A. AND VARIANTS ALA-207; ASP-545 AND HIS-605.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RA Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 4-615 FROM N.A.
RX MEDLINE=86176794; PubMed=3754331;
RA Tripodi M., Citarella F., Guida S., Galeffi P., Fantoni A.,
RA Cortese R.;
RT "cDNA sequence coding for human coagulation factor XII (Hageman).";
RL Nucleic Acids Res. 14:3146-3146 (1986).
RN [4]
RP SEQUENCE OF 14-615 FROM N.A.
RX MEDLINE=86033830; PubMed=3877053;
RA Cool D.E., Edgell C.-J.S., Louie G.V., Zoller M.J., Brayer G.D.,
RA McGillivray R.T.A.;
RT "Characterization of human blood coagulation factor XII cDNA.
RT Prediction of the primary structure of factor XII and the tertiary
RT structure of beta-factor XIIa.";
RL J. Biol. Chem. 260:13666-13676 (1985).
RN [5]
RP SEQUENCE OF 146-615 FROM N.A.
RX MEDLINE=86216049; PubMed=3011063;
RA Que B.G., Davie E.W.;
RT "Characterization of a cDNA coding for human factor XII (Hageman
RT factor).";
RL Biochemistry 25:1525-1528 (1986).
RN [6]
RP SEQUENCE OF 20-379.
RX MEDLINE=85182674; PubMed=3886654;
RA McMullen B.A., Fujikawa K.;
RT "Amino acid sequence of the heavy chain of human alpha-factor XIIa
RT (activated Hageman factor).";
RL J. Biol. Chem. 260:5328-5341 (1985).
RN [7]
RP SEQUENCE OF 354-362 AND 373-615.
RX MEDLINE=83291041; PubMed=6604055;
RA Fujikawa K., McMullen B.A.;
RT "Amino acid sequence of human beta-factor XIIa.";
RL J. Biol. Chem. 258:10924-10933 (1983).
RN [8]
RP SEQUENCE OF 561-615 FROM N.A.
RC TISSUE=Blood;

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RX MEDLINE=96133302; PubMed=8528215;
RA Schloesser M., Hofferbert S., Bartz U., Lutze G., Lammie B., Engel W.;
RT "The novel acceptor splice site mutation 1139c(G->A) in the factor
RT XII gene causes a truncated transcript in cross-reacting material
RT negative patients.";
RL Hum. Mol. Genet. 4:1235-1237 (1995).
RN [9]
RP CARBOHYDRATE-LINKAGE SITE THR-109.
RX MEDLINE=92184750; PubMed=1544894;
RA Harris R.J., Ling V.T., Spellman M.W.;
RT "O-linked fucose is present in the first epidermal growth factor
RT domain of factor XII but not protein C.";
RL J. Biol. Chem. 267:5102-5107 (1992).
RN [10]
RP VARIANT WASHINGTON D.C. SER-590.
RX MEDLINE=90046788; PubMed=2510163;
RA Miyata T., Kawabata S.-I., Iwanaga S., Takahashi I., Alving B.,
RA Saito H.;
RT "Coagulation factor XII (Hageman factor) Washington D.C.: inactive
RT factor XIIa results from Cys-571->Ser substitution.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:8319-8322 (1989).
RN [11]
RP VARIANT LOCARNO PRO-372.
RX MEDLINE=94325559; PubMed=8049433;
RA Hovinga J.K., Schaller J., Stricker H., Willemin W.A., Furlan M.,
RA Laemmle B.;
RT "Coagulation factor XII Locarno: the functional defect is caused by
RT the amino acid substitution Arg-353->Pro leading to loss of a
RT kallikrein cleavage site.";
RL Blood 84:1173-1181 (1994).
RN [12]
RP VARIANT TENRI CYS-53.
RX MEDLINE=9920785; PubMed=10361128;
RA Kondo S., Tokunaga F., Kawano S., Ono Y., Kumagai S., Koide T.;
RT "Factor XII Tenri, a novel cross-reacting material negative factor XII
RT deficiency, occurs through a proteasome-mediated degradation.";
RL Blood 93:4300-4308 (1999).
RN [13]
RP FUNCTION: Factor XII is a serum glycoprotein that participates in
CC the initiation of blood coagulation, fibrinolysis, and the
CC generation of bradykinin and angiotensin.
CC -!- FUNCTION: Cleaves selectively Arg-|-Ile bonds in factor
CC VII to form factor VIIa and factor XI to form factor Xla.
CC -!- PTM: O- AND N-GLYCOSYLATED.
CC -!- DISEASE: Defects in F12 do not cause any clinical symptoms. The
CC sole effect is that whole-blood clotting time is prolonged.
CC -!- MISCELLANEOUS: Factor XII, prekallikrein, and HMW kininogen form a
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor
CC XIIa activates factor XI to factor Xla.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 EGF-like domains.
CC -!- SIMILARITY: Contains 1 fibronectin type I domain.
CC -!- SIMILARITY: Contains 1 fibronectin type II domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; M31315; AAA70225.1; -
CC EMBL; AF538691; AAM57932.1; -
CC EMBL; M11723; AAA51986.1; -
CC EMBL; M17466; AAB59490.1; -
CC EMBL; M17464; AAB59490.1; JOINED.
CC EMBL; M17465; AAB59490.1; JOINED.
CC EMBL; M13147; AAB70224.1; -
CC EMBL; U71274; AAB51203.1; -
CC PIR; A29411; KFHU12.

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Db      272 DIRPWCFTV 279
|||||:|
RESULT 20
APOA_MACMU
ID APOA_MACMU STANDARD; PRT; 1420 AA.
AC P14417;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apo lipoprotein(a) (EC 3.4.21.-) (Apo(a)) (Lp(a)) (Fragment).
LN LPA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=5544;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=89174660; PubMed=2955643;
RT Tomlinson J.E., McLean J.W., Lawn R.M.;
RT "Rhesus monkey apolipoprotein(a) : Sequence, evolution, and sites of
RT synthesis."
RL J. Biol. Chem. 264:5957-5965(1989).
CC CC -1- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC (Lp(a)). It has serine proteinase activity and is able of
CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
CC Lp(a) may be a ligand for megalin/Gp 330.
CC -1- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibronectin and
CC decorin (By similarity).
CC -1- PFM: N- and O-glycosylated (By similarity).
CC -1- DISEASE: Elevated plasma concentrations of apo(a) and its
CC naturally occurring proteolytic fragments are correlated with
CC atherosclerosis. Homology with plasminogen kringle IV and V is
CC thought to underlie the atherogenicity of the protein, because the
CC fragments are competing with plasminogen for fibrin(ogen) binding.
CC -1- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC leading to the formation of the so called mini-Lp(a). Apo(a)
CC fragments accumulate in atherosclerotic lesions, where they may
CC promote thrombogenesis. O-glycosylation may limit the extent of
CC proteolytic fragmentation (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family S1, plasminogen subfamily.
CC -1- SIMILARITY: Contains at least 10 kringle domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J04635; AAA36833.1; -
CC PIR; A32869; A32869.
CC HSP; P00747; 2PK4.
CC MEROPS; S01.226; -.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR000001; Kringle
CC InterPro; IPR001254; Peptidase_S1
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00051; Kringle; 11.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 10.
CC SMART; SM00130; KR; 10.
CC SMART; SM00200; TRY2_SPC; 1.
CC PROSITE; PS00021; KRINGLE_1; 10.
CC PROSITE; PS00070; KRINGLE_2; 10.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
CC PROSITE; PS00134; TRYPSIN_HIS; FALSE NEG.
CC PROSITE; PS00135; TRYPSIN_SER; FALSE NEG.

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KW Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein;
KW Kringle; Repeat; Atherosclerosis.
FT NON_TER 1
FT DOMAIN 49 127 KRINGLE 1.
FT DOMAIN 163 241 KRINGLE 2.
FT DOMAIN 277 355 KRINGLE 3.
FT DOMAIN 391 469 KRINGLE 4.
FT DOMAIN 505 583 KRINGLE 5.
FT DOMAIN 619 697 KRINGLE 6.
FT DOMAIN 725 803 KRINGLE 7.
FT DOMAIN 839 917 KRINGLE 8.
FT DOMAIN 953 1031 KRINGLE 9.
FT DOMAIN 1067 1145 KRINGLE 10.
FT DOMAIN 1191 1420 SERINE PROTEASE.
SQ SEQUENCE 1420 AA; 158367 MW; BE102945E03C580E CRC64;
Query Match 29.1%; Score 161; DB 1; Length 1420;
Best Local Similarity 40.9%; Pred. No. 4.4e-10;
Matches 36; Conservative 9; Mismatches 31; Indels 12; Gaps 4;
QY 3 CYEENGHFGKASDTMGRPCLPWNSATVLO--QTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 1068 CHYENGQSRGTFSTVIGRTQCSHSMTPHGHKTPENHPNDLTM-----NYCRNPD 1122
QY 61 RRRPWCYOVGLKPLVQE--CMWHDCA 86
DB 1123 DTGPWCFT---MDPSVRREYCNLTRCS 1147
RESULT 21
KRM1_MOUSE STANDARD; PRT; 473 AA.
ID KRM1_MOUSE
AC Q99N43;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
DE and the nose (Dickkopf receptor).
GN KREMEN1 OR KREMEN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
RC TISSUE=Brain, and Kidney;
RX MEDLINE=21167372; PubMed=11267660;
RA Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K., Nakamura T.;
RT "Molecular cloning and characterization of Kremen, a novel kringle-containing transmembrane protein.";
RL Biochim. Biophys. Acta 1518:63-72(2001).
CC -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Wnt/beta-catenin signaling (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: In the adult, widely expressed with high levels in heart, lung, kidney, skeletal muscle and testis.
CC -!- DEVELOPMENTAL STAGE: In the embryo, expression is first detected on day 9 and increases up to day 18. Lower levels are found in adult. At 9.5 dpc, expression is localised to the apical ectodermal ridge (AER) of the developing fore- and hindlimb buds, the telencephalon and the first brachial arch. At 10.5 dpc, expression is also observed in the myotome and in sensory tissues such as the nasal pit and optic vesicle.
CC -!- SIMILARITY: Contains 1 CUB domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -!- SIMILARITY: Contains 1 WSC domain.

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CC -----
CC EMBL; AB059617; BAB40968.1; -
CC HSP; P00747; ICEA.
CC MGD; MGI:1933988; Kremen.
CC GO; GO:0016021; C:Integral to membrane; NAS.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR002899; WSC.
CC Pfam; PF00431; CUB; 1.
CC Pfam; PF0051; kringle; 1.
CC Pfam; PF01822; WSC; 1.
CC PRINTS; PD00018; KRINGLE.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00042; CUB; 1.
CC SMART; SM00130; KR; 1.
CC PROSITE; PS01180; CUB; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS00070; KRINGLE_2; 1.
CC KX Wnt signaling pathway; Signal; Transmembrane; Kringle.
FT SIGNAL 1 19
FT CHAIN 20 473 KREMEN PROTEIN 1.
FT DOMAIN 21 392 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 393 413 POTENTIAL.
FT DOMAIN 414 473 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 114 KRINGLE.
FT DOMAIN 120 210 WSC.
FT DOMAIN 214 321 CUB.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 217 217 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 255 255 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 345 345 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 473 AA; 51716 MW; 586827788BE3FDD1 CRC64;
Query Match 28.7%; Score 159; DB 1; Length 473;
Best Local Similarity 45.6%; Pred. No. 2.3e-10;
Matches 31; Conservative 7; Mismatches 26; Indels 4; Gaps 2;
QY 3 CYEENGHFGKASDTM--GRPCLPWNSATVLCQTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 32 CFTANGADYRGTSQSWTALQGGKPCLFWNE--TFQHPYNTLKYNGEGGLGHEHNYCRNPDG 89
QY 61 RRRPWCYV 68
DB 90 DVSPWCYV 97
RESULT 22
KRM1_MOUSE STANDARD; PRT; 473 AA.
ID KRM1_MOUSE
AC Q924S4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
DE KREMEN1 OR KREMEN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakamura T., Nakamura T.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Wnt/beta-catenin signaling (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- SIMILARITY: Contains 1 CUB domain.
CC -!- SIMILARITY: Contains 1 kringle domain.

CC -1- SIMILARITY: Contains 1 WSC domain.
 CC -----
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 CC -----
 CC EMBL; AB065090; BAB62003.1; -
 CC GO:0016021; C: integral to membrane; ISS.
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR002889; WSC.
 CC Pfam; PF00431; CUB; 1.
 CC Pfam; PF00051; Kringle; 1.
 CC Pfam; PF01822; WSC; 1.
 CC PRINTS; PR00018; KRINGLE.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS00021; KRINGLE_2; 1.
 CC PROSITE; PS000395; Kringle; 1.
 CC SMART; SM00042; CUB; 1.
 CC SMART; SM00130; KR; 1.
 CC SMART; SM00321; WSC; 1.
 CC PROSITE; PS01180; CUB; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS00021; KRINGLE_2; 1.
 CC Wnt signaling pathway; Signal; Transmembrane; Kringle.
 CC SIGNAL 1 19
 CC CHAIN 20 473
 CC KREMER PROTEIN 1.
 CC POTENTIAL.
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 393 413
 CC DOMAIN 414 473
 CC CYTOPLASMIC (POTENTIAL).
 CC KRINGLE.
 CC WSC.
 CC CUB.
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 59 59
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 217 217
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 255 255
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 293 293
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 333 333
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 345 345
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SEQUENCE 473 AA; 51869 MW; 9B510857DF856F08 CRC64;
 Query Match 28.7%; Score 159; DB 1; Length 473;
 Best Local Similarity 45.6%; Pred. No. 2.3e-10;
 Matches 31; Conservative 7; Mismatches 26; Indels 4; Gaps 2;
 QY 3 CYEGNGHYRGKASTDTM--GRPCLPWNSATVLOQTHAHSRDLQLGLGKHNYCRNPDN 60
 DB 32 CFTANGADYRGTSWTALQGGKPCLFWNE--TFQHPYNTLKYPNGEGGLGHEHNYCRNPDG 89
 QY 61 RRRPWCYV 68
 DB 90 DVSPWCYV 97
 RESULT 23
 ID KRM1_XENLA STANDARD; PRT; 452 AA.
 AC Q90Y90;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Kremen protein 1 precursor (Kringle-containing protein marking the eye
 DE and the nose) (Dickkopf receptor).
 GN KREMN1.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nakamura T.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
 CC to block wnt/beta-catenin signaling (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- SIMILARITY: Contains 1 CUB domain.
 CC -1- SIMILARITY: Contains 1 kringle domain.
 CC -1- SIMILARITY: Contains 1 WSC domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB070851; BAB64294.1; -
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR002889; WSC.
 CC Pfam; PF00431; CUB; 1.
 CC Pfam; PF00051; Kringle; 1.
 CC Pfam; PF01822; WSC; 1.
 CC PRINTS; PR00018; KRINGLE.
 CC PROSITE; PS000395; Kringle; 1.
 CC SMART; SM00042; CUB; 1.
 CC SMART; SM00130; KR; 1.
 CC SMART; SM00321; WSC; 1.
 CC PROSITE; PS01180; CUB; 1.
 CC PROSITE; PS00021; KRINGLE_1; 1.
 CC PROSITE; PS00021; KRINGLE_2; 1.
 CC Wnt signaling pathway; Glycoprotein; Kringle;
 CC Transmembrane; Signal.
 CC SIGNAL 1 22
 CC CHAIN 23 452
 CC KREMER PROTEIN 1.
 CC EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 370 390
 CC DOMAIN 391 452
 CC CYTOPLASMIC (POTENTIAL).
 CC KRINGLE.
 CC WSC.
 CC CUB.
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 57 57
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 215 215
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 253 253
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 291 291
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 328 328
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 344 344
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC SEQUENCE 452 AA; 50188 MW; ED24BCDIAF4564E2 CRC64;
 Query Match 28.5%; Score 158; DB 1; Length 452;
 Best Local Similarity 44.1%; Pred. No. 2.8e-10;
 Matches 30; Conservative 9; Mismatches 25; Indels 4; Gaps 2;
 QY 3 CYEGNGHYRGKASTDTM--GRPCLPWNSATVLOQTHAHSRDLQLGLGKHNYCRNPDN 60
 DB 30 CYTVNGADYRGTSWTALQGGKPCLFWNE--TFQHPYNTLKYPNGEGGLGHEHNYCRNPDG 87
 QY 61 RRRPWCYV 68
 DB 88 DVSPWCYV 95
 RESULT 24
 ID APOA_HUMAN STANDARD; PRT; 4548 AA.
 AC P08519;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Apolipoprotein(a) precursor (EC 3.4.21.-) (Apo(a)) (Lp(a)).
 GN LPA.
 OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89039109; PubMed=3670400; Eaton D.L., Chen E.Y.,
RA McLean J.W., Tomlison J.E., Kuang W.-J., Eaton D.L., Chen E.Y.,
RA Fless G.M., Scannu A.M., Lawn R.M.;
RT "cDNA sequence of human apolipoprotein(a) is homologous to
RL plasminogen.";
RL Nature 330:132-137(1987).
RN [2]
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=90076123; PubMed=2531657;
RA Salonen E.-M., Jauhainen M., Zardi L., Vaheri A., Ehnholm C.;
RT "Lipoprotein(a) binds to fibrinogen and has serine proteinase
RT activity capable of cleaving it.";
RL EMBO J. 8:4035-4040(1989).
RN [3]
RP REVIEW.
RX MEDLINE=90049223; PubMed=2530631;
RA Utermann G.;
RT "The mysteries of lipoprotein(a).";
RL Science 246:904-910(1989).
RN [4]
RP CHARACTERIZATION OF THE N- AND O-LINKED GLYCANS.
RX MEDLINE=21303595; PubMed=11294842;
RA Garner B., Merry A.H., Royce L., Harvey D.J., Rudd P.M., Thillet J.;
RT "Structural elucidation of the N- and O-glycans of human
RT apolipoprotein(a): role of o-glycans in conferring protease
RT resistance.";
RL J. Biol. Chem. 276:22200-22208(2001).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 4121-4208.
RX MEDLINE=96217891; PubMed=8642595;
RA Mikol V., Ligrasso P.V., Boettcher B.R.;
RT "Crystal structures of apolipoprotein(a) kringle IV27 free and
RT complexed with 6-aminohexanoic acid and with p-aminomethylbenzoic
RL acid: existence of novel and expected binding modes.";
RL J. Mol. Biol. 256:751-761(1996).
RN [6]
RP VARIANT ARG-4193.
RX MEDLINE=95002201; PubMed=7918682;
RA Scannu A.M., Lee J.C., Hinman J.;
RT "A single point mutation (Trp72-->Arg) in human apo(a) kringle 4-37
RT associated with a lysine binding defect in Lp(a).";
RL Biochim. Biophys. Acta 1227:41-45(1994).
CC -!- FUNCTION: Apo(a) is the main constituent of lipoprotein(a)
CC (Lp(a)). It has serine proteinase activity and is able of
CC autoproteolysis. Inhibits tissue-type plasminogen activator 1.
CC Lp(a) may be a ligand for megalin/Gp 330.
CC -!- SUBUNIT: Disulfide-linked to apo-B100. Binds to fibrinectin and
CC decorin.
CC -!- PTM: N- and O-glycosylated. The N-glycans are complex biantennary
CC structures present in either a mono- or disialylated state. The
CC O-glycans are mostly (80%) represented by the monosialylated core
CC type I structure, NeuNAcHex2-3Galbeta1-3GalNAc, with smaller
CC amounts of disialylated and non-sialylated O-glycans also
CC detected.
CC -!- DISEASE: Elevated plasma concentrations of apo(a) and its
CC naturally occurring proteolytic fragments are correlated with
CC atherosclerosis. Homology with plasminogen kringles IV and V is
CC thought to underlie the atherogenicity of the protein, because the
CC fragments are competing with plasminogen for fibrin(ogen) binding.
CC -!- MISCELLANEOUS: Apo(a) is known to be proteolytically cleaved,
CC leading to the formation of the so called mini-Lp(a). Apo(a)
CC fragments accumulate in atherosclerotic lesions, where they may
CC promote thrombogenesis. O-glycosylation may limit the extent of
CC proteolytic fragmentation.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 38 kringle domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X06290; CAA29618.1; --
DR PIR; S00657; S00657.
DR PDB; 1171; 13-JUN-01.
DR PDB; 1JFN; 28-JUN-02.
DR PDB; 1KIV; 18-MAY-99.
DR PDB; 3KIV; 18-MAY-99.
DR PDB; 4KIV; 18-MAY-99.
DR MEROPS; S01.226; --
DR Genew; HGNC:6667; LPA.
DR MIN; 152200; --
DR GO; GO:0004866; F:endorpeptidase inhibitor activity; TAS.
DR GO; GO:0008015; P:circulation; TAS.
DR GO; GO:0009405; P:pathogenesis; TAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle_S1.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 38.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringle; 38.
DR SMART; SM00130; KR; 38.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 38.
DR PROSITE; PS00070; KRINGLE_2; 38.
DR PROSITE; PS02040; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Lipid transport; Plasma; Glycoprotein;
KW Kringle; Repeat; Atherosclerosis; Signal; Polymorphism; 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 4548 APOLIPOPROTEIN(A).
FT DOMAIN 20 130 KRINGLE TYPE IV, 1.
FT DOMAIN 131 244 KRINGLE TYPE IV, 2.
FT DOMAIN 245 358 KRINGLE TYPE IV, 3.
FT DOMAIN 359 472 KRINGLE TYPE IV, 4.
FT DOMAIN 473 586 KRINGLE TYPE IV, 5.
FT DOMAIN 587 700 KRINGLE TYPE IV, 6.
FT DOMAIN 701 814 KRINGLE TYPE IV, 7.
FT DOMAIN 815 928 KRINGLE TYPE IV, 8.
FT DOMAIN 929 1042 KRINGLE TYPE IV, 9.
FT DOMAIN 1043 1156 KRINGLE TYPE IV, 10.
FT DOMAIN 1157 1270 KRINGLE TYPE IV, 11.
FT DOMAIN 1271 1384 KRINGLE TYPE IV, 12.
FT DOMAIN 1385 1498 KRINGLE TYPE IV, 13.
FT DOMAIN 1499 1612 KRINGLE TYPE IV, 14.
FT DOMAIN 1613 1726 KRINGLE TYPE IV, 15.
FT DOMAIN 1727 1840 KRINGLE TYPE IV, 16.
FT DOMAIN 1841 1954 KRINGLE TYPE IV, 17.
FT DOMAIN 1955 2068 KRINGLE TYPE IV, 18.
FT DOMAIN 2069 2182 KRINGLE TYPE IV, 19.
FT DOMAIN 2183 2296 KRINGLE TYPE IV, 20.
FT DOMAIN 2297 2410 KRINGLE TYPE IV, 21.
FT DOMAIN 2411 2524 KRINGLE TYPE IV, 22.
FT DOMAIN 2525 2638 KRINGLE TYPE IV, 23.
FT DOMAIN 2639 2752 KRINGLE TYPE IV, 24.
FT DOMAIN 2753 2866 KRINGLE TYPE IV, 25.
FT DOMAIN 2867 2980 KRINGLE TYPE IV, 26.
FT DOMAIN 2981 3094 KRINGLE TYPE IV, 27.
FT DOMAIN 3095 3208 KRINGLE TYPE IV, 28.
FT DOMAIN 3209 3322 KRINGLE TYPE IV, 29.
FT DOMAIN 3323 3436 KRINGLE TYPE IV, 30.
FT DOMAIN 3437 3550 KRINGLE TYPE IV, 31.
FT DOMAIN 3551 3664 KRINGLE TYPE IV, 32.
FT DOMAIN 3665 3770 KRINGLE TYPE IV, 33.

FT DOMAIN 3771 3884 KRINGLE TYPE IV, 34.
FT DOMAIN 3885 3998 KRINGLE TYPE IV, 35.
FT DOMAIN 3999 4112 KRINGLE TYPE IV, 36.
FT DOMAIN 4113 4226 KRINGLE TYPE IV, 37.
FT DOMAIN 4227 4340 KRINGLE TYPE V.
FT DOMAIN 4341 4454 SERINE PROTEASE.
FT ACT_SITE 4328 4548 CHARGE RELAY SYSTEM.
FT ACT_SITE 4412 4412 CHARGE RELAY SYSTEM.
FT ACT_SITE 4498 4498 CHARGE RELAY SYSTEM.
FT VARIANT 4193 4193 W -> R (LOSS OF LYSINE-SEPHAROSE BINDING).
SQ SEQUENCE 4548 AA; 501313 MW; 969215E96A465CSF CRC64;
Query Match 28.3%; Score 157; DB 1; Length 4548;
Best Local Similarity 34.2%; Pred. No. 4.2e-09;
Matches 40; Conservative 9; Mismatches 36; Indels 32; Gaps 6;
Qy 3 CYEGNGHYFGKASTDMGRCPLPMSATVLOQTYHAHRSAL---QLGLGKHNYCRNP 59
Db 3896 CYRGDQGSYGTLLTITGRCTQSWSS-----MTPWHRRIRPLYPNAGLTR-NYCRNPD 3949
Qy 60 NRBRPCVYQVGLKPLV--CEQVHDC-----ADGKKPSPPEE 96
Db 3950 ABIRPWCYT---MDPSVRWBYCNLTRCPVTSSVLTTPTVAPVPSTPEAPSEQAPPEK 4003
RESULT 25
KRM1_HUMAN
ID KRM1_HUMAN STANDARD; PRT; 475 AA.
AC Q96MU8; Q96Y70; Q96G55; Q96GUL;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Kremen protein 1 precursor (kringle-containing protein marking the eye
DE and the nose) (Dickkopf receptor).
GN KREMEIN OR KREMEIN
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NAKAMURA T., NAKAMURA T.;
RP SEQUENCE FROM N.A. (ISOFORM 1).
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RA Taghiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Maseo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Nagasuna M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isegai T.;
RA "NEDO human cDNA sequencing project";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clamp M., Smink L.J., Ainscow R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barclow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgman A.M., Buck D., Burgess J.,
RA Burill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grahm D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,

RA Martyn J.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawabaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuayama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qian Y., Ray L., Ren O., Shaull S., Sloan D., Song L.,
RA Zhang M., Zhang G., Chiesse S., Murray J., Miller N., Mix P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing J.,
RA Scheet P., Walker C., Wamley A., Wohldmann P., Pepin K., Nelson T.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.-J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Franconi I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22";
RL Nature 402:489-495(1999).
CC -!- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
CC to block Wnt/beta-catenin signaling (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q96MU8-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q96MU8-2; Sequence=VSP_003900;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Contains 1 CUB domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -!- SIMILARITY: Contains 1 WSC domain.
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CC -----
CC EMBL; AB059618; BAB40969.1; -;
CC EMBL; AK056425; BAB71180.1; -;
CC EMBL; Z95116; CAB62952.1; -;
CC EMBL; AL021393; CAB62959.1; -;
CC Genew; HGNC:17550; KREMEIN.
CC GO; GO:0016021; C:integral to membrane; ISS.
CC GO; GO:0005624; C:membrane fraction; TAS.
CC GO; GO:0007154; P:cell communication; TAS.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR002889; WSC.
CC Pfam; PF00431; CUB; 1.
CC Pfam; PF00051; Kringle; 1.
CC Pfam; PF01822; WSC; 1.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00042; CUB; 1.
CC SMART; SM00130; KR; 1.
CC PROSITE; PS01180; CUB; 1.
CC PROSITE; PS00021; KRINGLE; 1.
CC PROSITE; PS00021; KRINGLE_2; 1.

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KW Wnt signaling pathway; Signal; Transmembrane; Kringle;
KW Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 475
FT DOMAIN 21 394
FT TRANSMEM 395 415
FT DOMAIN 416 475
FT DOMAIN 433 475
FT DOMAIN 433 475
FT DOMAIN 433 475
FT DOMAIN 433 475
FT CARBOHYD 47 47
FT CARBOHYD 61 61
FT CARBOHYD 219 219
FT CARBOHYD 295 295
FT CARBOHYD 335 335
FT CARBOHYD 347 347
FT VARSPLIC 473 475
FT 2D -> ALODSEVSLWSQCPRSI (in isoform
FT /FTID=VSP 003900.
FT MISSING (IN REF. 1).
FT I -> V (IN REF. 2).
FT SEQUENCE 475 AA; 51898 MW; B7E86FD80F96A0A4 CRC64;

Query Match 28.2%; Score 156; DB 1; Length 475;
Best Local Similarity 44.1%; Pred. No. 5e-10;
Matches 30; Conservative 8; Mismatches 26; Indels 4; Gaps 2;

QY 3 CYEGNGHYRGKASTDTM--GRCLPWSATVLTQYTHAHRSDALQLGLGKHNYCRNPDN 60
DB 34 CFTANGADYRGTONWTALQGRKCLFWNE--TFQHPYNTLKYPNGEGLGKHNYCRNPDG 91
QY 61 RRRPWCYV 68
DB 92 DVSPWCYV 99

RESULT 26
FAIL_BOVIN STANDARD; PRT; 593 AA.
AC P98140;
AT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Coagulation factor XII precursor (EC 3.4.21.38) (Hageman factor)
DE (HAF) (Fragment).
DE F12.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94242782; PubMed=8186251;
RA Shibuya Y., Samba U., Okabe H., Kambata T., Yamamoto T.;
RT "Primary structure of bovine Hageman factor (blood coagulation factor
RT XII): comparison with human and guinea pig molecules."
RL Biochim. Biophys. Acta 1206:63-70(1994).
RN [2]
RP SEQUENCE OF 10-21; 350-364 AND 525-550.
RX MEDLINE=77182112; PubMed=861210;
RA Fujikawa K., Walsh A.K., Davie W.E.;
RT "Isolation and characterization of bovine factor XII (Hageman
RT factor).";
RL Biochemistry 16:2270-2278(1977).
CC -1- FUNCTION: factor XII is a serum glycoprotein that participates in
CC the initiation of blood coagulation, fibrinolysis, and the
CC generation of bradykinin and angiotensin.
CC -1- CATALYTIC ACTIVITY: Cleaves selectively Arg-|-Ile bonds in factor
CC VII to form factor VIIa and factor XI to form factor Xla.
CC -1- PTM: O- AND N-GLYCOSYLATED (BY SIMILARITY).
CC -1- MISCELLANEOUS: Factor XII, prekallikrein, and HNW kininogen form a
```

```
CC complex bound to an anionic surface. Prekallikrein is cleaved by
CC factor XII to form kallikrein, which then cleaves factor XII first
CC to alpha-factor XIIa and then to beta-factor XIIa. Alpha-factor
CC XIIa activates factor XI to factor Xla. Bovine factor XII is
CC cleaved only to alpha-factor XIIa as it lacks the trypsin/
CC kallikrein cleavage site.
CC -1- SIMILARITY: Belongs to peptidase family S1.
CC -1- SIMILARITY: Contains 2 EGF-like domains.
CC -1- SIMILARITY: Contains 1 fibronectin type I domain.
CC -1- SIMILARITY: Contains 1 fibronectin type II domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC -----
CC EMBL; S70164; AAB30804.2; --
CC PIR; S45281; S45281.
CC HSSP; P00763; LDPO.
CC MEROPS; S01.211; --
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR000083; Fibrinctn1.
CC InterPro; IPR000562; FN_Type_II.
CC InterPro; IPR006210; IgGF.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Peptidase_S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00008; EGF; 2.
CC Pfam; PF00039; fn1; 1.
CC Pfam; PF00040; fn2; 1.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00083; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00013; FNTYPEII.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000995; FN_Type_II; 1.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00181; EGF; 2.
CC SMART; SM00058; FN1; 1.
CC SMART; SM00059; FN2; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; Tryp_Spc; 1.
CC PROSITE; PS00022; EGF_1; 2.
CC PROSITE; PS01186; EGF_2; FALSE_NEG.
CC PROSITE; PS50026; EGF_3; 2.
CC PROSITE; PS01253; FIBRONECTIN_1; 1.
CC PROSITE; PS00023; FIBRONECTIN_2; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS50070; KRINGLE_2; 1.
CC PROSITE; PS50240; TRYPsin_DOM; 1.
CC PROSITE; PS00134; TRYPsin_HIS; 1.
CC PROSITE; PS00135; TRYPsin_SER; 1.
CC Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;
CC Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.
FT NON_TER 1
FT SIGNAL <1 9
FT CHAIN 10 349
FT CHAIN 350 593
FT DOMAIN 37 78
FT DOMAIN 84 121
FT DOMAIN 123 163
FT DOMAIN 164 200
FT DOMAIN 207 287
FT DOMAIN 297 333
FT DOMAIN 350 593
FT ACT_SITE 369 389
FT ACT_SITE 438 438
FT ACT_SITE 541 541
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PT DISULFID 88 100 BY SIMILARITY.
PT DISULFID 94 109 BY SIMILARITY.
PT DISULFID 111 120 BY SIMILARITY.
PT DISULFID 125 153 BY SIMILARITY.
PT DISULFID 151 170 BY SIMILARITY.
PT DISULFID 168 179 BY SIMILARITY.
PT DISULFID 173 188 BY SIMILARITY.
PT DISULFID 190 199 BY SIMILARITY.
PT DISULFID 207 287 BY SIMILARITY.
PT DISULFID 230 269 BY SIMILARITY.
PT DISULFID 258 282 BY SIMILARITY.
PT DISULFID 336 463 BY SIMILARITY.
PT DISULFID 374 390 BY SIMILARITY.
PT DISULFID 382 452 BY SIMILARITY.
PT DISULFID 413 416 BY SIMILARITY.
PT DISULFID 479 547 BY SIMILARITY.
PT DISULFID 510 526 BY SIMILARITY.
PT DISULFID 537 568 BY SIMILARITY.
PT CARBOHYD 99 99 O-LINKED (FUC) (BY SIMILARITY).
PT CARBOHYD 241 241 N-LINKED (GLNAC. . .) (POTENTIAL).
PT CARBOHYD 263 263 N-LINKED (GLNAC. . .) (POTENTIAL).
PT CARBOHYD 410 410 N-LINKED (GLNAC. . .) (POTENTIAL).
SQ SEQUENCE 593 AA; 65148 MW; 721592BA792ED61F CRC64;

Query Match 28.1%; Score 155.5; DB 1; Length 593;
Best Local Similarity 38.4%; Pred. No. 7.2e-10;
Matches 33; Conservative 9; Mismatches 37; Indels 7; Gaps 3;

Qy 2 TCYE-GNGHYRKGASTDNGRCLPWNATVLCQTY-HAHRSDALQLGLGHNYCRNP 58
Dy 206 SCYDRDRGLSYRGMAGTTLGAPCQSWAS----EATYVNTAEQVLNGLGDFHAFCRNP 261
Qy 59 DNRRRPWCYQVGLKPLVQECVHDC 84
Dy 262 DNDTRPWCFFIWKGRDLSWNYCRLAPC 287

RESULT 27
PLMN BOVIN
ID PLMN BOVIN STANDARD; PRT; 812 AA.
AC P06858; Q28162;
DT 01-JAN-1988 (Rel. 05, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-NOV-2004 (Rel. 45, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7).
GN PLG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_taxid=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Berglund L., Andersen M.D., Petersen T.E.;
RT "Cloning and characterization of the bovine plasminogen cDNA.";
RL Int. Dairy J. 5:593-603 (1995).
RN [2]
RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=8520306; PubMed=3946532;
RA Schaller J., Moser P.W., Danneberger-Muller G.A.K., Rosselet S.J.,
RA Kampfer U., Rickli E.E.;
RT "Complete amino acid sequence of bovine plasminogen. Comparison with
human plasminogen.";
RL Eur. J. Biochem. 149:267-278 (1985).
RN [3]
RP SEQUENCE OF 706-812 FROM N.A.
RX MEDLINE=85023311; PubMed=6148961;
RA Malinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxy-ribonucleic acid coding for
human and bovine plasminogen.";
RL Biochemistry 23:4243-4250 (1984).
RN [4]

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RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegthart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
plasminogen. Species specificity in relation to sialylation and
fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63 (1988).
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including
embryonic development, tissue remodeling, tumor invasion,
and inflammation; in ovulation it weakens the walls of the
Graafian follicle. It activates the urokinase-type plasminogen
activator, collagenases and several complement zymogens, such
as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin,
laminin and von Willebrand factor.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
products.
CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
activators, both plasminogen and its activator being bound to
fibrin. Cannot be activated with streptokinase.
CC -!- PTM: N-LINKED GLYCANS CONTAIN N-ACETYLGLUCOSAMINE AND SIALIC ACID.
O-LINKED GLYCANS CONSIST OF GAL-GALNAc DISACCHARIDE WITH IS.
CC MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES (MICROHETEROGENEITY).
CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
immediately after dissociation from the clot.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 5 kringle domains.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X79402; CAA55939.1; -
DR EMBL; K02935; AAA30714.1; -
DR PIR; S45046; PLBO.
DR MEROPS; P00747; 2PK4.
DR MEROPS; S01.233; -
DR GlycoSuiteDB; P06858; -
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; Kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 5.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;
Signal.
KW SIGNAL
FT CHAIN 1 26 PLASMINOGEN.
FT CHAIN 27 812 PLASMIN HEAVY CHAIN A.
FT CHAIN 594 812 PLASMIN LIGHT CHAIN B.
FT CHAIN

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inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.

-1- CATALYTIC ACTIVITY: Preferential cleavage: Lys-[Xaa > Arg]-Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

-1- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Activated with catalytic amounts of streptokinase.

-1- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.

-1- MISCELLANEOUS: In the presence of the inhibitor, the activation involves only cleavage after Arg-580, resulting in 2 chains held together by 2 disulfide bonds. Without the inhibitor, the activation involves also removal of the activation peptide.

-1- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.

-1- SIMILARITY: Contains 5 kringle domains.

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EMBL: J04697; AAA36901.1; --
 PIR: B32869; B30848.
 HSRP: P00747; 1PWK.
 MEROPS: S01.233; --
 InterPro: IPR003003; Cys_Ser_trypsin.
 InterPro: IPR000001; Kringle.
 InterPro: IPR003014; PAN.
 InterPro: IPR003609; Pan app.
 InterPro: IPR001254; Peptidase_S1.
 InterPro: IPR001314; Peptidase_S1A.
 InterPro: IPR003966; Peptidase_S1A_pr.
 Pfam: PF00051; kringle; 5.
 Pfam: PF00024; PAN; 1.
 Pfam: PF00089; trypsin; 1.
 PRINTS: PR00722; CHYMOTRYPSIN.
 PRINTS: PR00018; KRINGLE.
 PRINTS: PR01505; PROTHROMBIN.
 PRODOM: PD000395; kringle; 5.
 SMART: SM00130; KR; 4.
 SMART: SM00473; PAN AP; 1.
 PROSITE: PS00021; KRINGLE_1; 5.
 PROSITE: PS00070; KRINGLE_2; 5.
 PROSITE: PS02240; TRYPsin_DOM; 1.
 PROSITE: PS00134; TRYPsin_HIS; 1.
 PROSITE: PS00135; TRYPsin_SER; 1.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis; Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 810 PLASMINOGEN
 FT CHAIN 20 580 PLASMIN HEAVY CHAIN A.
 FT PEPTIDE 20 96 ACTIVATION PEPTIDE.
 FT CHAIN 97 580 PLASMIN SHORT FORM OF CHAIN A.
 FT CHAIN 581 810 PLASMIN LIGHT CHAIN B.
 FT DOMAIN 103 181 KRINGLE 1.
 FT DOMAIN 184 262 KRINGLE 2.
 FT DOMAIN 275 352 KRINGLE 3.
 FT DOMAIN 377 454 KRINGLE 4.
 FT DOMAIN 481 560 KRINGLE 5.
 FT DOMAIN 581 622 SERINE PROTEASE.
 FT ACT_SITE 622 CHARGE RELAY SYSTEM.
 FT ACT_SITE 665 CHARGE RELAY SYSTEM.
 FT ACT_SITE 760 760 CHARGE RELAY SYSTEM.
 FT BINDING 136 136 OMEGA-AMINOCARBOXYLIC ACIDS.

FT BINDING 158 158 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 172 172 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 432 432 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 445 445 OMEGA-AMINOCARBOXYLIC ACIDS.
 FT BINDING 134 134 FIBRIN.
 FT BINDING 136 136 FIBRIN.
 FT DISULFID 49 73 BY SIMILARITY.
 FT DISULFID 53 61 BY SIMILARITY.
 FT DISULFID 103 181 BY SIMILARITY.
 FT DISULFID 124 164 BY SIMILARITY.
 FT DISULFID 152 176 BY SIMILARITY.
 FT DISULFID 188 262 BY SIMILARITY.
 FT DISULFID 206 245 BY SIMILARITY.
 FT DISULFID 234 257 BY SIMILARITY.
 FT DISULFID 275 352 BY SIMILARITY.
 FT DISULFID 296 335 BY SIMILARITY.
 FT DISULFID 324 347 BY SIMILARITY.
 FT DISULFID 377 454 BY SIMILARITY.
 FT DISULFID 398 437 BY SIMILARITY.
 FT DISULFID 426 449 BY SIMILARITY.
 FT DISULFID 481 560 BY SIMILARITY.
 FT DISULFID 502 543 BY SIMILARITY.
 FT DISULFID 531 555 BY SIMILARITY.
 FT DISULFID 567 685 BY SIMILARITY.
 FT DISULFID 577 623 BY SIMILARITY.
 FT DISULFID 607 623 BY SIMILARITY.
 FT DISULFID 699 766 BY SIMILARITY.
 FT DISULFID 729 745 BY SIMILARITY.
 FT DISULFID 756 784 BY SIMILARITY.
 FT CARBOHYD 365 365 O-LINKED (GALNAc...) (BY SIMILARITY).
 FT SEQUENCE 810 AA; 90255 MW; A75E1C51A1A0F24A CRC64;
 Query Match 26.9%; Score 149; DB 1; Length 810;
 Best Local Similarity 36.4%; Pred. No. 5.4e-09;
 Matches 36; Conservative 12; Mismatches 35; Indels 16; Gaps 6;
 QY 3 CYEGNGHEFYRGKASDTDMGRECLPNSATVLQOYVHAHR---SDALQLGLGKHNYCRNP 59
 Db 377 CHGQGYRGVSTTTTGKXQSWSS-----MTPHHEKTPENFPNAGL-TMYICRNP 430
 QY 60 NRRPWCYVQVGLKPLV--QECVHDC--DGKXSSPP 94
 Db 431 ADKGWCFT--TDPVVRWEYCNLKCSGTEGVAAPP 466
 RESULT 30
 KRM2 HUMAN
 ID KRM2 HUMAN STANDARD; PRT; 462 AA.
 AC Q8NCW0; Q8NJ4; Q8NCW1; Q96GL8; Q9BTP9;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kremen protein 2 precursor (Kringle-containing protein marking the eye and the nose) (Dickkopf receptor 2).
 GN KREMEN2 OR KRM2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP Tanaka S., Sugimachi K.;
 RA "Human Kremen2 and Wnt signaling";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
 RC TISSUE=Ovarian carcinoma;
 RA Suzuki T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

RT "NEDO human cDNA sequencing project";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RC TISSUE=Brain, and Uterus;
RX MEDLINE=2238257; PubMed=12477932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Strausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
to block Wnt/beta-catenin signaling. Forms a ternary complex with
Dkk1 and LRP6 and induces rapid endocytosis and removal of the Wnt
receptor LRP6 from the plasma membrane (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q8NCW0-1; Sequences=Displayed;
CC Name=2; Synonyms=Kremen2a;
CC IsoId=Q8NCW0-2; Sequences=VSP_050509, VSP_050510;
CC Name=3; Synonyms=Kremen2b;
CC IsoId=Q8NCW0-3; Sequences=VSP_050511, VSP_050512;
CC Name=4; Synonyms=Kremen2c;
CC IsoId=Q8NCW0-4; Sequences=VSP_050513, VSP_050514;
CC -1- SIMILARITY: Contains 1 CUB domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -1- SIMILARITY: Contains 1 WSC domain.
CC -----
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CC -----
CC EMBL; AB086405; BAC00872.1; -
CC EMBL; AB086355; BAC00823.1; -
CC EMBL; AB086356; BAC00824.1; -
CC EMBL; AB086357; BAC00825.1; -
CC EMBL; AK027669; BAB55281.1; -
CC EMBL; AK075033; BAC11365.1; -
CC EMBL; BC003533; AAK03533.1; -
CC EMBL; BC009383; AAK09383.1; -
CC HSP; P00750; IPK2.
CC Genew; HGNC:18797; KREMEN2.
CC InterPro; IPR000859; CUB.
CC InterPro; IPR000001; Kringle.
CC Pfam; PF00431; CUB.1.
CC Pfam; PF00051; kringle.1.
CC Pfam; PF01822; WSC.1.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle.1.
CC SMART; SMC0042; CUB.1.
CC SMART; SMC0130; KR.1.

DR SMART; SMC0321; WSC.1.
DR PROSITE; PS01180; CUB.1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Wnt signaling pathway; Glycoprotein; Kringle; Signal; Transmembrane;
KW Alternative splicing.
FT SIGNAL 1 25
FT CHAIN 26 462
FT DOMAIN 26 364
FT TRANSMEM 365 387
FT DOMAIN 388 462
FT DOMAIN 35 119
FT DOMAIN 121 215
FT DOMAIN 219 326
FT CARBOHYD 49 49
FT CARBOHYD 222 222
FT CARBOHYD 244 244
FT CARBOHYD 351 351
FT VARSPLIC 394 424
FT VARSPLIC 425 462
FT VARSPLIC 367 420
FT VARSPLIC 421 462
FT VARSPLIC 367 399
FT VARSPLIC 400 462
FT CONFLICT 164 202
FT CONFLICT 285 285
FT CONFLICT 462 AA; 48849 MW; CE33015917A9AA68 CRC64;
SQ QUERY MATCH 26.8%; Score 148.5; DB 1; Length 462;
Best Local Similarity 42.0%; Pred. No. 3.4e-09;
Matches 29; Conservative 9; Mismatches 26; Indels 5; Gaps 2;
QY 3 CYENGCHFYRG---KASTDTMGPRCLPNSATVLQQTTHAHRSDALQLGLGKHNVCNPD 59
DB 36 CFQVNGADYRGHQNRTPRGAGRPCLFWDQTQ--QHSYSSASDPHGRWGLGAHNFRCNPD 93
QY 60 NRRRPWCYV 68
DB 94 GDVQPCYV 102
RESULT 31
ID HGFL HUMAN STANDARD; PRT; 711 AA.
AC P26927; Q13350; Q14870;
DT 01-AUG-1992 (Rel. 23, Created)
DI 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
stimulatory protein) (MSP) (Macrophage stimulating protein).
GN MST1 OR HGFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92002016; PubMed=1655021;
RA Han S., Stuart L.A., Frierzner Degen S.J.;

RT "Characterization of the DNF15S2 locus on human chromosome 3:
 FT identification of a gene coding for four kringle domains with
 RT homology to hepatocyte growth factor.";
 RL Biochemistry 30:9788-9780(1991).
 RN [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Liver;

RC MEDLINE=93340141; PubMed=8393443;

RA Yoshimura T., Yuhki N., Wang M.H., Skeel A., Leonard E.J.;

RT "Cloning, sequencing, and expression of human macrophage stimulating

protein (MSP, MST1), confirms MSP as a member of the family of kringle

proteins and locates the MSP gene on chromosome 3.";

RL J. Biol. Chem. 268:15461-15468(1993).

CC -!- FUNCTION: Probably has no proteolytic activity, since crucial AA

characteristic of serine proteases catalytic sites are not

conserved.

CC -!- P1M: MAY BE CLEAVED AFTER AA 484, TO YIELD A TWO-CHAIN MOLECULE

CC HELD TOGETHER BY DISULFIDE BONDS, OR TWO SEPARATE POLYPEPTIDES.

CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.

CC -!- SIMILARITY: Contains 4 kringle domains.

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 CC or send an email to license@sib-sib.ch).

CC EMBL; M74178; AAC50165.1; -

DR EMBL; U37055; AAC50471.1; -

DR EMBL; L11924; AAC59872.1; -

DR PIR; A40331; A47136.

DR HSSP; P00747; 2PK4.

DR MEROPS; S01.975; -

DR Genew; HGNC:7380; MST1.

DR MIM; 142408; -

DR InterPro; IPR009003; Cys Ser trypsin.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR003014; PAN.

DR InterPro; IPR003609; Pan_app.

DR InterPro; IPR001254; Peptidase S1.

DR InterPro; IPR001314; Peptidase S1A.

DR InterPro; IPR003966; Peptidase_S1A_pr.

DR Pfam; PF00051; kringle; 4.

DR Pfam; PF00024; PAN; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00018; KRINGLE.

DR PRINTS; PR01505; PROTHROMBIN.

DR ProDom; PD000395; Kringle; 4.

DR SMART; SM00130; KR; 4.

DR SMART; SM00473; PAN AP; 1.

DR SMART; SM00020; TRY_SPC; 1.

DR PROSITE; PS00021; KRINGLE_1; 4.

DR PROSITE; PS00070; KRINGLE_2; 4.

DR PROSITE; PS02040; TRYPSIN_DOM; 1.

KW Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal;

KW Polymorphism.

FT SIGNAL 1 18

FT CHAIN 19 711

FT DOMAIN 32 109

FT DOMAIN 110 186

FT DOMAIN 191 268

FT DOMAIN 283 361

FT DOMAIN 370 448

FT DOMAIN 484 711

FT DISULFID 56 78

FT DISULFID 60 66

FT DISULFID 110 186

FT DISULFID 131 169

FT DISULFID 157 181

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 191 268

FT DISULFID 194 324

FT DISULFID 212 251

FT DISULFID 240 263

FT DISULFID 283 361

FT DISULFID 304 343

FT DISULFID 332 355

FT DISULFID 370 448

FT DISULFID 391 431

FT DISULFID 419 443

FT DISULFID 468 588

FT DISULFID 507 523

FT DISULFID 602 667

FT DISULFID 632 646

FT DISULFID 657 685

FT CARBOHYD 72 72

FT CARBOHYD 296 296

FT CARBOHYD 615 615

FT VARIANT 13 13

FT VARIANT 212 212

FT VARIANT 676 676

FT CONFLICT 623 623

FT SEQUENCE 711 AA; 80379 MW; 596ED21F180290E4 CRC64;

Query Match 26.8%; Score 148.5; DB 1; Length 711;

Best Local Similarity 33.0%; Pred. No. 5.3e-09; Indels 13; Gaps 4;

Matches 31; Conservative 14; Mismatches 36;

2 TCYEGNGHFYRGKASTDTMGRCPLFWNSATVLCQTYHAHRSALQLGLG--KHNYCRNPD 59

282 SCFRGKGEGYRGATNTTITAGVPCQRWDA----QIPHQRFTPEKYACKDLRENFRCNPD 336

60 NRRRPWCYVQVGLKPLVQEC---WVHDCADGKKP 90

337 GSEAPWCFT---LRFGMAAFYQIRCTDDVRP 367

RESULT 32

PLMN_ERIEU

ID PLMN_ERIEU STANDARD; PRT; 810 AA.

AC Q29485;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Plasminogen precursor (EC 3.4.21.7).

GN PLG

OS Brinaceus europaeus (Western European hedgehog).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceus.

OX NCBI_TaxID=9365;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=96025778; PubMed=7592597;

RA Lawn R.M., Boonmark N.W., Schwartz K., Lindahl G.E., Wade D.P.,

RA Byrne C.D., Fong K.J., Meer K., Patthy L.;

RT "The recurring evolution of lipoprotein(a). Insights from cloning of

RT hedgehog apolipoprotein(a).";

RL J. Biol. Chem. 270:24004-24009(1995).

RN [2]

RP REVISIONS.

RA Lawn R.M.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as

CC a proteolytic factor in a variety of other processes including

CC embryonic development, tissue remodeling, tumor invasion, and

CC inflammation; in ovulation it weakens the walls of the Graafian

CC follicle. It activates the urokinase-type plasminogen activator,

CC collagenases and several complement zymogens, such as C1 and C5.

CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von

CC Willebrand factor.

Db 436 GPWCY 440

|||||

RESULT 33

ID	PLMN CANFA	STANDARD;	PRT;	333 AA.
AC	P80009;			
DT	01-NOV-1991 (Rel. 20, Created)			
DT	01-NOV-1991 (Rel. 20, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Plasminogen (EC 3.4.21.7) (Fragment).			
GN	PLG.			
ON	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
OX	[1]			
RN	SEQUENCE.			
RP	TISSUE=Plasma;			
RC	MEDLINE=90175423; PubMed=2626424;			
RX	Schaller J., Straub C., Kaemper U., Rickli E.E.;			
RA	"Complete amino acid sequence of canine miniplasminogen.";			
RT	Protein Seq. Data Anal. 2:445-450(1989).			
RL	-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as			
CC	a proteolytic factor in a variety of other processes including			
CC	embryonic development, tissue remodeling, tumor invasion, and			
CC	inflammation; in ovulation it weakens the walls of the Graafian			
CC	follicle. It activates the urokinase-type plasminogen activator,			
CC	collagenases and several complement zymogens, such as C1 and C5.			
CC	It cleaves fibrin, fibronectin, thrombospondin, laminin and von			
CC	Willebrand factor.			
CC	-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys- -Xaa > Arg- -Xaa;			
CC	higher selectivity than trypsin. Converts fibrin into soluble			
CC	products.			
CC	-!- ENZYME REGULATION: Converted into plasmin by plasminogen			
CC	activators, both plasminogen and its activator being bound to			
CC	fibrin. Activated with urokinase and high concentrations of			
CC	streptokinase.			
CC	-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin			
CC	immediately after dissociation from the clot.			
CC	-!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.			
CC	-!- SIMILARITY: Contains at least 1 kringle domain.			
DR	HSP; P00747; SHPG.			
DR	MEROPS, S01.233; -.			
DR	InterPro; IPR009003; Cys_Ser_trypsin.			
DR	InterPro; IPR000001; Kringle.			
DR	InterPro; IPR001254; Peptidase_S1.			
DR	InterPro; IPR001314; Peptidase_S1A.			
DR	InterPro; IPR003966; Peptidase_S1A_pr.			
DR	Pfam; PF00051; kringle; 1.			
DR	Pfam; PF00089; trypsin; 1.			
DR	PRINTS; PR00722; CHYMOTRYPSIN.			
DR	PRINTS; PR0018; KRINGLE.			
DR	PRINTS; PRO1505; PROTHROMBIN.			
DR	ProDom; PD000395; Kringle; 1.			
DR	SMART; SM00130; KR; 1.			
DR	SMART; SM00020; Tryp_SPC; 1.			
DR	PROSITE; PS00021; KRINGLE_1; 1.			
DR	PROSITE; PS00070; KRINGLE_2; 1.			
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
DR	PROSITE; PS00135; TRYPSIN_SER; 1.			
KW	Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;			
FT	Tissue remodeling; Blood coagulation; Kringle; Zymogen.			
FT	NON TER 1			
FT	CHAIN <1 103			
FT	CHAIN 104 333			
FT	DOMAIN 4 83			
FT	DOMAIN 104 333			
FT	DISULFID 4 83			
FT	DISULFID 25 66			
FT	DISULFID 54 78			

PT DISULFID 90 208 INTERCHAIN (BY SIMILARITY).
FT DISULFID 100 108 INTERCHAIN (BY SIMILARITY).
FT DISULFID 130 146 BY SIMILARITY.
FT DISULFID 222 289 BY SIMILARITY.
FT DISULFID 259 268 BY SIMILARITY.
FT DISULFID 272 307 BY SIMILARITY.
FT ACT_SITE 145 145 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 188 188 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 283 283 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 283 283 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 152 152 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 186 186 STREPTOKINASE-BINDING SITE (PROBABLE).
FT SITE 264 264 SITE OF SUBSTRATE SPECIFICITY
FT SITE 277 277 (BY SIMILARITY).
SQ SEQUENCE 333 AA; 36678 MW; C8C0271B6C6AC8D4 CRC64;
Query Match 26.7%; Score 148; DB 1; Length 333;
Best Local Similarity 38.8%; Pred. No. 2.7e-09;
Matches 40; Conservative 7; Mismatches 40; Indels 16; Gaps 6;
Qy 3 CYEGNGHFYRGKASTDTMGSPCLPWNATVLTQTYHAHR-----SDALQLGLGKHNCRNP 58
Db 4 CMFNGKGYRGKATTVGIPQCEWAA-----QEPHRSIFTPETNPQAGLEK-NYCRNP 57
Qy 59 D-NRRRWCYVQVGLKPLVOECMVHDC-----DGKPSPPPEE 96
Db 58 DGDVNGPWCYT-MNQKLFYCDVPQCVCSTSPDCGKQVPEPK 99
RESULT 34
PLMN_PIG STANDARD; PRT; 790 AA.
AC P06867;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7).
GN PLG.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9623;
RN [1]
RP SEQUENCE OF 1-560.
RA Schaller J., Marti T., Roessellet S.J., Kaempfer U., Rickli E.E.;
RT "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
of the carbohydrate attachment sites with the human and bovine
species.";
RL Fibrinolysis 1:91-102(1987).
RN [2]
RP SEQUENCE OF 450-790.
EX MEDLINE=85203907; PubMed=3846533;
RA Marti T., Schaller J., Rickli E.E.;
RT "Determination of the complete amino-acid sequence of porcine
miniplasminogen.";
RL Eur. J. Biochem. 149:279-285(1985).
RN [3]
RP CARBOHYDRATE-LINKAGE SITES.
EX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
Gerwig G.J., van Halbeek H., Vliegenhart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
plasminogen. Species specificity in relation to sialylation and
fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
a proteolytic factor in a variety of other processes including
embryonic development, tissue remodeling, tumor invasion, and
inflammation; in ovulation it weakens the walls of the Graafian
follicle. It activates the urokinase-type plasminogen activator,
collagenases and several complement zymogens, such as C1 and C5.
CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
Willebrand factor.

CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
higher selectivity than trypsin. Converts fibrin into soluble
products
CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
activators, both plasminogen and its activator being bound to
fibrin. Cannot be activated with streptokinase.
CC -!- PTM: N-LINKED GLYCANS CONTAINS N-ACETYLACTOSAMINE, SIALIC ACID AND
IS CORE FUCOSYLATED. O-LINKED GLYCANS CONSIST OF GAL-GALNAc.
CC DISACCHARIDE WITH IS MODIFIED WITH UP TO 2 SIALIC ACID RESIDUES
(MICROHETEROGENEITY).
CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
immediately after dissociation from the clot.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 5 kringle domains.
DR PIR: S03733; PLPG.
DR HSSP: P00747; SHPG.
DR MEROPS: S01.233;
DR GlycoSuiteDB, P06867;
DR InterPro: IPR009003; Cys_Ser_trypsin.
DR InterPro: IPR000001; Kringle.
DR InterPro: IPR003014; PAN.
DR InterPro: IPR003609; PAN_app.
DR InterPro: IPR001254; Peptidase_S1.
DR InterPro: IPR001314; Peptidase_S1.
DR InterPro: IPR003966; Peptidase_S1A_pr.
DR Pfam: PF00051; Kringle; 5.
DR Pfam: PF00024; PAN; 1.
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: PR00722; CHYMOTRYPSIN.
DR PRINTS: PR00181; KRINGLE.
DR PRINTS: PR01505; PROTHROMBIN.
DR ProDom: PD000395; Kringle; 5.
DR SMART: SM00130; KR; 5.
DR SMART: SM00473; PAN_AP; 1.
DR SMART: SM00020; TRY_SPC; 1.
DR PROSITE: PS00021; KRINGLE 1; 5.
DR PROSITE: PS50070; KRINGLE 2; 5.
DR PROSITE: PS50240; TRYPSIN_DOM; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; FALSE_NEG.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
FT CHAIN 1 560 PLASMIN HEAVY CHAIN A.
FT CHAIN 561 790 PLASMIN LIGHT CHAIN B.
FT DOMAIN 561 790 SERINE PROTEASE.
FT DOMAIN 84 162 KRINGLE 1.
FT DOMAIN 166 243 KRINGLE 2.
FT DOMAIN 256 333 KRINGLE 3.
FT DOMAIN 358 435 KRINGLE 4.
FT DOMAIN 461 540 KRINGLE 5.
FT ACT_SITE 602 602 CHARGE RELAY SYSTEM.
FT ACT_SITE 645 645 CHARGE RELAY SYSTEM.
FT ACT_SITE 740 740 CHARGE RELAY SYSTEM.
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .).
FT CARBOHYD 340 340 /FTID=CAR_000019.
FT CARBOHYD 340 340 O-LINKED (GALNAc. . .).
FT /FTID=CAR_000020.
SQ SEQUENCE 790 AA; 88592 MW; F04EA06E74BCD58E CRC64;
Query Match 26.7%; Score 148; DB 1; Length 790;
Best Local Similarity 38.2%; Pred. No. 6.8e-09;
Matches 34; Conservative 8; Mismatches 33; Indels 14; Gaps 5;
Qy 3 CYEGNGHFYRGKASTDTMGSPCLPWNATVLTQTYHAHR-----SDALQLGLGKHNCRNP 59
Db 358 CYRGNGESYRGTSSTITGRKQSW-----VSMTPHREKTPGNFPNAGL-TMYCRNP 411
Qy 60 NERRWCYVQVGLKPLV--QECMVHDCAD 86
Db 412 ADKSPWCYT---TDRVRWEYCNLKKCE 437
RESULT 35

HGFL_MOUSE
ID HGFL_MOUSE STANDARD; PRT; 716 AA.
AC P26928;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor-like protein precursor (Macrophage
stimulatory protein) (MSP).
GN MST1 OR HGFL.
OS Mus musculus. (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Liver;
RA MEDLINE=92002017; PubMed=1832957;
RX Friesner Degen S.G.; Stuart L.A.; Han S.; Jamison C.S.;
RT "Characterization of the mouse cDNA and gene coding for a hepatocyte
growth factor-like protein: expression during development.";
RL Biochemistry 30:9781-9791(1991).
CC -!- FUNCTION: Probably has no proteolytic activity, since crucial AA
characteristic of serine proteases catalytic sites are not
conserved.
CC -!- TISSUE SPECIFICITY: Liver. Lower levels in lung, placenta and
adrenal.
CC -!- DEVELOPMENTAL STAGE: Is expressed at low levels during gestation.
CC Just before birth the level increases dramatically and remains
stable afterwards.
CC -!- PTM: MAY BE CLEAVED AFTER AA 488, TO YIELD A TWO-CHAIN MOLECULE
HELD TOGETHER BY DISULFIDE BONDS, OR CLEAVED INTO TWO SEPARATE
POLYPEPTIDES.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 4 kringle domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; M74180; AAA50166.1; -.
CC EMBL; M74181; AAA50167.1; -.
CC PIR; A40332; A40332.
CC HSP; P00747; IGRN.
CC MEROPS; S01.975; -.
CC MGD; MGI:96080; Mst1.
CC GO; GO:0007566; P:embryo implantation; IC.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR003014; PAN.
CC InterPro; IPR003609; PAN_app.
CC InterPro; IPR001254; Peptidase S1.
CC InterPro; IPR001314; Peptidase S1A.
CC InterPro; IPR003966; Peptidase_S1A_pr.
CC Pfam; PF00051; Kringle; 4.
CC Pfam; PF00024; PAN; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC PRINTS; PR01505; PROTHROMBIN.
CC ProDom; PD000395; Kringle; 4.
CC SMART; SM00130; KR; 4.
CC SMART; SM00473; PAN AP; 1.
CC SMART; SM00020; TRYPSIN; 1.
CC PROSITE; PS00021; KRINGLE_1; 4.
CC PROSITE; PS00070; KRINGLE_2; 4.
CC PROSITE; PS00240; TRYPSIN_DOM; 1.
KW Kringle; Glycoprotein; Serine protease homolog; Repeat; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 716 HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN.

FT DOMAIN 19 109 PAP.
FT DOMAIN 110 186 KRINGLE 1.
FT DOMAIN 191 268 KRINGLE 2.
FT DOMAIN 292 370 KRINGLE 3.
FT DOMAIN 379 457 KRINGLE 4.
FT DOMAIN 489 716 SERINE PROTEASE-LIKE.
FT DISULFID 56 78 BY SIMILARITY.
FT DISULFID 60 66 BY SIMILARITY.
FT DISULFID 110 186 BY SIMILARITY.
FT DISULFID 131 169 BY SIMILARITY.
FT DISULFID 157 181 BY SIMILARITY.
FT DISULFID 191 268 BY SIMILARITY.
FT DISULFID 194 333 INTERCHAIN (BY SIMILARITY).
FT DISULFID 212 251 BY SIMILARITY.
FT DISULFID 240 263 BY SIMILARITY.
FT DISULFID 292 370 BY SIMILARITY.
FT DISULFID 313 352 BY SIMILARITY.
FT DISULFID 341 364 BY SIMILARITY.
FT DISULFID 379 457 BY SIMILARITY.
FT DISULFID 400 440 BY SIMILARITY.
FT DISULFID 428 452 BY SIMILARITY.
FT DISULFID 477 593 INTERCHAIN (BY SIMILARITY).
FT DISULFID 512 528 BY SIMILARITY.
FT DISULFID 607 672 BY SIMILARITY.
FT DISULFID 637 651 BY SIMILARITY.
FT DISULFID 662 690 BY SIMILARITY.
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 305 305 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 620 620 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 P -> O (IN GENOMIC SEQUENCE).
SQ SEQUENCE 716 AA; 80588 MW; BBCE02EF85213ACC CRC64;
Query Match 26.6%; Score 147.5; DB 1; Length 716;
Best Local Similarity 36.5%; Pred. No. 7e-09;
Matches 38; Conservative 11; Mismatches 34; Indels 21; Gaps 7;
Qy 3 CYENGHFYKASTDTMGRCPLPNSATVLTQYTHAHR-----SDALQLGLGHNYCRN 57
Db 379 CYHSGQYGRSVSKTKGVQCQHSSET-----PHKQFTPTSPAQGL-EANFCRN 430
Qy 58 PD-NRRPWCYVQVGLKP--LVQECMVHDCADGKKPS--SPPEE 96
Db 431 PDGDSHGWCYT--LDPDILFDYCALQRCDDDDPPSILDPDQ 471
RESULT 36
ID ROR2 HUMAN STANDARD; PRT; 943 AA.
AC Q01974; Q9HAV7; Q9HB61;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor
(EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2).
GN ROR2 OR NTRKR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93100347; PubMed=1334494;
RA Maslakowski P.; Carroll R.D.;
RT "A novel family of cell surface receptors with tyrosine kinase-like
domain.";
RL J. Biol. Chem. 267:26181-26190(1992).
RN [2]
RP SEQUENCE OF 34-943 FROM N.A., AND VARIANT ILE-819.
RX MEDLINE=20164326; PubMed=10700182;
RA Oldridge M.; Fortuna A.M.; Maringa M.; Propping P.; Mansour S.;
RA Pollitt C.; DeChiara T.M.; Kimble R.B.; Valenzuela D.M.;
RA Yancopoulos G.D.; Wilkie A.O.M.;

"Dominant mutations in ROR2, encoding an orphan receptor tyrosine kinase, cause brachydactyly type B";
 Nat. Genet. 24:275-278(2000).
 [3]
 RN SEQUENCE OF 34-574 FROM N.A. AND VARIANT THR-245.
 RX MEDLINE=20442029; PubMed=10986040;
 RA Schwabe G.C., Tinschert S., Buschow C., Meinecke P., Wolff G.,
 RA Gillesen-Kaeschach G., Oldridge M., Wilkie A.O.M., Koeneck R.,
 RA Mundlos S.;
 RT "Distinct mutations in the receptor tyrosine kinase gene ROR2 cause
 RT brachydactyly type B";
 RL Am. J. Hum. Genet. 67:822-831(2000).
 RN [4]
 RN VARIANTS RRS CYS-184; TRP-189; TRP-366 AND LYS-620.
 RX MEDLINE=20392394; PubMed=10932186;
 RA Afzal A.R., Rajab A., Fenske C.D., Oldridge M., Elanko N.,
 RA Ternes-Pereira E., Tucsyesz B., Munday V.A., Patton M.A.,
 RA Wilkie A.O.M., Jeffery S.;
 RT "Recessive Robinow syndrome, allelic to dominant brachydactyly type B,
 RT is caused by mutation of ROR2";
 RL Nat. Genet. 25:419-422(2000).
 RN [5]
 RN VARIANT RRS TYR-182.
 RX MEDLINE=20392395; PubMed=10932187;
 RA van Bokhoven H., Celli J., Kayserili H., van Beusekom E., Balci S.,
 RA Brussel W., Skovby F., Kerr B., Percin E.F., Akarsu N., Brunner H.G.;
 RL Nat. Genet. 26:383-383(2000).
 CC -!- FUNCTION: Tyrosine-protein kinase receptor which may be involved
 CC in the early formation of the chondrocytes. It seems to be
 CC required for cartilage and growth plate development.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- DEVELOPMENTAL SPAG: Expressed at high levels during early
 CC embryonic development. The expression levels drop strongly around
 CC day 16 and there are only very low levels in adult tissues.
 CC -!- DISEASE: Defects in ROR2 are a cause of brachydactyly type B1
 CC (BDB1) [MIM:113000]. BDB1 is an autosomal dominant skeletal
 CC disorder characterized by hypoplasia/aplasia of distal phalanges
 CC and nails. In BDB1 the middle phalanges are short but in addition
 CC the terminal phalanges are rudimentary or absent. Both fingers and
 CC toes are affected. The thumbs and big toes are usually deformed.
 CC -!- DISEASE: Defects in ROR2 are a cause of recessive Robinow syndrome
 CC (RRS) [MIM:268310]. RRS is an autosomal disorder characterized by
 CC skeletal dysplasia with generalized limb bone shortening,
 CC segmental defects of the spine, brachydactyly and a dysmorphic
 CC facial appearance.
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
 CC subfamily.
 CC -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 kringle domain.
 CC -----
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 CC -----
 DR EMBL; M97639; AAA60276.1; -;
 DR EMBL; AF294796; AAG01184.2; -;
 DR EMBL; AF254747; AAG01184.2; JOINED.
 DR EMBL; AF254746; AAG01184.2; JOINED.
 DR EMBL; AF254749; AAG01184.2; JOINED.

DR EMBL; AF254750; AAG01184.2; JOINED.
 DR EMBL; AF254751; AAG01184.2; JOINED.
 DR EMBL; AF254752; AAG01184.2; JOINED.
 DR EMBL; AF254753; AAG01184.2; JOINED.
 DR EMBL; AF279762; AAG33132.1; -;
 DR EMBL; AF279763; AAG33132.1; -;
 DR EMBL; AF279764; AAG33132.1; JOINED.
 DR EMBL; AF279765; AAG33132.1; JOINED.
 DR EMBL; AF279766; AAG33132.1; JOINED.
 DR EMBL; AF279767; AAG33132.1; JOINED.
 DR EMBL; AF279768; AAG33132.1; JOINED.
 DR EMBL; AF279769; AAG33132.1; JOINED.
 DR EMBL; AF279770; AAG33132.1; JOINED.
 DR PIR; B45082; B45082.
 DR HSPD; P00747; 1KRN.
 DR Genew; HGNC:10257; ROR2.
 DR MIM; 602337; -;
 DR MIM; 113000; -;
 DR MIM; 268310; -;
 DR GO; GO:0005897; C: integral to plasma membrane; TAS.
 DR GO; GO:0004714; F: transmembrane receptor protein tyrosine kin. . . ; TAS.
 DR GO; GO:0007275; P: development; TAS.
 DR GO; GO:0007165; P: signal transduction; TAS.
 DR InterPro; IPR000024; Fz domain.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003598; IG C2.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR006266; Tyr_kinase_AS.
 DR Pfam; PF01392; Fz; 1.
 DR Pfam; PF00047; Ig; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000395; Kringle; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00408; IGC2; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS50038; FZ; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS50070; KRINGLE 2; 1.
 DR PROSITE; PS00107; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00011; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Receptor;
 KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
 KW Immunoglobulin domain; Developmental protein; Polymorphism;
 KW Disease mutation.
 FT SIGNAL 1 33
 FT CHAIN 34 943
 FT TYROSINE-PROTEIN KINASE TRANSMEMBRANE
 FT RECEPTOR ROR2.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE C2-TYPE.
 FT FZ.
 FT KRINGLE.
 FT PROTEIN KINASE.
 FT SER/THR-RICH.
 FT PRO-RICH.
 FT SER/THR-RICH.
 FT ATP (BY SIMILARITY).
 FT ATP (BY SIMILARITY).
 FT BY SIMILARITY.
 FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT BY SIMILARITY.
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT C -> Y (in RRS).
 FT VARIANT 182

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FT VARIANT 184 184 /FTID=VAR_010911.
FT R -> C (in RRS).
FT /FTID=VAR_010768.
FT VARIANT 189 189 R -> W (in RRS).
FT /FTID=VAR_010769.
FT VARIANT 245 245 A -> T.
FT /FTID=VAR_010912.
FT VARIANT 366 366 R -> W (in RRS).
FT /FTID=VAR_010770.
FT VARIANT 620 620 N -> K (in RRS).
FT /FTID=VAR_010771.
FT VARIANT 819 819 V -> I.
FT /FTID=VAR_010913.
SQ SEQUENCE 943 AA; 104726 MW; DBAC1E4622B5ECA0 CRC64;

Query Match 26.6%; Score 147.5; DB 1; Length 943;
Best Local Similarity 39.3%; Pred. No. 9.3e-09;
Matches 33; Conservative 10; Mismatches 36; Indels 5; Gaps 4;

QY 3 CYEGNGHYRGKASTDTMGRPCLPWNSATVLAQTYHAHRSALQGLGKHYCRNPDNR 62
Db 316 CYNGSGVYRGASTYKSHQCQPW--ALQHPHSHLSLSTDPPELG-GGHAYCRNPGQM 372

QY 63 R-PWCYVQVGLKPLVQECWVHDC 85
Db 373 EGPWCFTQ-KNKNVRELCDVPSCS 395

RESULT 37
ROR2_MOUSE STANDARD; PRT; 944 AA.
ID AC Q9Z138;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor ROR2 precursor
DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 2)
DE (mROR2).
DE GN
OS Mus musculus (Mouse).
OC Mammalia; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99248426; PubMed=10231392;
RA Oishi T., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J.,
RA Hata T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.,
RT "Spatio-temporally regulated expression of receptor tyrosine kinases,
RT mKor1, mKor2, during mouse development: implications in development
RT and function of the nervous system.";
RL Genes Cells 4:41-56(1999).
[2]
RN CHARACTERIZATION.
RX MEDLINE=20164325; PubMed=10700181;
RA DeChiara T.M., Kimble R.B., Poueymirou W.T., Rojas J., Masiakowski P.,
RA Valenzuela D.M., Yancopoulos G.D.;
RT "Ror2, encoding a receptor-like tyrosine kinase, is required for
RT cartilage and growth plate development.";
RL Nat. Genet. 24:271-274(2000).
CC -1- FUNCTION: Tyrosine-protein kinase receptor which may be involved
CC in the early formation of the chondrocytes. It seems to be
CC required for cartilage and growth plate development.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
CC subfamily.
CC -1- SIMILARITY: Contains 1 frizzled (FZ) domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB010384; BAA75481.1; -.
CC HSP; P00747; SHPG.
CC MGD; MG11347521; Ror2.
CC GO; GO:0001501; P:skeletal development; IMP.
CC InterPro; IPR000024; Fz_domain.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_C2.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR001245; Tyr_kinase.
CC InterPro; IPR008266; Tyr_kinase_AS.
CC Pfam; PF01392; Fz; 1.
CC Pfam; PF00047; Ig; 1.
CC Pfam; PF00031; kringle; 1.
CC Pfam; PF00069; pkinase; 1.
CC PRINTS; PR00018; KRINGLE.
CC PRINTS; PR00109; TYRKINASE.
CC PRODOM; PD000395; Kringle; 1.
CC PRODOM; PD000001; Prot_kinase; 1.
CC SMART; SMO0408; IGC2; 1.
CC SMART; SMO0130; KR; 1.
CC SMART; SMO0219; TyKc; 1.
CC PROSITE; PS50038; FZ; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.
CC PROSITE; PS00070; KRINGLE_2; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC Transferrase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KW Immunoglobulin domain; Developmental protein.
FT SIGNAL 1 33
FT CHAIN 34 944
FT TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT RECEPTOR ROR2.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT IG-LIKE C2-TYPE.
FT FZ.
FT KRINGLE.
FT PROTEIN KINASE.
FT SER/THR-RICH.
FT PRO-RICH.
FT SER/THR-RICH.
FT NP_BIND 479 487
FT BINDING 507 507
FT ACT_SITE 615 615
FT MOD_RES 646 646
FT DISULFID 83 135
FT CARBOHYD 70 70
FT CARBOHYD 188 188
FT CARBOHYD 318 318
SQ SEQUENCE 944 AA; 105050 MW; CD2EEBC710387A56 CRC64;

Query Match 26.6%; Score 147.5; DB 1; Length 944;
Best Local Similarity 41.4%; Pred. No. 9.3e-09;
Matches 36; Conservative 9; Mismatches 31; Indels 11; Gaps 6;

QY 3 CYEGNGHYRGKASTDTMGRPCLPWNSATVLAQTYHAHRSALQGLGKHYCRNPD 59
Db 316 CYNGSGVYRGASTYKSHQCQPW--ALQHPHSHLSLSTDPPELG-GGHAYCRNPG 369

QY 60 NRRR-PWCYVQVGLKPLVQECWVHDC 85
Db 370 GMEGFWCFTQ-KNKNVRELCDVPSCS 395

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Query Match      26.4%; Score 146.5; DB 1; Length 461;
Best Local Similarity 42.0%; Pred. No. 5.7e-09;
Matches 29; Conservative 8; Mismatches 27; Indels 5; Gaps 2;

QY 3 CYEGNGHFYRGK--ASTDTMGRPCLPWNSATVLTQTYHAHRSDALQLGLGKKNYCRNPD 59
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Db 35 CFQVNGADYRGHQNYTGPRGAGRPCLFWDQ--QHSYSSASDPQGRWGLGAHFRNPD 92
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 60 NRRRPWCYV 68
   : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 93 GDVQPCYV 101

RESULT 39
PLMN HUMAN
ID PLMN HUMAN STANDARD; PRT; 810 AA.
AC P00747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
GN PLG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANT ASN-472.
RX MEDLINE=90203879; PubMed=2318848;
RA Petersen T.E., Martzen M.R., Ichinose A., Davie E.W.;
RT "Characterization of the gene for human plasminogen, a key proenzyme
   in the fibrinolytic system.";
RL J. Biol. Chem. 265:6104-6111(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87162490; PubMed=3030813;
RA Forsgren M., Raden B., Israelsen M., Larsson K., Heden L.-O.;
RT "Molecular cloning and characterization of a full-length cDNA clone
   for human plasminogen.";
RL FEBS Lett. 213:254-260(1987).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS LYS-57; GLN-133; HIS-261; TRP-408;
RX ASN-472; VAL-494 AND TRP-523.
RA Rieder M.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,
RA Rajkumar N., Toth E.J., Yi Q., Nickerson D.A.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 20-810, AND VARIANT ASN-472.
RA Sottrup-Jensen L., Petersen T.E., Magnusson S.;
RL Submitted (JUL-1977) to the PIR data bank.
RN [5]
RP SEQUENCE OF 292-810 FROM N.A.
RX MEDLINE=85023311; PubMed=6148961;
RA Malinowski D.P., Sadler J.E., Davie E.W.;
RT "Characterization of a complementary deoxyribonucleic acid coding for
   human and bovine plasminogen.";
RL Biochemistry 23:4243-4250(1984).
RN [6]
RP SEQUENCE OF 20-100.
RX MEDLINE=75093329; PubMed=122932;
RA Wiman B., Wallen P.;
RT "Structural relationship between 'glutamic acid' and 'lysine' forms
   of human plasminogen and their interaction with the NH2-terminal
   activation peptide as studied by affinity chromatography.";
RL Eur. J. Biochem. 50:489-494(1975).
RN [7]
RP SEQUENCE OF 95-580; 581-626; 657-700 AND VARIANT ASN-472.
RA Sottrup-Jensen L., Claessens H., Zajdel M., Petersen T.E., Magnusson S.;
RL (in) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.);
RL Progress in chemical fibrinolysis and thrombolysis, pp.3:191-209,
RL Raven Press, New York (1978).
RN [8]
RP SEQUENCE OF 483-604.
```


RX MEDLINE=76043692; PubMed=126863;
RA Wiman B., Wallen P.;
RT "Amino-acid sequence of the cyanogen-bromide fragment from human
RT plasminogen that forms the linkage between the plasmin chains.";
RL Eur. J. Biochem. 58:539-547(1975).
RN [9]
RP SEQUENCE OF 581-810.
RX MEDLINE=77225245; PubMed=142009;
RA Wiman B.;
RT "Primary structure of the B-chain of human plasmin.";
RL Eur. J. Biochem. 76:129-137(1977).
RN [10]
RP ACTIVE SITE.
RX MEDLINE=73149248; PubMed=4594729;
RA Robbins K.C., Bernabe P., Arzaadon L., Summaria L.;
RT "The primary structure of human plasminogen. II. The histidine loop
RT of human plasmin: light (B) chain active center histidine sequence.";
RL J. Biol. Chem. 248:1631-1633(1973).
RN [11]
RP ACTIVE SITE.
RX MEDLINE=69234739; PubMed=4240117;
RA Grobkopf W.R., Summaria L., Robbins K.C.;
RT "Studies on the active center of human plasmin. Partial amino acid
RT sequence of a peptide containing the active center serine residue.";
RL J. Biol. Chem. 244:3590-3597(1969).
RN [12]
RP OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES.
RX MEDLINE=82213905; PubMed=6919539;
RA Trexler M., Valli Z., Pathy L.;
RT "Structure of the omega-aminocarboxylic acid-binding sites of human
RT plasminogen. Arginine 70 and aspartic acid 56 are essential for
RT binding of ligand by kringle 4.";
RL J. Biol. Chem. 257:7401-7406(1982).
RN [13]
RP FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES.
RX MEDLINE=85054794; PubMed=6094526;
RA Valli Z., Pathy L.;
RT "The fibrin-binding site of human plasminogen. Arginines 32 and 34
RT are essential for fibrin affinity of the kringle 1 domain.";
RL J. Biol. Chem. 259:13690-13694(1984).
RN [14]
RP PHOSPHORYLATION SITE SER-597.
RX MEDLINE=97345939; PubMed=9201958;
RA Wang H., Prorok M., Bretthauer R.K., Castellino F.J.;
RT "Serine-578 is a major phosphorylation locus in human plasma
RT plasminogen.";
RL Biochemistry 36:8100-8106(1997).
RN [15]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=88185329; PubMed=3356193;
RA Marti T., Schaller J., Rickli E.E., Schmid K., Kamerling J.P.,
RA Gerwig G.J., van Halbeek H., Vliegthart J.F.;
RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
RT plasminogen. Species specificity in relation to sialylation and
RT fucosylation patterns.";
RL Eur. J. Biochem. 173:57-63(1988).
RN [16]
RP CARBOHYDRATE-LINKAGE SITE SER-268.
RX MEDLINE=97207306; PubMed=9054441;
RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Enghild J.J.,
RA Pizzo S.V.;
RT "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of
RT human plasminogen 2.";
RL J. Biol. Chem. 272:7408-7411(1997).
RN [17]
RP CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE.
RX MEDLINE=95042728; PubMed=7525077;
RA O'Reilly M.S., Holmgren L., Shing Y., Chen C., Rosenthal R.A.,
RA Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
RT "Angiostatin: a novel angiogenesis inhibitor that mediates the
RT suppression of metastases by a Lewis lung carcinoma.";
RL Cell 79:315-328(1994).
RN [18]

RP CHARACTERIZATION OF ANGIOSTATIN.
RX MEDLINE=97238710; PubMed=9102221;
RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W.,
RA Lapcevic R., Nacy C.A.;
RT "A recombinant human angiotensin protein inhibits experimental primary
RT and metastatic cancer.";
RL Cancer Res. 57:1329-1334(1997).
RN [19]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461.
RX MEDLINE=92031502; PubMed=1657148;
RA Mulichak A.M., Tulinsky A., Ravichandran K.G.;
RT "Crystal and molecular structure of human plasminogen kringle 4
RT refined at 1.9-A resolution.";
RL Biochemistry 30:10576-10588(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461.
RX MEDLINE=92031503; PubMed=1657149;
RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulichak A.M.;
RT "The refined structure of the epsilon-aminocaproic acid complex of
RT human plasminogen kringle 4.";
RL Biochemistry 30:10589-10594(1991).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454.
RA Stec B., Yamano A., Whitlow M., Tester M.M.;
RT "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K.
RT A possible structural role of disordered residues.";
RL Acta Crystallogr. D 53:169-178(1997).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181.
RX MEDLINE=96180681; PubMed=8611560;
RA Mathews I.I., Vanderhoff-Hanover P., Castellino F.J., Tulinsky A.;
RT "Crystal structures of the recombinant kringle 1 domain of human
RT plasminogen in complexes with the ligands epsilon-aminocaproic acid
RT and trans-4-(aminomethyl)cyclohexane-1-carboxylic acid.";
RL Biochemistry 35:2567-2576(1996).
RN [23]
RP X-RAY CRYSTALLOGRAPHY (1.66 ANGSTROMS) OF 480-563.
RX MEDLINE=98198034; PubMed=9521645;
RA Chang Y., Mochalkin I., McCance S.G., Cheng B., Tulinsky A.,
RA Castellino F.J.;
RT "Structure and ligand binding determinants of the recombinant kringle
RT 5 domain of human plasminogen.";
RL Biochemistry 37:3258-3271(1998).
RN [24]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237157; PubMed=8181475;
RA Rejzante M.R., Llinas M.;
RT "1H-NMR assignments and secondary structure of human plasminogen
RT kringle 1.";
RL Eur. J. Biochem. 221:927-937(1994).
RN [25]
RP STRUCTURE BY NMR OF 96-184.
RX MEDLINE=94237158; PubMed=8181476;
RA Rejzante M.R., Llinas M.;
RT "Solution structure of the epsilon-aminohexanoic acid complex of
RT human plasminogen kringle 1.";
RL Eur. J. Biochem. 221:939-949(1994).
RN [26]
RP STRUCTURE BY NMR OF 183-354.
RX MEDLINE=96194156; PubMed=8652577;
RA Soehndel S., Hu C.-K., Marti D., Affolter M., Schaller J., Llinas M.,
RA Rickli E.E.;
RT "Recombinant gene expression and 1H NMR characteristics of the
RT kringle (2 + 3) supermodule: spectroscopic/functional individuality
RT of plasminogen kringle domains.";
RL Biochemistry 35:2357-2364(1996).
RN [27]
RP STRUCTURE BY NMR OF 374-461.
RX MEDLINE=90219023; PubMed=2157850;

Query Match 26.4%; Score 146.5; DB 1; Length 810;
Best Local Similarity 37.4%; Pred. No. 1e-08;
Matches 37; Conservative 13; Mismatches 32; Indels 17; Gaps 7;

QY 3 CYBGNHGFYRGKASTDMGRPCLPMNSATVLOQTYHAHR---SDALQLGLGKHNYCRNPD 59
DB 377 CYHGDGQSYRGTSSTTTGKKQCSWSS-----MTPRHQKTPENYFNAGL-TMYNCRNPD 430
QY 60 NRPRPCVYQVGLKPLV--QECMVHDCADGKKPS--SPP 94
DB 431 ADKGPWCFT---TDPSSVRWEYCNLKKCS-GTEASVVAPP 465

RESULT 40
ROR1_HUMAN STANDARD; PRT; 937 AA.
AC Q01973; Q92776;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor ROR1 precursor
DE (EC 2.7.1.112) (Neurotrophic tyrosine kinase, receptor-related 1).
GN ROR1 OR NTRK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN J. Biol. Chem. 267:26181-26190(1992).
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RX MEDLINE=93100347; PubMed=1334494;
RA Maslakowski P., Carroll R.D.;
RT "A novel family of cell surface receptors with tyrosine kinase-like domain";
RT J. Biol. Chem. 267:26181-26190(1992).
RL (2)
RN SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=97030043; PubMed=8875995;
RA Reddy U.R., Phatak S., Pleasure D.;
RT "Human neural tissues express a truncated Ror1 receptor tyrosine kinase, lacking both extracellular and transmembrane domains";
RT Oncogene 13:1555-1559(1996).
RL (1)
CC -!- FUNCTION: Tyrosine-protein kinase receptor whose role is not yet clear.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q01973-1; Sequence=Displayed;
CC Name=Short; Synonyms=ROR1;
CC IsoId=Q01973-2; Sequence=VSP_005008;
CC -!- TISSUE SPECIFICITY: Expressed strongly in human heart, lung, and kidney, but weakly in the CNS. The short isoform is strongly expressed in fetal and adult CNS and in a variety of human cancers, including those originating from CNS or PNS neuroectoderm.
CC -!- DEVELOPMENTAL STAGE: Expressed at high levels during early embryonic development. The expression levels drop strongly around day 16 and there are only very low levels in adult tissues.
CC -!- SIMILARITY: Belongs to the tyr family of protein kinases. ROR subfamily.
CC -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
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CC -----
CC EMBL; M97675; AAA60275.1; -;
CC EMBL; U38894; AAC50714.1; -;

PIR; A45082; A45082.
HSSP; P00747; ICEA.
Genew; HGNC:10256; ROR1.
MIM; 602336; -;
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004714; F:transmembrane receptor protein tyrosine kin. ; TAS.
DR GO; GO:0007169; F:transmembrane receptor protein tyrosine kin. ; TAS.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; Igc2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00219; Ty-Kc; 1.
DR PROSITE; PS00038; FZ; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS00111; PROTEIN KINASE_DW; 1.
DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
KW Transferase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW Transmembrane; signal; Glycoprotein; Kringle; Phosphorylation;
KW Immunoglobulin domain; Alternative splicing.
FT SIGNAL 1 29
FT CHAIN 30 937
FT DOMAIN 30 406
FT TRANSMEM 407 427
FT DOMAIN 428 937
FT DOMAIN 42 147
FT DOMAIN 165 299
FT DOMAIN 312 391
FT DOMAIN 473 746
FT DOMAIN 753 782
FT DOMAIN 784 851
FT DOMAIN 853 876
FT NP_BIND 479 487
FT BINDING 506 506
FT ACT_SITE 615 615
FT MOD_RES 645 645
FT DISULFID 79 131
FT CARBOHYD 47 47
FT CARBOHYD 66 66
FT CARBOHYD 184 184
FT CARBOHYD 315 315
FT VARSPPLIC 1 549
FT SEQUENCE 937 AA; 104312 MW; 0D0694DBF29F4773 CRC64;
SQ
Query Match 26.4%; Score 146; DB 1; Length 937;
Best Local Similarity 44.1%; Pred. No. 1.4e-08;
Matches 30; Conservative 5; Mismatches 25; Indels 8; Gaps 3;
QY 3 CYBGNHGFYRGKASTDMGRPCLPMNSATVLOQTYHAHRSDALQLGLGKHNYCRNPD 60
DB 313 CYNSTGVYRGVTSVTKSGRQCQPNWS-----QYPHTHTFTALFPPLNGHSGYCRNPGN 367
QY 61 RRR-PWCY 67
DB 368 QKEAPWCF 375

KW Transferase; Tyrosine-protein kinase; ATP-binding; Receptor;
KW Transmembrane; Signal; Glycoprotein; Kringle; Phosphorylation;
KW Immunoglobulin domain.
FT SIGNAL 1 29
FT CHAIN 30 937
FT TYROSINE-PROTEIN KINASE TRANSMEMBRANE
FT RECEPTOR RORL.
FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 407 427
FT POTENTIAL.
FT DOMAIN 428 937
FT CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 141
FT IG-LIKE C2-TYPE.
FT DOMAIN 165 299
FT FZ.
FT DOMAIN 312 391
FT KRINGLE.
FT DOMAIN 473 746
FT PROTEIN KINASE.
FT DOMAIN 753 782
FT SER/THR-RICH.
FT DOMAIN 784 851
FT PRO-RICH.
FT DOMAIN 853 876
FT SER/THR-RICH.
FT NP_BIND 479 487
FT ATP (BY SIMILARITY).
FT BINDING 506 506
FT ATP (BY SIMILARITY).
FT ACT_SITE 615 615
FT BY SIMILARITY.
FT MOD_RES 645 645
FT PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT DISULFID 79 131
FT BY SIMILARITY.
FT CARBOHYD 47 47
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 66 66
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184
FT N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315
FT N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 937 AA; 104156 MW; D728733E67D1782C CRC64;
Query Match 25.4%; Score 146; DB 1; Length 937;
Best Local Similarity 44.1%; Pred. No. 1.4e-08;
Matches 30; Conservative 5; Mismatches 25; Indels 8; Gaps 3;
QY 3 CYEENGHFGKASTDTMGPRCLPWNSATVLQOTYHAHRSDALQLG--LGSHNYCRPN 60
DB 313 CYNSTGVYRGTSVTKSGRCQCPWNS-----QYPHTSFALRFPPLNGSHYCRPN 367
QY 61 RRR-PWCY 67
DB 368 QKEAPWCF 375
RESULT 42
PLMN_MOUSE STANDARD; PRT; 812 AA.
AC P20918; Q8CIS2; Q91WJ5;
DT 01-FEB-1991 (Rel. 17, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiostatin].
GN PLG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91184812; PubMed=2081600;
RA Degen S.J., Bell S.M., Schaefer L.A., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse plasminogen and
RT localization of the gene to mouse chromosome 17.";
RL Genomics 8:49-61(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RA Brathwaite M.; Maeltz P., Qian Y., Dudekula D., Schlessinger D.,
RA Nagaraja R.;
RT "Genomic sequence analysis in the mouse t-complex region.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RESULT 41
RORL_MOUSE STANDARD; PRT; 937 AA.
AC Q9Z139;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor RORL precursor
DE [EC 2.7.1.112] (Neurotrophic tyrosine kinase, receptor-related 1)
DE (RORL).
GN RORL OR NTRKRL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99248426; PubMed=102311392;
RA Gishi I., Takeuchi S., Hashimoto R., Nagabukuro A., Ueda T., Liu Z.J.,
RA Hatta T., Akira S., Matsuda Y., Yamamura H., Otani H., Minami Y.;
RT "Spatio-temporally regulated expression of receptor tyrosine kinases,
RT mRor1, mRor2, during mouse development: implications in development
RT and function of the nervous system.";
RL Genes Cells 4:41-56(1999).
CC -!- FUNCTION: Tyrosine-protein kinase receptor whose role is not yet
CC clear.
CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
CC subfamily.
CC -!- SIMILARITY: Contains 1 frizzled (FZ) domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB010383; BAA75480.1; .
DR HSP; P00747; ICEA
DR MGD; MGI:1347520; Rorl.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TVR; 1.

DR	EMBL; AY134430; AAN15805.1; -	1	19	SIGNAL
DR	PIR; A38514; PLMS	20	812	PLASMINOGEN.
DR	HSP; P00747; LEWK.	20	581	PLASMIN HEAVY CHAIN A.
DR	MEROPI; S01.233; -	20	97	ACTIVATION PEPTIDE
DR	MGB; MGI:97620; PIG.	98	581	PLASMIN SHORT FORM OF CHAIN A.
DR	GO; GO:0016506; F:apoptosis activator activity; IDA.	98	436	ANGIOSTATIN.
DR	GO; GO:0006915; P:apoptosis; IDA.	582	812	PLASMIN LIGHT CHAIN B.
DR	GO; GO:0009003; Cys Ser trypsin.	103	181	KRINGLE 1.
DR	InterPro; IPR009001; Kringl	184	262	KRINGLE 2.
DR	InterPro; IPR000001; Kringl	275	352	KRINGLE 3.
DR	InterPro; IPR003014; PAN	377	454	KRINGLE 4.
DR	InterPro; IPR003609; Pan_app	481	560	KRINGLE 5.
DR	InterPro; IPR001254; Peptidase_S1	582	812	SERINE PROTEASE
DR	InterPro; IPR001314; Peptidase_S1A	624	624	CHARGE RELAY SYSTEM (BY SIMILARITY).
DR	InterPro; IPR003966; Peptidase_S1A_pr	657	667	CHARGE RELAY SYSTEM (BY SIMILARITY).
DR	Pfam; PF00051; kringl; 5.	762	762	CHARGE RELAY SYSTEM (BY SIMILARITY).
DR	Pfam; PF00024; PAN; 1.	49	73	BY SIMILARITY.
DR	Pfam; PF00089; trypsin; 1.	53	61	BY SIMILARITY.
DR	PRINTS; P300722; CHYMOTRYPSIN.	103	181	BY SIMILARITY.
DR	PRINTS; P300018; KRINGLE	124	164	BY SIMILARITY.
DR	PRINTS; P301505; PROTHROMBIN	122	176	BY SIMILARITY.
DR	ProDom; P000395; kringl; 4.	185	262	BY SIMILARITY.
DR	SMART; SM00130; KR; 5.	188	316	BY SIMILARITY.
DR	SMART; SM00473; PAN AP; 1.	206	245	BY SIMILARITY.
DR	SMART; SM00020; TRYD_SPC; 1.	224	257	BY SIMILARITY.
DR	PROSITE; PS00021; KRINGLE 1; 5.	275	352	BY SIMILARITY.
DR	PROSITE; PS00070; KRINGLE 2; 5.	296	335	BY SIMILARITY.
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.	324	347	BY SIMILARITY.
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	377	454	BY SIMILARITY.
DR	PROSITE; PS00135; TRYPSIN_SER; 1.	377	454	BY SIMILARITY.
DR	Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;	384	437	BY SIMILARITY.
KW	Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat;	426	449	BY SIMILARITY.
KW	Signal.	481	560	BY SIMILARITY.
FT	FT CHAIN	502	543	BY SIMILARITY.
FT	FT CHAIN	531	555	BY SIMILARITY.
FT	FT PEPTIDE	568	687	INTERCHAIN (BY SIMILARITY).
FT	FT CHAIN	578	586	INTERCHAIN (BY SIMILARITY).
FT	FT CHAIN	609	625	BY SIMILARITY.
FT	FT CHAIN	701	768	BY SIMILARITY.
FT	FT CHAIN	731	747	BY SIMILARITY.
FT	FT CHAIN	758	786	BY SIMILARITY.
FT	FT CHAIN	235	235	R -> H (IN REF. 1).
FT	FT CHAIN			CONFLICT

```

FT CONFLICT 525 525 G -> D (IN REF. 1).
FT CONFLICT 649 649 S -> L (IN REF. 1).
SQ SEQUENCE 812 AA; 90781 MW; 2417326086A2FFD2 CRC64;

Query Match 26.1%; Score 144.5; DB 1; Length 812;
Best Local Similarity 32.7%; Pred. No. 1.7e-08;
Matches 33; Conservative 8; Mismatches 47; Indels 13; Gaps 4;

QY 3 CYEKGHFYRGASDTWGRCPPLNWSATVLOOTYHARSALQLGLG--KHYNCRNPDN 60
DB 275 CLKRGYNYRGVTVSVGSKTCQKRW-----EQPHRHNTPEPFPCKNLEBNCRNPDG 329

QY 61 RRRPQYVQVGLKPLVQECMVHCDAGKKP-----SSPPEE 96
DB 330 ETAPWCYT-TDSQLRWEYCEIIPSCSSASPDQSDSSVPPEE 369

RESULT 43
RORI DROME
ID RORI DROME STANDARD; PRT; 685 AA.
AC Q24488;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tyrosine-protein kinase transmembrane receptor Ror precursor
DE (EC 2.7.1.112) (GROr).
GN ROR OR CG4926.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=Canton-S; TISSUE=Larval brain;
RX MEDLINE=93348222; PubMed=8394009;
RA Wilson C. Goherdan D. C. I. Steller H.;
RT "Ror", a potential neurotrophic receptor gene, encodes a Drosophila
RT homolog of the vertebrate Ror family of Trk-related receptor tyrosine
RT kinases."
RL Proc. Natl. Acad. Sci. U.S.A. 90:7109-7113(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Change M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.P., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C.J., Gabrielian A.B., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwa C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Wang X.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.N., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "the genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE OF 545-597 FROM N.A.
RX MEDLINE=98401146; PubMed=9731193;
RA Oates A.C., Wollberg P., Achen M.G., Wilks A.F.;
RT "Sampling the genomic pool of protein tyrosine kinase genes using the
RT polymerase chain reaction with genomic DNA."
RL Biochem. Biophys. Res. Commun. 249:660-667(1998).
CC -/- FUNCTION: Tyrosine-protein kinase receptor that functions during
CC early stages of neuronal development.
CC -/- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -/- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -/- TISSUE SPECIFICITY: Expressed in neurons of the developing nervous
CC system.
CC -/- SIMILARITY: Belongs to the Tyr family of protein kinases. ROR
CC subfamily.
CC -/- SIMILARITY: Contains 1 frizzled (FZ) domain.
CC -/- SIMILARITY: Contains 1 kringle domain.
CC -----
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CC -----
DR EMBL; L20297; AAA28860.1; -.
DR EMBL; AE003628; AAF52885.1; -.
DR EMBL; AJ002908; CAA05743.1; -.
DR PIR; A48289; A48289.
DR HSP; P11362; IFKG.
DR FlyBase; FBgn0010407; Ror.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; NAS.
DR GO; GO:0007417; P:central nervous system development; IEP.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002011; Recepttyrkinil.
DR InterPro; IPR001245; Tyr_kinase_AS.
DR InterPro; IPR006266; Tyr_kinase_AS.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00330; KR; 1.
DR SMART; SM00219; TyRK; 1.
DR PROSITE; PS00038; FZ; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00239; RECEPTOR_TYR_KIN_II; 1.
DR Transmembrane; Kinase; Tyrosine-protein kinase; ATP-binding; Receptor;
DR Developmental protein.
FT SIGNAL 1 24
FT CHAIN 25 685 TYROSINE-PROTEIN KINASE TRANSMEMBRANE

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FT DOMAIN 25 317 RECEPTOR ROR
FT TRANSMEM 318 338 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 339 685 POTENTIAL.
FT CYTOPLASMIC 36 225 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 236 310 FZ.
FT DOMAIN 410 677 KRINGLE.
FT NP_BIND 416 424 PROTEIN KINASE.
FT BINDING 442 442 ATP (BY SIMILARITY).
FT ACT_SITE 539 539 ATP (BY SIMILARITY).
FT MOD_RES 565 565 BY SIMILARITY.
FT MOD_RES 569 569 PHOSPHORYLATION (AUTO-) (BY
FT MOD_RES 570 570 SIMILARITY).
FT CARBOHYD 45 45 PHOSPHORYLATION (AUTO-) (BY
FT CARBOHYD 63 63 SIMILARITY).
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 685 AA; 526162D27D5FD7C7 CRC64;

Query Match 25.1%; Score 139; DB 1; Length 685;
Best Local Similarity 34.5%; Pred. NO. 6e-08;
Matches 30; Conservative 19; Mismatches 28; Indels 10; Gaps 5;

Oy 1 KTCVEGNGHYRGKASDTMGRCLPWNGATVLOQTYHAHRSDALQGLGKKNYCRNPDN 60
Db 235 ENCWEDGSIYRGVANVSASGKCLAW--SWLMKEI-----SDFPEL-IGQ-NYCRNPGS 285

Oy 61 -RRRPWCYOVGLKPLVQSCWHDGAD 86
Db 286 VENSPPWCVDSSRIELCDIPKCAD 312

RESULT 44
HGF_MOUSE STANDARD; PRT; 728 AA.
ID -HGF_MOUSE STANDARD; PRT; 728 AA.
AC Q08048; Q61662; Q64007;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN HGF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT), AND SEQUENCE OF 496-504.
RC TISSUE=Mammary fibroblast;
RX MEDLINE=94183257; PubMed=8135822;
RA Sasaki M., Nishio M., Sasaki T., Enami J.;
RT "Identification of mouse mammary fibroblast-derived mammary growth
factor as hepatocyte growth factor."
RL Biochem. Biophys. Res. Commun. 199;772-779(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94363381; PubMed=8081873;
RA Lee C.C., Kozak C.A., Yamada K.M.;
RT "Structure, genetic mapping, and expression of the mouse Hgf/scatter
factor gene."
RL Cell Adhes. Commun. 1:101-111(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=94060105; PubMed=8241272;
RA Liu Y., Michalopoulos G.K., Zarnegar R.;
RT "Molecular cloning and characterization of cDNA encoding mouse
hepatocyte growth factor."

```

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RL CC Biochim. Biophys. Acta 1216:299-303(1993).
CC -!- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC hepatocyte cells, seems to be an hepatotrophic factor, and acts as
CC growth factor for a broad spectrum of tissues and cell types. It
CC has no detectable protease activity.
CC -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC disulfide bond.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q08048-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q08048-2; Sequence=VSP_005408;
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 4 kringle domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D10212; BAA01064.1; -
CC EMBL; D10213; BAA01065.1; -
CC EMBL; S71816; AAB31855.1; -
CC EMBL; X72307; CAAS1054.1; ALT_INIT.
CC PIR; JC2117; A60185.
CC HSSP; P14210; 1BHT.
CC MESOPS; S01_982; -
CC MGD; MGI:96079; Hgf.
CC InterPro; IPR009003; Cys_Ser_trypsin.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR003014; PAN.
CC InterPro; IPR003609; Pan app.
CC InterPro; IPR01254; Peptidase S1.
CC InterPro; IPR001314; Peptidase_S1A.
CC Pfam; PF00051; Kringle; 4.
CC Pfam; PF00024; PAN; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 4.
CC SMART; SM00130; KR; 4.
CC SMART; SM00473; PAN AP; 1.
CC SMART; SM00020; Tryp_Sec; 1.
CC PROSITE; PS00021; KRINGLE_1; 4.
CC PROSITE; PS00070; KRINGLE_2; 4.
CC PROSITE; PS50240; TRYPSIN_DOM; 1.
CC Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
CC Signal; Alternative splicing; Pyrrolidone carboxylic acid.
FT SIGNAL 1 32 BY SIMILARITY.
FT CHAIN 33 495 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
FT CHAIN 496 728 HEPATOCYTE GROWTH FACTOR BETA CHAIN.
FT MOD_RES 33 33 PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
FT DOMAIN 33 128 PAP.
FT DOMAIN 129 207 KRINGLE 1.
FT DOMAIN 212 289 KRINGLE 2.
FT DOMAIN 306 384 KRINGLE 3.
FT DOMAIN 392 470 KRINGLE 4.
FT DOMAIN 496 728 SERINE PROTEASE-LIKE.
FT DISULFID 71 97 BY SIMILARITY.
FT DISULFID 75 85 BY SIMILARITY.
FT DISULFID 488 607 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 656 656 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPPLIC 163 167 Missing (in isoform Short).
FT CONFLICT 344 344 /FTid=VSP_005408.
FT CONFLICT 344 N -> K (IN REF. 2).

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FT CONFLICT 479 479 V -> L (IN REF. 2).
FT CONFLICT 564 564 R -> H (IN REF. 3).
SQ SEQUENCE 728 AA; 82944 MW; A0381FC497534328 CRC64;

Query Match
Best Local Similarity 24.8%; Score 137.5; DB 1; Length 728;
Matches 31; Conservative 12; Mismatches 35; Indels 19; Gaps 4;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWNASATVLOQTYHAHRSDALQLGLG-----KHNYCRNP 58
Db 306 CIQGGEGYRGTTINWGIPIQRWDS-----QYPKHDTITPENFKCKDLRENYCRNP 358

QY 59 DNRERPWCY-----VOVGLKPLVQECMV---HDCADG 87
Db 359 DGAESPWCFTTDPNIRVGVCSPKCDVSSGQDCYRG 395

RESULT 46
HGF_HUMAN
ID HGF_HUMAN STANDARD; PRT; 728 AA.
AC P14210; Q9BYL9; Q9UDU6;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN HGF OR HPTA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=91340155; PubMed=1831432;
RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
RT "Organization of the human hepatocyte growth factor-encoding gene.";
RL Gene 102:213-219(1991).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Placenta;

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DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN AP; 1.
DR SMART; SM00020; TYD_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
DR PROSITE; PSS0240; TRYPSIN_DOM; 1.
KW Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
KW signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 32
FT CHAIN 33 495
FT CHAIN 496 728
FT MOD_RES 33 33
FT DOMAIN 33 128
FT DOMAIN 129 207
FT DOMAIN 212 289
FT DOMAIN 306 384
FT DOMAIN 392 470
FT DOMAIN 496 728
FT DISULFID 71 97
FT DISULFID 75 85
FT DISULFID 488 607
FT CARBOHYD 295 295
FT CARBOHYD 403 403
FT CARBOHYD 569 569
FT CARBOHYD 656 656
SQ SEQUENCE 728 AA; 82905 MW; 3E0BF1F96ADCEDEFF CRC64;

Query Match 24.5%; Score 135.5; DB 1; Length 728;
Best Local Similarity 32.0%; Pred. No. 1.6e-07;
Matches 31; Conservative 11; Mismatches 36; Indels 19; Gaps 4;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWNASATVLOQTYHAHRSDALQLGLG-----KHNYCRNP 58
Db 306 CIQGGEGYRGTTINWGIPIQRWDS-----QYPKHDTITPENFKCKDLRENYCRNP 358

QY 59 DNRERPWCY-----VOVGLKPLVQECMV---HDCADG 87
Db 359 DGAESPWCFTTDPNIRVGVCSPKCDVSSGQDCYRG 395

RESULT 46
HGF_HUMAN
ID HGF_HUMAN STANDARD; PRT; 728 AA.
AC P14210; Q9BYL9; Q9UDU6;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hepatocyte growth factor precursor (Scatter factor) (SF)
DE (Hepatopoietin A).
GN HGF OR HPTA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RP MEDLINE=91340155; PubMed=1831432;
RA Seki T., Hagiya M., Shimonishi M., Nakamura T., Shimizu S.;
RT "Organization of the human hepatocyte growth factor-encoding gene.";
RL Gene 102:213-219(1991).
RN [2]
RP SEQUENCE FROM N.A.
RP TISSUE=Placenta;

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RX MEDLINE=89392017; PubMed=2528952;
RA Miyazawa K., Tsubouchi H., Naka D., Takahashi K., Okigaki M.,
RA Arakaki N., Nakayama H., Hirono S., Sakiyama O., Takahashi K.,
RA Gohda E., Daikuhara Y., Kitamura N.;
RT "Molecular cloning and sequence analysis of cDNA for human hepatocyte
RT growth factor.";
RL Biochem. Biophys. Res. Commun. 163:967-973(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025062; PubMed=2145836;
RA Seki T., Ihara I., Sugimura A., Shimonishi M., Nishizawa T.,
RA Asami O., Hagiya M., Nakamura T., Shimizu S.;
RT "Isolation and expression of cDNA for different forms of hepatocyte
RT growth factor and expression of cDNA for different forms of hepatocyte
RL Biochem. Biophys. Res. Commun. 172:321-327(1990).
RN [4]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 55-73 AND 495-520.
RC TISSUE=Liver;
RX MEDLINE=90666676; PubMed=2531289;
RA Nakamura T., Nishizawa T., Hagiya M., Seki T., Shimonishi M.,
RA Sugimura A., Tashiro K., Shimizu S.;
RT "Molecular cloning and expression of human hepatocyte growth factor.";
RL Nature 342:440-443(1989).
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic fibroblast;
RX MEDLINE=91334393; PubMed=1831266;
RA Weidner K.M., Arakaki N., Hartmann G., Vandekerkhove J., Weingart S.,
RA Rieder H., Fonatsch C., Tsubouchi H., Hishida T., Daikuhara Y.,
RA Birchemier W.;
RT "Evidence for the identity of human scatter factor and human
RT hepatocyte growth factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:7001-7005(1991).
RN [6]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Livingston R.J., Daniels M.R., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Courtney L., Elliot G., Angell S.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 249-695 FROM N.A.
RX MEDLINE=91369928; PubMed=1832556;
RA Miyazawa K., Kitamura A., Kitamura N.;
RT "Structural organization and the transcription initiation site of the
RT human hepatocyte growth factor gene.";
RL Biochemistry 30:9170-9176(1991).
RN [9]
RP SIGNAL SEQUENCE CLEAVAGE SITE.
RX MEDLINE=91207365; PubMed=1826837;
RA Yoshiyama Y., Arakaki N., Naka D., Takahashi K., Hirono S., Kondo J.,
RA Nakayama H., Gohda E., Kitamura N., Tsubouchi H., Ishii T.,
RA Hishida T., Daikuhara Y.;
RT "Identification of the N-terminal residue of the heavy chain of both
RT native and recombinant human hepatocyte growth factor.";
RL Biochem. Biophys. Res. Commun. 175:660-667(1991).
RN [10]
RP CARBOHYDRATE-LINKAGE SITE THR-476.
RX MEDLINE=9129192; PubMed=1482348;
RA Shimizu N., Hara H., Sogabe T., Sakai H., Ihara I., Inoue H.,
RA Nakamura T., Shimizu S.;
RT "Hepatocyte growth factor is linked by O-glycosylated oligosaccharide
RT on the alpha chain.";
RL Biochem. Biophys. Res. Commun. 189:1329-1335(1992).
RN [11]
RP MUTAGENESIS.
RX MEDLINE=92331602; PubMed=1321034;
RA Lokker N.A., Mark M.R., Luis E.A., Bennett G.L., Robbins K.A.,
RA Baker J.B., Godowski P.J.;

"Structure-function analysis of hepatocyte growth factor:
RT identification of variants that lack mitogenic activity yet retain
RT high affinity receptor binding.";
RL EMBO J. 11:2503-2510(1992).
RN [12]
RP STRUCTURE BY NMR OF 31-127.
RX MEDLINE=98154323; PubMed=9493272;
RA Zhou H., Mazulla M.J., Kaufman J.D., Stahl S.J., Wingfield P.T.,
RA Rubin J.S., Bottaro D.P., Byrd R.A.;
RT "The solution structure of the N-terminal domain of hepatocyte growth
RT factor reveals a potential heparin-binding site.";
RN Structure 6:109-116(1998).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 35-210.
RX MEDLINE=99036858; PubMed=9817840;
RA Utsch M., Lokker N.A., Godowski P.J., de Vos A.M.;
RT "Crystal structure of the NK1 fragment of human hepatocyte growth
RT factor at 2.0-A resolution.";
RN Structure 6:1383-1393(1998).
RN CC
CC -!- FUNCTION: HGF is a potent mitogen for mature parenchymal
CC hepatocyte cells, seems to be an hepatotrophic factor, and acts
CC as growth factor for a broad spectrum of tissues and cell types.
CC It has no detectable protease activity.
CC -!- SUBUNIT: Dimer of an alpha chain and a beta chain linked by a
CC disulfide bond.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
CC -!- SIMILARITY: Contains 4 kringle domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D90334; BAA14348.1; -
CC EMBL; D90318; BAA14348.1; JOINED.
CC EMBL; D90319; BAA14348.1; JOINED.
CC EMBL; D90320; BAA14348.1; JOINED.
CC EMBL; D90322; BAA14348.1; JOINED.
CC EMBL; D90323; BAA14348.1; JOINED.
CC EMBL; D90324; BAA14348.1; JOINED.
CC EMBL; D90325; BAA14348.1; JOINED.
CC EMBL; D90326; BAA14348.1; JOINED.
CC EMBL; D90327; BAA14348.1; JOINED.
CC EMBL; D90328; BAA14348.1; JOINED.
CC EMBL; D90329; BAA14348.1; JOINED.
CC EMBL; D90330; BAA14348.1; JOINED.
CC EMBL; D90331; BAA14348.1; JOINED.
CC EMBL; D90332; BAA14348.1; JOINED.
CC EMBL; D90333; BAA14348.1; JOINED.
CC EMBL; M29145; AAA52650.1; -
CC EMBL; M60718; AAA52648.1; -
CC EMBL; X16323; CAA34387.1; -
CC EMBL; M73239; AAA64239.1; -
CC EMBL; M73240; AAA64297.1; -
CC EMBL; AY246560; AAO61091.1; -
CC EMBL; AC004960; AAC71655.1; -
CC EMBL; M75983; AAG53460.1; -
CC EMBL; M75972; AAG53460.1; JOINED.
CC EMBL; M75973; AAG53460.1; JOINED.
CC EMBL; M75974; AAG53460.1; JOINED.
CC EMBL; M75975; AAG53460.1; JOINED.
CC EMBL; M75976; AAG53460.1; JOINED.
CC EMBL; M75977; AAG53460.1; JOINED.
CC EMBL; M75978; AAG53460.1; JOINED.
CC EMBL; M75979; AAG53460.1; JOINED.
CC EMBL; M75980; AAG53460.1; JOINED.
CC EMBL; M75981; AAG53460.1; JOINED.
CC EMBL; M75982; AAG53460.1; JOINED.
CC PIR; JH0579; JH0579.
CC PDB; 2HGF; 24-JUN-98.

DR PDB; 1BHT; 18-NOV-98.
DR PDB; INK1; 29-DEC-99.
DR MEROPS; S01.376; -
DR GlycosuitedB; P14210; -
DR Genew; HGNC:4893; HGF.
DR MIM; 142409; -
DR GO; GO:0008083; P: growth factor activity; NAS.
DR GO; GO:0007087; P: mitosis; NAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan app.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; Kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR0018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00021; KRINGLE_1; 4.
DR PROSITE; PS00070; KRINGLE_2; 4.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR Growth factor; Kringle; Glycoprotein; Serine protease homolog; Repeat;
KW Signal; 3D-structure; Polymorphism; Pyrrolidone carboxylic acid.
FT SIGNAL 1 31
FT CHAIN 32 494 HEPATOCYTE GROWTH FACTOR ALPHA CHAIN.
FT CHAIN 495 728 HEPATOCYTE GROWTH FACTOR BETA CHAIN.
FT MOD_RES 32 32 PYRROLIDONE CARBOXYLIC ACID.
FT DOMAIN 32 127 PAP.

Query Match 24.1%; Score 133.5; DB 1; Length 728;
Best Local Similarity 34.7%; Pred No. 2.7e-07;
Matches 33; Conservative 10; Mismatches 37; Indels 15; Gaps 5;

Qy 3 CYEGNGHFYRGKASTDTMGRLPCLPWSATVLOQTYFAHRSALQGLGKHNYCRNPDN 60
Db 305 CIOGQGEYRGTVTWINGIPQWRDS----QYPHEHDMTPENFKCDLRENYCRNPDG 359

Qy 61 RRRPWY-----VOVGLKPLVQEC-MVH--DCADG 87
Db 360 SESPWCFTTDPNIRVGYSQIENCDMSHQDQYRG 394

RESULT 47
ID PLMN PETWA STANDARD; PRT; 325 AA.
AC F33574;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Plasminogen (EC 3.4.21.7) (Fragments).
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hypercoartia;
OC Petromyzontiformes; Petromyzontidae; Petromyzon.
OX NCBI_TaxID=7757;
RN [1]
RP SEQUENCE.
RA Affolter M., Schaller J., Rickli E.E.;
RT "Isolation, characterization and partial amino acid sequence of
RT lamprey plasminogen."
RL Protein Seq. Data Anal. 5:207-211 (1993).
CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
CC a proteolytic factor in a variety of other processes including
CC embryonic development, tissue remodeling, tumor invasion,
CC and inflammation.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
CC higher selectivity than trypsin. Converts fibrin into soluble
CC products.
CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.

CC -!- SIMILARITY: Contains at least 2 kringle domains.
DR PIR; S33879; S33879.
DR HSSP; P00747; SHPG.
DR MEROPS; S01.233; -
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; TRYPSIN; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
KW Tissue remodeling; Blood coagulation; Kringle; Zymogen.
FT NON_CONS 15 16
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Query Match 23.6%; Score 131; DB 1; Length 325;
Best Local Similarity 32.9%; Pred. No. 2.2e-07;
Matches 28; Conservative 5; Mismatches 36; Indels 16; Gaps 2;

Qy 3 CYEGNGHFYRGKASTDTMGRLPCLPWSATVLOQTYFAHRSALQGLGKHNYCRNPDN 62
Db 81 CVKGTGEGYRGTAALTVSGKACQAWASQT-----PGDVYSCQGLVSNYCRNPDGK 131

Qy 63 RPMCYYVQVGLKPLVQECMVHDCADG 87
Db 132 LPWCYT-----TEYCNVPSCTGG 149

RESULT 48
ID THRB MOUSE STANDARD; PRT; 618 AA.
AC P12221;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Prothrombin precursor (EC 3.4.21.5).
GN F2 OR CF2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Liver;
RX MEDLINE=91025553; PubMed=2222810;
RA Friezner Degen S.J., Schaffer L.A., Jamison C.S., Grant S.G.,
RA Fitzgibbon J.J., Pai J.-A., Chapman V.M., Elliott R.W.;
RT "Characterization of the cDNA coding for mouse prothrombin and
RT localization of the gene on mouse chromosome 2.";
RL DNA Cell Biol. 9:487-498 (1990).
RN [2]
RP SEQUENCE FROM N.A.

CC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=2238257; PubMed=1277932;
RA Klausner R.L., Feingold E.A., Grouse L.H., Shemen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murry D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.C.,
RA Blakesley R.W., Touchman J.W., Green E.B., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [3]
RP SEQUENCE OF 384-618 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92212913; PubMed=1557383;
RA Banfield D.K., Macgillivray R.T.,
RT "Partial characterization of vertebrate prothrombin cDNAs:
RT amplification and sequence analysis of the B chain of thrombin from
RT nine different species";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2779-2783 (1992).
CC -!- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XI, and, in complex with thrombomodulin, protein C.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -!- FROM THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOomal
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
CC OF PROTHROMBIN TO THROMBIN.
CC -!- MISCELLANEOUS: Prothrombin is activated on the surface of a
CC phospholipid membrane that binds the amino end of prothrombin and
CC factors Va and Xa in Ca-dependent interactions; factor Xa removes
CC the activation peptide and cleaves the remaining part into light
CC and heavy chains. The activation process starts slowly because
CC factor V itself has to be activated by the initial, small amounts
CC of thrombin.
CC -!- MISCELLANEOUS: Thrombin can itself cleave the amino terminal
CC fragment (fragment 1) of the prothrombin, prior to its activation
CC by factor Xa.
CC -!- SIMILARITY: Belongs to peptidase family S1.
CC -!- SIMILARITY: Contains 2 kringle domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; X52308; CAA36548.1; -;
CC EMBL; BC013662; AAH13662.1; -;
CC EMBL; M81394; AAA04035.1; -;
CC F01; A35827; A35827.
CC HSPF; P00734; 1B7X.
CC MEROPS; S01.217; -;
CC MGI; 88380; F2.
CC InterPro; IPR009003; Cys Ser trypsin.
CC InterPro; IPR002383; GLA_blood.
CC InterPro; IPR000001; Kringle.

DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR InterPro; IPR000294; VitK_dep_GLA.
DR Pfam; PF00594; gla; 1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PRO0722; CHYMOTRYPSIN.
DR PRINTS; PRO0001; GLABLOOD.
DR PRINTS; PRO0018; KRINGLE.
DR PRINTS; PRO1505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00069; GLA; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM0020; TRYPSIN; 1.
DR PROSITE; PS00011; GLU-CARBOXYLATION; 1.
DR PROSITE; PS00021; KRINGLE 1; 2.
DR PROSITE; PS00070; KRINGLE 2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Blood coagulation; Plasma; Calcium-binding; Glycoprotein; Repeat;
KW Vitamin K; Zymogen; Gamma-carboxyglutamic acid; Acute phase; Liver;
KW Hydrolase; Serine protease; Kringle; Signal.
FT SIGNAL 1 24
FT PROPEP 25 43
FT CHAIN 44 618
FT PEPTIDE 44 200
FT PEPTIDE 201 324
FT CHAIN 325 360
FT CHAIN 361 618
FT DOMAIN 109 187
FT DOMAIN 215 292
FT DOMAIN 361 618
FT SITE 200 201
FT SITE 324 325
FT SITE 360 361
FT ACT_SITE 403 403
FT ACT_SITE 459 459
FT ACT_SITE 565 565
FT MOD_RES 50 50
FT MOD_RES 51 51
FT MOD_RES 58 58
FT MOD_RES 60 60
FT MOD_RES 63 63
FT MOD_RES 64 64
FT MOD_RES 69 69
FT MOD_RES 70 70
FT MOD_RES 73 73
FT MOD_RES 76 76
FT DISULFID 91 104
FT DISULFID 109 187
FT DISULFID 130 170
FT DISULFID 158 182
FT DISULFID 215 293
FT DISULFID 236 276
FT DISULFID 264 288
FT DISULFID 333 479
FT DISULFID 388 404
FT DISULFID 533 547
FT DISULFID 561 591
FT CARBOHYD 122 122
FT CARBOHYD 144 144
FT CARBOHYD 413 413
FT CARBOHYD 553 553
SQ SEQUENCE 618 AA; 70268 MW; B89F719A9AFD601E0 CEC64;
Query Match 22.7%; Score 125.5; DB 1; Length 618;
Best Local Similarity 31.8%; Pred. No. 1.8e-06;
Matches 27; Conservative 13; Mismatches 40; Indels 5; Gaps 3;
QY 3 CYEGNGHYRGKASDTWGRCLPNSATVLQQTVAHRSALQLGLGKHVCRNPD-NR 61

Db 215 CUTEGRYQGNLAVTTIGSPCLPWNLSIPAKTSLKYQDFPEVKL---VENFCRNPDWDE 271
 QY 62 RPPWCYVQVGLKPLVQECMVHDCAD 86
 Db 272 EGACWCYV-AGQGDPEYCNLYCEE 295

RESULT 49
 PLMN_SHEEP
 ID PLMN_SHEEP STANDARD; PRT; 343 AA.
 AC P81286;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Plasminogen (EC 3.4.21.7) (Fragment).
 GN PLG.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93149995; PubMed=1492092;
 RA Schaller J., Straub C., Kamper U., Rickli E.E.;
 RT "Complete amino acid sequence of ovine miniplasminogen.";
 RL Protein Seq. Data Anal. 5:21-25(1992).
 CC -!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willebrand factor.
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!- ENZYME REGULATION: Converted into plasmin by plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot plasminogen
 CC -!- SIMILARITY: Belongs to peptidase family S1. Plasminogen subfamily.
 CC -!- SIMILARITY: Contains at least 2 kringle domains.
 DR PIR; B61545; B61545.
 DR HSP; P00747; 5HPG.
 DR MEROPS; S01.233; -.
 DR InterPro; IPR009003; Cys Ser trypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001234; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR InterPro; IPR003966; Peptidase_S1A_pr.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR01505; PROTHROMBIN.
 DR ProDom; PD000395; kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp SPC; 1.
 DR PROSITE; PS00021; KRINGLE 1; 1.
 DR PROSITE; PS00070; KRINGLE 2; 1.
 DR PROSITE; PS00240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Hydrolase; Serine protease; Plasma; Glycoprotein; Fibrinolysis;
 KW Tissue remodeling; Blood coagulation; Kringle; Zymogen; Repeat.
 FT NON_TER 1 1
 FT DOMAIN <1 140 HEAVY CHAIN A.
 FT DOMAIN 141 >343 LIGHT CHAIN A.
 FT DOMAIN <1 17 KRINGLE 4.

FT DOMAIN 41 120 KRINGLE 5.
 FT DOMAIN 114 341 SERINE PROTEASE.
 FT ACT_SITE 181 CHARGE RELAY SYSTEM.
 FT ACT_SITE 224 CHARGE RELAY SYSTEM.
 FT ACT_SITE 319 CHARGE RELAY SYSTEM.
 FT NON_TER 343 343
 SQ SEQUENCE 343 AA; 37662 MW; 8DF6EBA92D596EE0 CRC64;

Query Match 22.5%; Score 124.5; DB 1; Length 343;
 Best local similarity 35.3%; Pred. No. 1.2e-06;
 Matches 36; Conservative 8; Mismatches 43; Indels 15; Gaps 6;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWNLSATVLOQTYHAH---RSDALQLGLGHNYCRNP 58
 Db 15 CMLGIGKYGKATTVAGVPCQEWAA-----QEPHKGIFPTETNPRAGLEK-NYCRNP 68
 QY 59 D-NRRRPWCYVQVGLKPLVQECMVHDCA---DGKPPSSPPEE 96
 Db 69 DGDVNGFWCYT-TNPKLFYCDIPQCESSFDGCKPKVEPKK 109

RESULT 50
 THRB_HUMAN
 ID THRB_HUMAN STANDARD; PRT; 622 AA.
 AC P00734;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5) (Coagulation factor II).
 GN F2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88077877; PubMed=2825773;
 RA Degen S.J.F., Davie E.W.;
 RT "Nucleotide sequence of the gene for human prothrombin.";
 RL Biochemistry 26:6165-6177(1987).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT MET-165.
 RA Rieder M.J., Arnel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
 RA Ouna M., Peel C.L., Toth E.J., Yi Q., Nickerson D.A.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 8-622 FROM N.A.
 RX MEDLINE=83231469; PubMed=6305407;
 RA Degen S.J.F., McGallivray R.T.A., Davie E.W.;
 RT "Characterization of the complementary deoxyribonucleic acid and gene
 RT coding for human prothrombin.";
 RL Biochemistry 22:2087-2097(1983).
 RN [4]
 RP SEQUENCE OF 44-314.
 RX MEDLINE=77193964; PubMed=266717;
 RA Walz D.A., Hewett-Emmett D., Sesegs W.H.;
 RT "Amino acid sequence of human prothrombin fragments 1 and 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
 RN [5]
 RP SEQUENCE OF 315-622.
 RX MEDLINE=77207112; PubMed=873923;
 RA Butkowski R.J., Eliot J., Downing M.R., Mann K.G.;
 RT "Primary structure of human prothrombin 2 and alpha-thrombin.";
 RL J. Biol. Chem. 252:4942-4957(1977).
 RN [6]
 RP PROCESSING.
 RX MEDLINE=87008532; PubMed=3759958;
 RA Rabiet M.J., Blashill A., Furie B., Furie B.C.;
 RT "Prothrombin fragment 1 X 2 X 3, a major product of prothrombin
 RT activation in human plasma.";
 RL J. Biol. Chem. 261:13210-13215(1986).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RP MEDLINE=90059942; PubMed=2503108;
RA Bode W., Mayr I., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
RT "The refined 1.9 A crystal structure of human alpha-thrombin;
RT interaction with D-Phe-Pro-Arg chloromethylketone and significance of
RT the Tyr-Pro-Pro-Trp insertion segment.";
RL EMBO J. 8:3467-3475 (1989).
RN [18]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RP MEDLINE=90327074; PubMed=2374926;
RA Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,
RA Roitsch C., Fenton J.W. II;
RT "The structure of a complex of recombinant hirudin and human alpha-
RT thrombin.";
RL Science 249:277-280 (1990).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RP MEDLINE=94350942; PubMed=8071320;
RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,
RA Correa P.E., Fenton J.W. II, Tulinsky A.;
RT "Crystallographic structure of human gamma-thrombin.";
RL J. Biol. Chem. 269:22000-22006 (1994).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RP MEDLINE=97357286; PubMed=9214615;
RA van de Loch A., Bode W., Huber R., le Bonniec B.F., Stone S.R.,
RA Esmen C.T., Stubbs M.T.;
RT "The thrombin E192Q-BPTI complex reveals gross structural
RT rearrangements: implications for the interaction with antithrombin
RT and thrombomodulin.";
RL EMBO J. 16:2977-2984 (1997).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.
RP MEDLINE=99162521; PubMed=10051558;
RA Guinto E.R., Caccia S., Rose T., Fuetterer K., Wakeman G., di Cera E.;
RT "Unexpected crucial role of residue 225 in serine proteases.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:1852-1857 (1999).
RN [12]
RP VARIANT DYSPROTHROMBINEMIA CYS-314.
RP MEDLINE=87033739; PubMed=3771562;
RA Rabiet M.-J., Fuzie B.C., Fuzie B.;
RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine
RT for arginine at residue 273.";
RL J. Biol. Chem. 261:15045-15048 (1986).
RN [13]
RP VARIANT DYSPROTHROMBINEMIA ALA-509.
RP MEDLINE=95313001; PubMed=7792730;
RA Degen S.J.F., McDowell S.A., Sparks L.M., Scharer I.;
RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by
RT substitution of Glu-466 by Ala.";
RL Thromb. Haemost. 73:203-209 (1995).
RN [14]
RP VARIANTS DYSPROTHROMBINEMIA THR-380 AND HIS-431.
RP MEDLINE=93043342; PubMed=1421398;
RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,
RA Yamaguchi K.;
RT "Prothrombin Hini: a compound heterozygote for two dysfunctional
RT prothrombin molecules (Met-337-->Thr and Arg-388-->His).";
RL Blood 80:2275-2280 (1992).
RN [15]
RP VARIANT DYSPROTHROMBINEMIA HIS-314.
RP MEDLINE=95169898; PubMed=7865694;
RA James H.L., Kim D.J., Zheng D.-Q., Girolami A.;
RA "Prothrombin Padua I: incomplete activation due to an amino acid
RT substitution at a factor Xa cleavage site.";
RL Blood Coagul. Fibrinolysis 5:841-844 (1994).
RN [16]
RP VARIANT DYSPROTHROMBINEMIA CYS-425.
RP MEDLINE=89207504; PubMed=3242619;
RA Henriksen R.A., Mann K.G.;
RT "Identification of the primary structural defect in the dysfibrinogen
RT thrombin Quick I: substitution of cysteine for arginine-382.";
RL Biochemistry 27:9160-9165 (1988).
RN [17]
RP VARIANT DYSPROTHROMBINEMIA VAL-601.
RP MEDLINE=89247398; PubMed=2719946;
RA Henriksen R.A., Mann K.G.;
RT "Substitution of valine for glycine-558 in the congenital dysfibrinogen
RT thrombin Quick II alters primary substrate specificity.";
RL Biochemistry 28:2078-2082 (1989).
RN [18]
RP VARIANT DYSPROTHROMBINEMIA ALA-509.
RP MEDLINE=92378975; PubMed=1354985;
RA Miyata T., Aruga R., Uneyama H., Bezeaud A., Guillin M.-C.,
RA Iwanaga S.;
RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine
RT reduces the fibrinogen clotting activity and the esterase activity.";
RL Biochemistry 31:7457-7462 (1992).
RN [19]
RP VARIANT DYSPROTHROMBINEMIA TRP-461.
RP MEDLINE=87185407; PubMed=3567158;
RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,
RA Iwanaga S.;
RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan
RT that impairs the fibrinogen clotting activity of derived thrombin
RT Tokushima.";
RL Biochemistry 26:1117-1122 (1987).
RN [20]
RP VARIANT DYSPROTHROMBINEMIA TRP-461.
RP MEDLINE=87101511; PubMed=3801671;
RA Inomoto T., Shirakami A., Kawauchi S., Shigeakiyo T., Saito S.,
RA Miyoshi K., Morita T., Iwanaga S.;
RT "Prothrombin Tokushima: Characterization of dysfunctional thrombin
RT derived from a variant of human prothrombin.";
RL Blood 69:565-569 (1987).
RN [21]
RP VARIANT DYSPROTHROMBINEMIA TRP-461.
RP MEDLINE=92256895; PubMed=1349838;
RA Iwahana H., Yoshimoto K., Shigeakiyo T., Shirakami A., Saito S.,
RA Itakura M.;
RT "Detection of a single base substitution of the gene for prothrombin
RT Tokushima. The application of PCR-SSCP for the genetic and molecular
RT analysis of dysprothrombinemia.";
RL Int. J. Hematol. 55:93-100 (1992).
RN [22]
RP VARIANT DYSPROTHROMBINEMIA LYS-200.
RP MEDLINE=83204687; PubMed=6405779;
RA Board P.G., Shaw D.C.;
RT "Determination of the amino acid substitution in human prothrombin
RT type 3 (157 Glu leads to Lys) and the localization of a third
RT thrombin cleavage site.";
RL Br. J. Haematol. 54:245-254 (1983).
RN [23]
RP VARIANTS MET-165 AND THR-386.
RP MEDLINE=99318093; PubMed=10391209;
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nimesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RT "Characterization of single-nucleotide polymorphisms in coding regions
RT of human genes.";
RL Nat. Genet. 22:231-238 (1999).
RN [24]
RP ERRATUM.
RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
RA Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nimesh J., Ziaugra L.,
RA Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
RA Lander E.S.;
RL Nat. Genet. 23:373-373 (1999).
CC -!- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys,
CC converts fibrinogen to fibrin and activates factors V, VII, VIII,
CC XIII, and, in complex with thrombomodulin, protein C.
CC -!- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates
CC fibrinogen to fibrin and releases fibrinopeptide A and B.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,

CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION

Query Match 22.4%; Score 124; DB 1; Length 622;
Best Local Similarity 38.8%; Pred. No. 2.6e-06;
Matches 26; Conservative 8; Mismatches 29; Indels 4; Gaps 2;

QY 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYYAHRSDALQGLGKHNYCRNPD-NR 61
Db 213 CVPDRGQYQGR LAVTTHTGLPCLAWASQAQKALS KHD FNSAVQL---VENFCRNPDGDE 269
QY 62 RRPWCYV 68
Db 270 EGVWCYV 276

Search completed: May 25, 2004, 14:53:57
Job time : 4.70202 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2004, 14:44:05 ; Search time 15.9018 Seconds
(without alignments)
1904.795 Million cell updates/sec

Title: US-09-880-503-9

Perfect score: 554

Sequence: 1 KTCVGNHFRGKASTDTM.....QECMVHDCADGKFPSPPEE 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

- SPREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriaph:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	495	89.4	154	Q96SE8	Q96SE8 homo sapien
2	440	79.4	433	Q8MIL0	Q8MIL0 oryctolagus
3	440	79.4	433	Q8MHV7	Q8MHV7 oryctolagus
4	422	76.2	157	Q9TVB8	Q9TVB8 bos taurus
5	408	73.6	231	Q8C6L2	Q8C6L2 mus musculu
6	337.5	60.9	214	Q9XIT0	Q9XIT0 oryctolagus
7	236.5	42.7	564	Q8MKB1	Q8MKB1 oryctolagus
8	226	40.8	291	Q7Z7N2	Q7Z7N2 homo sapien
9	226	40.8	516	Q9BU99	Q9BU99 homo sapien
10	226	40.8	562	Q86YK8	Q86YK8 homo sapien
11	218.5	39.4	90	Q8NG20	Q8NG20 homo sapien
12	218.5	39.4	395	Q9BZW1	Q9BZW1 homo sapien
13	211	38.1	562	Q8SQ23	Q8SQ23 sus scrofa
14	210	37.9	517	Q8KOD2	Q8KOD2 mus musculu
15	205	37.0	540	Q80DY7	Q80DY7 meleagris g
16	199.5	36.0	560	Q14520	Q14520 homo sapien

17	191	34.5	202	13	Q90675	Q90675 gallus gall
18	188	33.9	653	11	Q8VCS4	Q8VCS4 mus musculu
19	187.5	33.8	597	11	Q35727	Q35727 mus musculu
20	187.5	33.8	609	11	Q80YCS	Q80YCS mus musculu
21	178.5	32.2	616	6	Q97507	Q97507 sus scrofa
22	172.5	31.1	421	13	Q8AXX3	Q8AXX3 xenopus lae
23	170.5	30.8	615	4	Q81ZZ5	Q81ZZ5 homo sapien
24	167	30.1	947	13	Q8AXY6	Q8AXY6 gallus gall
25	166	30.0	263	13	Q7SXB3	Q7SXB3 brachydanio
26	158	28.5	454	6	Q46506	Q46506 papio hamad
27	157	28.3	113	4	Q9UIR5	Q9UIR5 homo sapien
28	154	27.8	806	6	Q18783	Q18783 macropus eu
29	153.5	27.7	801	11	Q8K008	Q8K008 mus musculu
30	153.5	27.7	944	11	Q8C3W2	Q8C3W2 mus musculu
31	153.5	27.7	944	11	Q8BSP6	Q8BSP6 mus musculu
32	153	27.6	113	4	Q9UIR7	Q9UIR7 homo sapien
33	151.5	27.3	359	6	Q8WNR1	Q8WNR1 canis famli
34	150	27.1	812	11	Q9R0W3	Q9R0W3 rattus norv
35	149	26.9	716	13	Q91691	Q91691 xenopus lae
36	148	26.7	105	4	Q9UIR8	Q9UIR8 homo sapien
37	147.5	26.6	567	4	Q13208	Q13208 homo sapien
38	147.5	26.6	648	4	Q9HIV4	Q9HIV4 homo sapien
39	147.5	26.6	716	11	Q9IXG8	Q9IXG8 mus musculu
40	147	26.5	113	4	Q9UIR6	Q9UIR6 homo sapien
41	146.5	26.4	810	4	Q15146	Q15146 homo sapien
42	146	26.4	393	4	Q9BRB6	Q9BRB6 homo sapien
43	146	26.4	937	11	Q8BNP9	Q8BNP9 mus musculu
44	146	26.4	937	11	Q8BG10	Q8BG10 mus musculu
45	145.5	26.3	313	13	Q9PU78	Q9PU78 crocodylus
46	145	26.2	902	5	Q17576	Q17576 caenorhabdi
47	145	26.2	928	5	Q9BLY1	Q9BLY1 caenorhabdi
48	143.5	25.9	709	13	Q90ZN6	Q90ZN6 brachydanio
49	143	25.8	2869	6	Q28398	Q28398 erinaceus e
50	142.5	25.7	213	11	Q81123	Q81123 mus musculu
51	142.5	25.7	264	11	Q81122	Q81122 mus musculu
52	142.5	25.7	264	11	Q7TMJ8	Q7TMJ8 mus musculu
53	141	25.5	759	11	Q7TP84	Q7TP84 rattus norv
54	140	25.3	132	4	Q16609	Q16609 homo sapien
55	140	25.3	930	13	Q8AV69	Q8AV69 xenopus lae
56	138.5	25.0	704	13	Q90865	Q90865 gallus gall
57	138.5	25.0	709	13	Q7ZTN9	Q7ZTN9 xenopus lae
58	138.5	25.0	717	13	P70006	P70006 xenopus lae
59	138	24.9	1145	5	Q9BXL8	Q9BXL8 aplysia cal
60	137.5	24.8	716	11	P70521	P70521 rattus norv
61	137.5	24.8	728	11	Q8C9G5	Q8C9G5 mus musculu
62	137	24.7	334	6	Q46507	Q46507 papio hamad
63	135.5	24.5	553	13	Q7Z292	Q7Z292 brachydanio
64	135	24.4	429	13	Q8AVB0	Q8AVB0 brachydanio
65	134.5	24.3	730	6	Q867B7	Q867B7 canis famli
66	133.5	24.1	145	6	Q28911	Q28911 macaca fasc
67	133.5	24.1	215	13	Q42341	Q42341 gallus gall
68	133.5	24.1	726	13	Q90978	Q90978 gallus gall
69	131.5	23.7	234	4	Q86YW2	Q86YW2 homo sapien
70	131.5	23.7	263	4	Q00318	Q00318 homo sapien
71	131.5	23.7	263	4	Q8NCU9	Q8NCU9 homo sapien
72	131.5	23.7	263	4	Q96PE7	Q96PE7 homo sapien
73	131	23.6	95	4	Q8N696	Q8N696 homo sapien
74	129	23.3	594	5	P91823	P91823 caenorhabdi
75	127.5	23.0	710	13	Q91402	Q91402 xenopus. he

ALIGNMENTS

RESULT 1

Q96SE8 PRELIMINARY; PRT; 154 AA.
ID Q96SE8
AC Q96SE8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Urokinase-type plasminogen activator amino-terminal fragment.
GN ATF.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fu J., Bai X., Ruan C.;
RT "Cloning and expression of the amino-terminal fragment of human
RT urokinase-type plasminogen activator.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bai X., Fu J., Wang W., Xi X., Ruan C.;
RT "Overexpression of the amino-terminal fragment of human urokinase-type
RT plasminogen activator in breast cancer cells results in decreased
RT tumor invasion, growth and angiogenesis.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AY029537; AAK38734.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00020; KRINGLE_2; 1.
DR InterPro; IPR006210; EGF.
DR PIRSF; PIRSF001144; Urokinase; Kringle.
KW Glycoprotein; Kinase; Kringle.
SQ SEQUENCE 154 AA; 17305 MW; A3CF2PCFF505572 CRC64;

Query Match 89.4%; Score 495; DB 4; Length 154;
Best Local Similarity 98.9%; Pred. No. 1.7e-50;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFRGKASTDTMGRCPLPWNATVLOQTYHAHRSALQLGLGKHNCRNPDN 60
DB 68 KTCYEGNGHFRGKASTDTMGRCPLPWNATVLOQTYHAHRSALQLGLGKHNCRNPDN 127

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
DB 128 RRRPWCYVQVGLKPLVQECMVHDCADG 154

RESULT 2
QSMILO
ID QSMILO PRELIMINARY; PRT; 433 AA.
AC QSMILO;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Urokinase-type plasminogen activator.
GN PLAU.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22155945; PubMed=12149463;
RA Falkenberg M., Tom C., DeYoung M.B., Wen S., Linnemann R.,
RA Dichek D.A.;
RT "Increased expression of urokinase during atherosclerotic lesion
RT development causes arterial constriction and lumen loss, and
RT accelerates lesion growth.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10665-10670 (2002).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AY122285; AAM83187.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004235; F:trypsin activity; IEA.
DR GO; GO:0006508; F:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR008293; Pept_S1A_UPA.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PIRSF; PIRSF001144; Urokinase; Kringle; 1.
KW Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SQ SEQUENCE 433 AA; 48375 MW; 65E64F36415549B0 CRC64;

Query Match 79.4%; Score 440; DB 6; Length 433;
Best Local Similarity 78.7%; Pred. No. 1.7e-43;
Matches 74; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFRGKASTDTMGRCPLPWNATVLOQTYHAHRSALQLGLGKHNCRNPDN 60
DB 70 KTCYEGNGHFRGKASTDTMGRCPLPWNATVLOQTYHAHRSALQLGLGKHNCRNPDN 129

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPP 94
DB 130 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPP 163

RESULT 3
QSMHY7
ID QSMHY7 PRELIMINARY; PRT; 433 AA.
AC QSMHY7;
DT 01-OCT-2002 (TremBLrel. 22, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Urokinase-type plasminogen activator.
GN UROKINASE.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugiki M., Yoshida E., Anai K., Maruyama M.,
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yano W., Watanabe M.;
RT "Oryctolagus cuniculus urokinase-type plasminogen activator, mRNA,
RT complete cds.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AY029517; AAK40239.1; -.
DR EMBL; AB087224; BAC02685.1; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.

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DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase S1A.
DR InterPro; IPR008293; Pept S1A_UPA.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp Spc; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR PIRSF; PIRSF001144; Urk plasm act; 1.
KW Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SQ SEQUENCE 433 AA; 48444 MW; 6D335A371010A6EE CRC64;

Query Match 79.4%; Score 440; DB 6; Length 433;
Best Local Similarity 78.7%; Pred. No. 1.7e-43;
Matches 74; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDN 60
DB 70 KTCYEGNGHSGYRGKANTDMDPRCLAWNSANVLTXYHAHRPDALQGLGKHNYCRNPDH 129

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPP 94
DB 130 QRRPWCYVQVGLKPLVQECMVHDCSSGKKPALPP 163

RESULT 4
Q9TVAB PRELIMINARY; PRT; 157 AA.
ID Q9TVAB;
AC Q9TVAB;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Urokinase plasminogen activator (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=21071388; PubMed=11204721;
RA Balcerzak D., Querengesser L., Dixon W.T., Baracos V.E.;
RT "Coordinate expression of matrix-degrading proteinases and their
activators and inhibitors in bovine skeletal muscle.";
RL J. Anim. Sci. 79:94-107(2001).
CC 1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
ENBL; AF144761; AAD30301.1; -.
DR HSSP; P00749; IURK.
DR GO; GO:0016301; F:kinase activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Glycoprotein; Kinase; Kringle.
FT NON_TER 1
FT NON_TER 157
SQ SEQUENCE 157 AA; 17858 MW; A768D6C72C1FBFB7 CRC64;

InterPro; IPR006209; EGF like.
InterPro; IPR000001; Kringle.
InterPro; IPR001254; Peptidase S1.
InterPro; IPR001314; Peptidase S1A.
InterPro; IPR008293; Pept S1A_UPA.
Pfam; PF00051; Kringle; 1.
Pfam; PF00089; trypsin; 1.
PRINTS; PR00722; CHYMOTRYPSIN.
PRINTS; PR00018; KRINGLE.
ProDom; PD000395; Kringle; 1.
SMART; SM00130; KR; 1.
SMART; SM00020; Tryp Spc; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS00021; KRINGLE_1; 1.
PROSITE; PS00070; KRINGLE_2; 1.
PROSITE; PS0240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PIRSF; PIRSF001144; Urk plasm act; 1.
KW Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
SQ SEQUENCE 433 AA; 48444 MW; 6D335A371010A6EE CRC64;

Query Match 76.2%; Score 422; DB 6; Length 157;
Best Local Similarity 75.0%; Pred. No. 7.4e-42;
Matches 72; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDN 60
DB 36 KTCYEGNGHSGYRGKANTDMDPRCLAWNSPTVLLKMYHAHRSDALQGLGKHNYCRNPDN 95

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPP 96
DB 96 QRRPWCYVQVGLKPLVQECMVHDCSVGKSPSSPREK 131

RESULT 5
Q8C6L2 PRELIMINARY; PRT; 231 AA.
ID Q8C6L2;
AC Q8C6L2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen activator (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR ENBL; AK054349; BAC35743.1; -.
DR PIR; PT0534; PT0534.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
FT NON_TER 231
FT NON_TER 231
SQ SEQUENCE 231 AA; 25510 MW; 25E8980A682737F2 CRC64;

Query Match 73.6%; Score 408; DB 11; Length 231;
Best Local Similarity 70.8%; Pred. No. 5.1e-40;
Matches 68; Conservative 12; Mismatches 16; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDN 60
DB 69 KTCYEGNGDSYRGKANTDTKGRPCLANAPAVLKPYNAHRPDAISLGLGKHNYCRNPDN 128

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPP 96
DB 129 QRRPWCYVQVGLKPLVQECMVHDCSVGKSPSSVDQ 164

RESULT 6
Q9XT70 PRELIMINARY; PRT; 214 AA.
ID Q9XT70;
AC Q9XT70;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Urokinase-type plasminogen activator (Fragment).
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Yin J., Idell S.;
RT "Partial mRNA of rabbit uPA.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AF097647; AAD39351.1; -.
DR HSPB; P00749; 1BJN.
DR MEROPS; S01_231; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; Kringle; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Glycoprotein; Hydrolase; Kinase; Kringle; Protease; Serine protease.
FT NON TER 214
SQ SEQUENCE 214 AA; 24314 MW; 69975C41C32B0D7E CRC64;

Query Match 60.9%; Score 337.5; DB 6; Length 214;
Best Local Similarity 79.7%; Pred. No. 9.8e-32;
Matches 59; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 20 MGRCLPWNATVLPQOYTHAHRSDALQGLGKKNYCRNPDRPWCYVQVGLKPLVQEC 79
Db 1 MDRCLAWNANVLTQYTHAHRSDALQGLGKKNYCRNPDRPWCYVQVGLKPLVQEC 60

Qy 80 MVHDCADGKPPSP 94
Db 61 KVHD-SSGKKPALPP 74

RESULT 7
Q8MKBI ID Q8MKBI PRELIMINARY; PRT; 564 AA.
AC Q8MKBI
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tissue-type plasminogen activator.
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Sugiki M., Yoshida E., Anai K., Maruyama M.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
DR EMBL; AY029518; AAK40240.1; -.
DR GO; GO:0005576; C:extracellular; IEA.

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DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00039; EGF; 1.
DR Pfam; PF00051; Kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00131; EGF; 1.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_Spc; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 564 AA; 62726 MW; 459D8BAC6D4A937C CRC64;

Query Match 42.7%; Score 236.5; DB 6; Length 564;
Best Local Similarity 46.8%; Pred. No. 2.4e-19;
Matches 44; Conservative 12; Mismatches 37; Indels 1; Gaps 1;

Qy 3 CYEGNGHPYRGKASTDTMGRECLPWNATVLPQOYTHAHRSDALQGLGKKNYCRNPDR 62
Db 217 CYLKGQAYRGTHTLTTGASCLPWNMLVGEKYTAQSNALGLGKKNYCRNPDR 276

Qy 63 RPWCYVQVGLKPLVQECMVHDCAD-GKKPPSPPE 95
Db 277 KPWCYVGLKPLVQECVDPQCATCGLRQDKQP 310

RESULT 8
Q727N2 ID Q727N2 PRELIMINARY; PRT; 291 AA.
AC Q727N2
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Plasminogen activator, tissue type isoform 2.
GN PLAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA Ahearn M.O., Kuldane S.A., Rajkumar N., Toth E.J., Yi Q.,
RA Nickerson D.A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291060; AAP34246.1; -.
DR SEQUENCE 291 AA; 32191 MW; 874E38C52F50EFID CRC64;

Query Match 40.8%; Score 226; DB 4; Length 291;
Best Local Similarity 47.7%; Pred. No. 2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

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QY 2 TCYEGNGHFGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDR 61
 Db 126 TCYEDQGISYRGTSWSTAESGAECTNWNSSALAKPYSGRRPDALRLGLGNHNYCRNPDRD 185
 QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
 Db 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 9
 Q9BU99 PRELIMINARY; PRT; 516 AA.
 ID Q9BU99
 AC Q9BU99;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to plasminogen activator, tissue.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Skin;
 RA Strausberg R.;
 RL Submitted (Feb-2001) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
 DR EMBL; BC002795; AA02795.1; -.
 DR HSSP; P00750; IASH.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; P:peptidase activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR006210; IEGF.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00181; EGF_1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; TRYPsin_DOM; 1.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
 KW Serine protease.
 SQ SEQUENCE 516 AA; 57370 MW; BAB31901FDC96800 CRC64;

Query Match 40.8%; Score 226; DB 4; Length 516;
 Best Local Similarity 47.7%; Pred. No. 3.8e-18;
 Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
 QY 2 TCYEGNGHFGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDR 61
 Db 80 TCYEDQGISYRGTSWSTAESGAECTNWNSSALAKPYSGRRPDALRLGLGNHNYCRNPDRD 139
 QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
 Db 140 SKPCYVFKAGKYSSEFCSTPACSEG 165

RESULT 10
 Q86YK8 PRELIMINARY; PRT; 562 AA.
 ID Q86YK8
 AC Q86YK8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Tissue plasminogen activator.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu Y., Xu L., Zeng Y., He X.;
 RL "CDNA of tissue plasminogen activator";
 RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY221101; AAC34406.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0005508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR000083; Fibrinctn1.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Peptidase_S1.
 DR InterPro; IPR001314; Peptidase_S1A.
 DR Pfam; PF00008; EGF_1.
 DR Pfam; PF00039; fn1; 1.
 DR Pfam; PF00051; Kringle; 2.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 2.
 DR SMART; SM00058; FNI; 1.
 DR SMART; SM00130; KR; 2.
 DR SMART; SM00020; Tryp_Spc; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 2.
 DR PROSITE; PS00070; KRINGLE_2; 2.
 DR PROSITE; PS00240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 SQ SEQUENCE 562 AA; 62902 MW; 837D98392F6EDDIF CRC64;

Query Match 40.8%; Score 226; DB 4; Length 562;
 Best Local Similarity 47.7%; Pred. No. 4.1e-18;
 Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
 QY 2 TCYEGNGHFGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDR 61
 Db 126 TCYEDQGISYRGTSWSTAESGAECTNWNSSALAKPYSGRRPDALRLGLGNHNYCRNPDRD 185
 QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
 Db 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 11
 Q8NG20 PRELIMINARY; PRT; 90 AA.
 ID Q8NG20
 AC Q8NG20;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Plasminogen/activator kringle.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

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RN [1]
RA SEQUENCE FROM N.A.
RP Dou D.;
RT "Production of kringle fragment.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF282882; AAM52248.1; -.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Glycoprotein; Kringle.
SQ SEQUENCE 90 AA; 9804 MW; A33887F9DF4C7B1 CRC64;

Query Match 39.4%; Score 218.5; DB 4; Length 90;
Best Local Similarity 49.4%; Pred. No. 4.2e-18;
Matches 41; Conservative 5; Mismatches 36; Indels 1; Gaps 1;

QY 3 CYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRS DALQLGLGKHNYCRNPDNR 62
DB 8 CYFGNGSAVGRGTHSLTESGASCLPWSMILIGKVYTAQNPSAQLGLGKHNYCRNPDGDA 67
QY 63 RPYCYVQVGLKPLVQSCMWHDC A 85
DB 68 KPWCIYT-TNPRKLYDYCDVPEQCA 89

RESULT 12
Q9BZW1 PRELIMINARY; PRT; 395 AA.
AC Q9BZW1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Neocatal thrombolytic agent alpha-form (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dou D.;
RT "A brain-type plasminogen activator.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF260825; AAK11956.1; -.
DR HSSP; P00750; 1PK2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_Trypsin.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_SPC; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00039; FN1; 1.
DR PROSITE; PS00051; kringle; 1.
DR PROSITE; PS00134; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00335; TRYPSIN_SER; 1.
DR EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;

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DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS0134; TRYPSIN_HIS; 1.
DR PROSITE; PS0135; TRYPSIN_SER; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
FT NON TER 395
SQ SEQUENCE 395 AA; 44323 MW; 3FBD4A2F0B7C11C8 CRC64;

Query Match 39.4%; Score 218.5; DB 4; Length 395;
Best Local Similarity 44.7%; Pred. No. 2.2e-17;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;

QY 3 CYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRS DALQLGLGKHNYCRNPDNR 62
DB 48 CYFGNGSAVGRGTHSLTESGASCLPWSMILIGKVYTAQNPSAQLGLGKHNYCRNPDGDA 107
QY 63 RPYCYVQVGLKPLVQSCMWHDC A-GKPSPP 95
DB 108 KPWCHVLNRRRLTWYCDVPCSTCGLRQYSQPQ 141

RESULT 13
Q8SQ23 PRELIMINARY; PRT; 562 AA.
AC Q8SQ23;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE T-plasminogen activator.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Ding Y.; Xue J.; Bartlett J.D.;
RT "Plasminogen activator in tooth tissues.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DR EMBL; AF364605; AAM00297.1; -.
DR HSSP; P00761; 1AN1.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_Trypsin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR006210; ISGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00181; EGF; 1.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00335; TRYPSIN_SER; 1.
DR EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;

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KW Serine protease.
SQ SEQUENCE 562 AA; 63668 MW; F9E5B4C77CB10188 CRC64;

Query Match 38.1%; Score 211; DB 6; Length 562;
Best Local Similarity 43.2%; Pred. No. 2.4e-16;
Matches 38; Conservative 10; Mismatches 40; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASDTMGPRCLPWNATVLQOTYHAHRSALQGLGKHNYCRNPDR 61
DB 126 TCYEDQGITYRGTSWTESGAEACWNWISGLASPMYNGRRPDAVKLGLGNHYCRNPDKD 185

QY 62 RRPWCYVQGLKPLVQECMWHDCADGKK 89
DB 186 SKPWCYIFKAEKSPDFCSTACTKEKE 213

RESULT 14
Q8K0D2 PRELIMINARY; PRT; 517 AA.
ID AC Q8K0D2
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; BC031775; AAH31775.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001891; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 3.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS0134; TRYPSIN_HIS; 1.
DR PROSITE; PS0135; TRYPSIN_SER; 1.
KW Hypothetical protein; EGF-like domain; Glycoprotein; Hydrolase;
KW Kringle; Protease; Serine protease.
SQ SEQUENCE 517 AA; 57326 MW; 3855A4203A5EA59 CRC64;

Query Match 37.9%; Score 210; DB 11; Length 517;
Best Local Similarity 43.5%; Pred. No. 2.9e-16;
Matches 40; Conservative 14; Mismatches 34; Indels 4; Gaps 2;

QY 3 CYEGNGHFYRGKASDTMGPRCLPWNATVLQOTYHAHRSALQGLGKHNYCRNPDR 62
DB 151 CYVGGSYRGKSVKTVNQNPCLYWNHLLQETYNMFMEAEATHGIAEHFRCRNPDDGH 210

QY 63 RRPWCYVQGLKPLVQECMWHDCADGKKPSSP 93
DB 211 KPWCFVKVNSEKVKWEYCDVTVC---PVPDTP 239

RESULT 15
Q800Y7 PRELIMINARY; PRT; 540 AA.
ID AC Q800Y7
DT 01-JUN-2003 (TREMELrel. 24, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hepatocyte growth factor activator (fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2122796; PubMed=12128063;
RA Holsberger D.R.; Becker A.E.; Thurston R.J.; Rice C.D.;
RT "Expression of a hepatocyte growth-factor activator protein in turkey
(R) (Meleagris gallopavo) deferent duct epithelial cells.";
RL Comp. Biochem. Physiol. 132:769-777(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Holsberger D.R.; Becker A.E.; Thurston R.J.; Rice C.D.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; A216598; AAC46038.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; Fibrinctn.
DR InterPro; IPR00562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; TYP_SPC; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRINECTIN_1; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS0240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
FT NON TER 1 540
FT NON TER 540
SQ SEQUENCE 540 AA; 61159 MW; 0BB3B489C0B577F CRC64;

Query Match 37.0%; Score 205; DB 13; Length 540;
Best Local Similarity 41.3%; Pred. No. 1.2e-15;
Matches 38; Conservative 12; Mismatches 40; Indels 2; Gaps 1;

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QY 3 CYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSALQGLGKHNVCNPNDR 62
Db 179 CYRGNGTEYRGAKTITISGSLPWSNLLYRELHVDVSERKAVQLGGLGFPFVCNPNDR 236
QY 63 RPWCYVQVGLKPLVQECMVHDCADGKPKSPSP 94
Db 239 KWCYIMKDNSLSWEYCNITSASRER--RPP 268

RESULT 16
Q14520 PRELIMINARY; PRT; 560 AA.
AC Q14520; 000663;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE HGF activator like protein (hyaluronan binding protein 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitamura N.,
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96425001; PubMed=8827452;
RA Choi-Miura N.H., Tobe T., Sumiya J., Nakano Y., Sano Y., Mazda T.,
RA Tomita M.;
RT "Purification and characterization of a novel hyaluronan-binding
RT protein (PHBP) from human plasma: it has three EGF, a kringle and a
RT serine protease domain, similar to hepatocyte growth factor
RT activator."
RL J. Biochem. 119:1157-1165(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Kidney;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; D49742; BAA08576.1; -
DR EMBL; S83182; AAB46909.1; -
DR EMBL; BC031412; AAB31412.1; -
DR PIR; JC4795; JC4795.
DR HSSP; P00763; LDPO.
DR MEROPS; S01.033; -
DR Genew; HGNC:4798; HAP2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0005539; F:glycosaminoglycan binding; TAS.
DR GO; GO:0007155; P:cell adhesion; TAS.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR008209; EGF-like.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 3.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS50240; TRYPSIN_HIS; 1.
DR PROSITE; PS00134; TRYPSIN_SER; 1.
DR EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;
KW Serine protease.
SQ SEQUENCE 560 AA; 62671 MW; 5C1907230784ACD4 CRC64;

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Query Match 36.0%; Score 199.5; DB 4; Length 560;
Best Local Similarity 40.2%; Pred. No. 5.5e-15;
Matches 39; Conservative 15; Mismatches 40; Indels 3; Gaps 2;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSALQGLGKHNVCNPNDR 62
Db 194 CYVGDGYSYRGKVNRTVQHQACLYNNSHLLQENYMFEDAEATHGIGHNFCRNPD 253
QY 63 RPWCYVQVGLKPLVQECMVHDC--DGKKPSPSP 96
Db 254 KPCFKIKVTNDKVKWEYCDVSACSADQVAYPEESPTE 290

RESULT 17
Q90675 PRELIMINARY; PRT; 202 AA.
AC Q90675;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Tissue-type plasminogen activator (Fragment).
GN TPA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=White Leghorn;
RX MEDLINE=97195025; PubMed=9047000;
RA Johnson A.L., Bridgham J.T., Anthony R.V.;
RT "Expression of avian urokinase and tissue-type plasminogen activator
RT messenger ribonucleic acid during follicle development and atresia."
RL Biol. Reprod. 56:581-588(1997).
CC -1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DR EMBL; U31988; AAA74955.1; -
DR HSSP; P00750; LRTF.
DR MEROPS; S01.232; -
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
FT NON_TER 1
FT NON_TER 202
SQ SEQUENCE 202 AA; 23148 MW; 049DB42941D83AFC CRC64;

Query Match 34.5%; Score 191; DB 13; Length 202;
Best Local Similarity 43.9%; Pred. No. 1.8e-14;
Matches 36; Conservative 7; Mismatches 39; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSALQGLGKHNVCNPNDR 62
Db 41 CYTGNGLAYRGTRSRKSGFSLPWNVFLTSKIYTALEEQRRALGLGKHNVCNPD 100
QY 63 RPWCYVQVGLKPLVQECMVHDC 84
Db 101 QPWCHWKDRQLTWBYCDVPPQC 122

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2 TCVEGNHGYRGKASTDTMGRPCLPWNSATVLQCTY-HAHRSDALQLGLGKHNYCRPN 60

Db 216 TCYEGRLSYRGAGTQSGAPCQRW----TVEATYRNMTKQALSWGLGHAFCRPN 271

QY 61 RRPWCYVQVGLKPLVQECWVHDC-----ADGKPSPP 94

Db 272 DTRPWCYVMSGDRLSWDYCGLEQCQTPTFAPLVVPSQESPSQAP 317

RESULT 20

Q80YC5 PRELIMINARY; PRT; 509 AA.

AC Q80YC5; (TREMBlrel. 24, Created)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Similar to coagulation factor XII (Hageman factor) (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Liver;

RA Strausberg R.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC049867; AH49867.1; --

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR009003; Cys Ser_trypsin.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR000083; Fibrinctn1.

DR InterPro; IPR000562; FN_Type_II.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR Pfam; PF00008; EGF_2.

DR Pfam; PF00039; fn1; 1.

DR Pfam; PF00040; fn2; 1.

DR Pfam; PF00051; kringle; 1.

DR Pfam; PF00051; kringle; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00013; FNTYPEII.

DR PRINTS; PR00018; KRINGLE.

DR ProDom; PD000995; FN_Type_II; 1.

DR ProDom; PD000395; Kringle; 1.

DR SMART; SM00181; EGF_2.

DR SMART; SM00179; EGF_CA; 2.

DR SMART; SM00058; FN1; 1.

DR SMART; SM00059; FN2; 1.

DR SMART; SM00130; KR; 1.

DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00022; EGF_1; 2.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS01253; FIBRONECTIN_1; 1.

DR PROSITE; PS00023; FIBRONECTIN_2; 1.

DR PROSITE; PS00021; KRINGLE_1; 1.

DR PROSITE; PS00070; KRINGLE_2; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

FT NON TER

SQ SEQUENCE 609 AA; 66783 MW; DF97D4DB2369B6D2 CRC64;

Query Match 33.8%; Score 187.5; DB 11; Length 609;

Best Local Similarity 37.7%; Pred.No.1.6e-13;

Matches 40; Conservative 10; Mismatches 39; Indels 17; Gaps 3;

QY 2 TCYEGHGFYRGKASTMTGRCLPWN SATVLQOY-HAHRSDALQLGLGKHNCRPN 60

Db 228 TCYEGRLSYRGAGTQSGAPCQRW----TVEATYRNMTKQALSWGLGHAFCRPN 283

QY 61 RRPWCYVQVGLKPLVQECWVHDC-----ADGKPSPP 94

Db 284 DTRPWCYVMSGDRLSWDYCGLEQCQTPTFAPLVVPSQESPSQAP 329

RESULT 21

Q97507 PRELIMINARY; PRT; 616 AA.

AC Q97507; (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Similar to coagulation factor XII (Hageman factor) (Fragment).

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Takahashi T.; Kihara T.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

DR EMBL; AB022426; BAA37148.1; --

DR HSSP; P00763; IDPO.

DR MEROPS; S01.211; --

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0004235; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR009003; Cys Ser_trypsin.

DR InterPro; IPR000742; EGF_2.

DR InterPro; IPR000083; Fibrinctn1.

DR InterPro; IPR006209; EGF-like.

DR InterPro; IPR000562; FN_Type_II.

DR InterPro; IPR008210; IEGF.

DR InterPro; IPR000001; Kringle.

DR InterPro; IPR001254; Peptidase_S1.

DR InterPro; IPR001314; Peptidase_S1A.

DR Pfam; PF00039; fn1; 1.

DR Pfam; PF00040; fn2; 1.

DR Pfam; PF00051; kringle; 1.

DR Pfam; PF00089; trypsin; 1.

DR PRINTS; PR00722; CHYMOTRYPSIN.

DR PRINTS; PR00013; FNTYPEII.

DR PRINTS; PR00018; KRINGLE.

DR ProDom; PD000995; FN_Type_II; 1.

DR ProDom; PD000395; Kringle; 1.

DR SMART; SM00181; EGF_2.

DR SMART; SM00058; FN1; 1.

DR SMART; SM00059; FN2; 1.

DR SMART; SM00130; KR; 1.

DR SMART; SM00020; Tryp_Spc; 1.

DR PROSITE; PS00022; EGF_1; 2.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS01253; FIBRONECTIN_1; 1.

DR PROSITE; PS00023; FIBRONECTIN_2; 1.

DR PROSITE; PS00021; KRINGLE_1; 1.

DR PROSITE; PS00070; KRINGLE_2; 1.

DR PROSITE; PS00240; TRYPSIN_DOM; 1.

DR PROSITE; PS00134; TRYPSIN_HIS; 1.

DR PROSITE; PS00135; TRYPSIN_SER; 1.

KW EGF-like domain; Glycoprotein; Hydrolase; Kringle; Protease;

KW Serine protease.

SQ SEQUENCE 616 AA; 68012 MW; 4C5FE3D71EBBD1A9 CRC64;

Query Match 32.2%; Score 178.5; DB 6; Length 616;

```
Best Local Similarity 41.2%; Pred. No. 1.9e-12;
Matches 42; Conservative 7; Mismatches 40; Indels 13; Gaps 4;

QY 3 CYEGNGHFGYRGKASTDTMGRPCLPWNSATVLOQTY-HAHRSDALQGLGKHNYCRPNDR 61
DB 217 CYSDRGLSYRGMAQTTLTGAPCPWAS-----EATYNNMTAEQALNWLGLGHAFCRPNPD 272
QY 62 RRPWCYVQVGLKPLVQECMVHOCAD--GKKP-----SSPPE 95
DB 273 TRPWCYVWRGDQLSWOYCKLARQAPIGEAAPPILFTQSPSE 314

RESULT 22
Q8AXX3 PRELIMINARY; PRT; 421 AA.
AC Q8AXX3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Kremen2.
GN KRM2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-22308973; PubMed-12421700;
RA Davidson G., Mao B., Del Barco Barrantes I., Niehrs C.;
RT "Kremen proteins interact with Dickkopf1 to regulate anteroposterior
RT CNS patterning.";
RL Development 129:5587-5596(2002).
DR EMBL; AV150813; AAN64661.1; -.
DR InterPro; IPR000859; CUB.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR002889; WSC.
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF01822; WSC; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00321; WSC; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00021; KRINGLE; 1; 1.
DR PROSITE; PS50070; KRINGLE; 2; 1.
SQ SEQUENCE 421 AA; 46274 MW; 74D04DB1682CD15F CRC64;

Query Match 31.1%; Score 172.5; DB 13; Length 421;
Best Local Similarity 50.7%; Pred. No. 6.2e-12;
Matches 34; Conservative 4; Mismatches 26; Indels 3; Gaps 2;

QY 3 CYEGNGHFGYRGKAS-TDTMGRPCLPWNSATVLOQTYHAHRSDALQGLGKHNYCRPNDR 61
DB 29 CFTVNGRDYRGTVSQAGPETPCLYNQTT--QHLNQAQSDPDGELGLGNHNYCRPNPD 86
QY 62 RRPWCYV 68
DB 87 VQPCYV 93

RESULT 23
Q8IZZ5 PRELIMINARY; PRT; 615 AA.
AC Q8IZZ5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Coagulation factor XII-Mie.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada H., Nishiooka J., Nakatani K., Kasai Y., Abe Y., Nobori T.;
RT "Molecular characterization of coagulation factor XII-Mie.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB095845; BAC23095.1; -.
DR GO; GO:000576; C:extracellular; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys Ser trypsin.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR000083; Fibrinctni.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00008; EGF; 2.
DR Pfam; PF00039; fn1; 1.
DR Pfam; PF00040; fn2; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00013; ENTPEII.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; FN_Type_II; 1.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00181; EGF; 2.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00058; FN1; 1.
DR SMART; SM00059; FN2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01253; FIBRONECTIN_1; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 615 AA; 67735 MW; 030508870A0C7EDB CRC64;

Query Match 30.8%; Score 170.5; DB 4; Length 615;
Best Local Similarity 48.5%; Pred. No. 1.6e-11;
Matches 33; Conservative 6; Mismatches 24; Indels 5; Gaps 2;

QY 2 TCYEGNGHFGYRGKASTDTMGRPCLPWNSATVLOQTY-HAHRSDALQGLGKHNYCRPNDR 60
DB 216 SCYDGRGLSYRGARTTLTGAPCPWAS----EATYNNVTAEQARNWGLGHAFCRPNDR 271
QY 61 RRPWCYV 68
DB 272 DIRPWCYV 279

RESULT 24
Q8AXY6 PRELIMINARY; PRT; 947 AA.
AC Q8AXY6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Muscle-specific receptor tyrosine kinase Musk.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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OC Gallus.
OX NCBI_TaxID=9031;
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=20538710; PubMed=11083926;
RA Ip F.C., Glass D.G., Gies D.R., Cheung J., Lai K.O., Fu A.K.,
RA Yancopoulos G.D., Ip N.Y.;
RT "Cloning and characterization of muscle-specific kinase in chicken."
RL Mol. Cell. Neurosci. 16:661-673(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Gies D., Glass D.J., Yancopoulos G.D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY143173; AA05008.1;
DR GO:0016020; C:membrane; IEA.
DR GO:0005874; C:microtubule; IEA.
DR GO:0005524; F:ATP binding; IEA.
DR GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO:0005198; F:structural molecule activity; IEA.
DR GO:0004898; F:transmembrane receptor activity; IEA.
DR GO:0007275; F:development; IEA.
DR GO:0007018; P:microtubule-based movement; IEA.
DR GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR002453; Beta_tubulin.
DR InterPro; IPR000024; Pz_domain.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF01392; Ig; 1.
DR Pfam; PF00047; Ig; 3.
DR Pfam; PF00051; Kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00038; F2; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00228; TUBULIN_E_AUTOREG; 1.
KW Receptor; Kinase.
SQ SEQUENCE 947 AA; 10558 MW; E6C3FCC5796CC88E CRC64;

Query Match 30.1%; Score 167; DB 13; Length 947;
Best Local Similarity 35.9%; Pred. No. 6.8e-11;
Matches 42; Conservative 8; Mismatches 29; Indels 38; Gaps 8;
QY 1 KTCYEGNHFYRGKASTDTMGRCPLPWNASATVLOQTYHAHSDALQLGLGKXCRPN 51
DB 463 RTCYSGNGQYQGWANVTASGIPQKWS-----DQAPHLHRRTPQVPFELSDA----- 510
QY 52 HNYCRNP--DNRRPWCYQVGLKPLV--QECMWHDCADG-----KKPSS-----PP 94
DB 511 ENYCNPGENERPCWYTK---DSVTWEYCVSPCGDASLSLGRKNGETQNLPP 564

RESULT 25
Q7SXB3

ID Q7SXB3 PRELIMINARY; PRT; 263 AA.
AC O7SXB3;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Body;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055675; AAH55675.1; --
SQ Hypothetical protein.
QY SEQUENCE 263 AA; 28777 MW; 8BEBC117EC7C8A58 CRC64;

Query Match 30.0%; Score 166; DB 13; Length 263;
Best Local Similarity 35.7%; Pred. No. 2.2e-11;
Matches 35; Conservative 9; Mismatches 44; Indels 10; Gaps 3;
QY 1 KTCYEGNHFYRGKASTDTMGRCPLPWNASATVLOQTYHAHSDALQLGLGKXCRPN 60
DB 23 KDCITNGEDYRGTOQKTSSTCLSMKSLNL-----KPKDSQTVGVGDHFCRPPDG 74
QY 61 RRRPWCYQVGLKPLVQECMWHDCADGKKPSSP-PEE 96
DB 75 SNKPWCYVSGSGGETKKEACIRICQDQNAEAPPEE 112

RESULT 26
O46506 PRELIMINARY; PRT; 454 AA.
ID O46506
AC O46506
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Apolipoprotein a (Fragment).
GN BABAOA.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Buthera; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.

Cox L.A., Jett C., Hixson J.E.;
"Molecular Basis of the Apolipoprotein (a) Null Phenotype: A Splice Site Mutation is Associated with Deletion of a Single Exon in a Null Allele."
Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-1- SIMILARITY: CONTAINS 2 KRINGLE DOMAINS.
DR EMBL; AF029691; AAB97886.1; -.
DR HSSP; P00747; 2PK4.
DR MEROPS; S01.999; -.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 2.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 2.
DR SMART; SM00130; KR; 2.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 2.
DR PROSITE; PS00070; KRINGLE_2; 2.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
DR Glycoprotein; Hydrolase; Kringle; Lipoprotein; Protease;
KW Serine protease.
FT NON_TER 1
SQ SEQUENCE 454 AA; 50041 MW; 974E30744C187B2F CRC64;
Query Match 28.5%; Score 158; DB 6; Length 454;
Best Local Similarity 39.8%; Pred. No. 3.5e-10;
Matches 35; Conservative 10; Mismatches 31; Indels 12; Gaps 4;
QY 3 CYEGNGHFYRGKASTDTMGRCPLPWSATVQ--OTYHAHRSALQGLGKHNYCRNP 60
DB 102 CYHGGQSVRGSTFTTGTGTCQSSMTPHQKTPENHNDGLTW-----NYCRPDA 156
QY 61 RRRPNCYVQGLKPLV--QECMVHDCAD 86
DB 157 DTGPNCF--MDPSIRWEYCNLTRCSD 181
RESULT 27
Q9UIR5 PRELIMINARY; PRT; 113 AA.
AC Q9UIR5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21181705; PubMed=11285247;
RA Ogorekova M., Kraft H.G., Ehnholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV types 6 to 10 domain affect lip(a) plasma concentrations and have different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158663; AAF03680.1; JOINED.
DR EMBL; AF158662; AAF03680.1; JOINED.
DR HSSP; P00747; 1PMK.
DR InterPro; IPR000001; Kringle.

Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
KW Glycoprotein; Kringle; Lipoprotein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12685 MW; F3D65681D9B5253A CRC64;
Query Match 28.3%; Score 157; DB 4; Length 113;
Best Local Similarity 34.8%; Pred. No. 9.9e-11;
Matches 39; Conservative 13; Mismatches 36; Indels 24; Gaps 6;
QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATV--LQOTYHAHRSALQGLGKHNYCRNP 58
DB 9 RCYHNGQSVRGSTFTTGTGTCQSSMTPHRQRTPEYNDGLTW-----NYCRNP 63
QY 59 DNRERPNCYVQGLKPLV--QECMVHDCADG-----KKPS-SPPEE 96
DB 64 DADTGPWCFT--MDPSIRWEYCNLTRCSDTGTGTVVAPPTVIQVPSLGPSE 112
RESULT 28
O18783 PRELIMINARY; PRT; 806 AA.
AC O18783;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Plasminogen.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RC MEDLINE=98004511; PubMed=9342350;
RA Lawn R.M., Schwartz K., Patthy L.;
RT "Convergent evolution of apolipoprotein(a) in primates and hedgehog.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:11992-11997(1997).
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.
DR EMBL; AF012297; AAB65760.1; -.
DR HSSP; P00747; 5HPG.
DR MEROPS; S01.233; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0003809; F:thrombin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0007596; P:blood coagulation; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 5.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 5.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; Tryp_SPC; 1.
DR PROSITE; PS00021; KRINGLE_1; 5.
DR PROSITE; PS00070; KRINGLE_2; 5.


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Qy 60 NRRR-PWCYVQVGLKPLVQECMVHDC--DGKK 89
Db 370 GQMEGFWCFQ-QKNVRVELCDVPPCSPRDGSK 401

RESULT 31
Q8BSP6 PRELIMINARY; PRT; 944 AA.
ID QBSP6
AC QBSP6
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Receptor tyrosine kinase-like orphan receptor 2.
GN ROR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
PC STAIN=CS7BL/6J; TISSUE=Forelimb;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK031112; BAC27258.1; --
DR MGI; MGI:1347521; Ror2.
DR GO; GO:0001501; P:Skeletal development; IMP.
DR InterPro; IPR000024; Fz domain.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR01245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000395; Kzingle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrK; 1.
DR PROSITE; PS50038; Fz; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS50070; KRINGLE 2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
SQ SEQUENCE 944 AA; 105053 MW; 1BBD416BE3170401 CRC64;

Query Match 27.7%; Score 153.5; DB 11; Length 944;
Best Local Similarity 41.9%; Pred. No. 2.7e-09;
Matches 39; Conservative 9; Mismatches 32; Indels 13; Gaps 7;

Qy 3 CYEGNGHYRGKASTDTGRCPLPWSATVLCQTYHAHR---SDALQGLGKHNYCRNPD 59
Db 316 CYNGSGADYRGWASTTKSGHQCPW-----ALQHP-HSHRLSSTFPFELG-GGHAYCRNPG 369

Qy 60 NRRR-PWCYVQVGLKPLVQECMVHDC--DGKK 89
Db 370 GQMEGFWCFQ-QKNVRVELCDVPPCSPRDGSK 401

RESULT 32
Q9UIR7 PRELIMINARY; PRT; 113 AA.
ID Q9UIR7
AC Q9UIR7
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
PC MEDLINE=21181705; PubMed=11285247;
RX Godelkova M., Kraft H.G., Enholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158659; AAF03678.1; JOINED.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS50070; KRINGLE_2; 1.
DR KW Glycoprotein; Kringle; Lipoprotein.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12815 MW; 4F50ADF8708548CB CRC64;

Query Match 27.6%; Score 153; DB 4; Length 113;
Best Local Similarity 39.3%; Pred. No. 2.9e-10;
Matches 33; Conservative 8; Mismatches 35; Indels 8; Gaps 3;

Qy 3 CYEGNGHYRGKASTDTGRCPLPWSATVLCQTYHAHRSDALQGLGKHNYCRNPDNR 62
Db 11 CYHGDSYRGSGFSTVTGRTCSHSMT---PHGHQRTTEYYPNGGLTRNYCRNPD 67

Qy 63 RPWCYVQVGLKPLV--QECMVHDC 84
Db 68 RPWCYT---MDPSVRWEYCNLTRC 88

RESULT 33
Q8WNR1 PRELIMINARY; PRT; 359 AA.
ID Q8WNR1
AC Q8WNR1
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Plasminogen (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Pirie-Shepherd S.R., Coffman K.T., Resnick D., Chan R., Kisker O.,
RA Folkman J., Waters D.J.;
RT "Angiostatin is Detectable in the Urine of Dogs with Spontaneous Bone
RT Cancer.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DDJ databases.
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; AY069985; AAL58519.1; --
DR GO; GO:0005509; F:calcium ion binding; IEA.
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RESULTS 38
Q9H1V4
ID Q9H1V4 PRELIMINARY; PRT; 648 AA.
AC Q9H1V4;

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Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
CC EMBL; BC010551; AAH10551.1; -.
DR HSSP; P00761; 1ANI.
DR MGD; MGI:96080; Mat1.
DR GO; GO:0007566; P:embryo implantation; IC.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR003966; Peptidase_S1A_pr.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR01505; PROTHROMBIN.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
DR SMART; SM00020; TRY_P_SPC; 1.
DR PROSITE; PS00021; KRINGLE 1; 4.
DR PROSITE; PS00070; KRINGLE 2; 4.
DR PROSITE; PS00240; TRYPSIN_DOM; 1.
DR KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease.
SQ SEQUENCE 716 AA; 80693 MW; 12474C48A7D4B46D CRC64;

Query Match 26.8%; Score 147.5; DB 11; Length 716;
Best Local Similarity 36.5%; Pred.No.1e-08;
Matches 38; Conservative 11; Mismatches 34; Indels 21; Gaps 7;

QY 3 CYEGNGHFYRGKASTDTMGRCPLPWNSATVLQYTHAHR-----SDALQLGLGHNYCRN 57
Db 379 CYHSGSEQYRGVSVKTRKGVCQHNSET-----PHKPFQPTFSAPQAGL-EANFCRN 430

QY 58 PD-NRRRPPCYQVGLKP--LVQECMVHDCADGKKFS--SPPEE 96
Db 431 PDGDSHGPGWYT---LDPDILFDYCALQRCDDDQPPSILDPPDQ 471

RESULT 40
Q9UIR6 PRELIMINARY; PRT; 113 AA.
ID Q9UIR6
AC Q9UIR6;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Apolipoprotein(a) (Fragment).
GN APOA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21181705; PubMed=11285247;
RA Ogorekova M., Kraft H.G., Enholm C., Utermann G.;
RT "Single nucleotide polymorphisms in exons of the apo(a) kringles IV
RT types 6 to 10 domain affect Lp(a) plasma concentrations and have
RT different patterns in Africans and Caucasians.";
RL Hum. Mol. Genet. 10:815-824(2001).
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AF158661; AAF03679.1; -.
DR EMBL; AF158660; AAF03679.1; JOINED.
DR HSSP; P00747; 2PK4.
DR InterPro; IPR000001; Kringle.
DR Pfam; PF00051; kringle; 1.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 1.
DR SMART; SMC0130; KR; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.

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DR PROSITE, PSS0070; KRINGLE_2; 1.  
KW Glycoprotein; Kringle; Lipoprotein.  
FT NON_TER 113 113  
SQ SEQUENCE 113 AA; 12697 MW; 51D461D9C66312E CRC64;  
  
Query Match 26.5%; Score 147; DB 4; Length 113;  
Best Local Similarity 36.0%; Pred. No. 1.5e-09;  
Matches 31; Conservative 14; Mismatches 33; Indels 8; Gaps 4;  
  
Qy 3 CYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQGLGKHNYCRNPDR 62  
Db 11 CYHGGRSYRGISSTVTGRTQSWSS--MIPHWQRTPEVNPAGL--TENYCRNPDSGK 67  
  
Qy 63 RWCIVQVGLKPLV--QECNVHDCAD 86  
Db 68 QPWCYT--TDCVRWEYCNLTQCS 90  
  
RESULT 41  
Q15146 PRELIMINARY; PRT; 810 AA.  
AC Q15146;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Plasminogen precursor.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Tissue=Liver;  
RA Browne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,  
RA Mitchell D., Robinson J.H.;  
RT "Expression of recombinant human plasminogen and aglycoplasminogen in  
RT HeLa cells."  
RL Fibinolysis; 0:0-0(1991).  
CC -1- SIMILARITY: CONTAINS 5 KRINGLE DOMAINS.  
DR EMBL; M74220; AAA36451.1; --  
DR HSP; P00747; 2PK4.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004263; F:chymotrypsin activity; IEA.  
DR GO; GO:0008233; F:peptidase activity; IEA.  
DR GO; GO:0003809; F:thrombin activity; IEA.  
DR GO; GO:0004295; F:trypsin activity; IEA.  
DR GO; GO:0007596; P:blood coagulation; IEA.  
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
DR InterPro; IPR009003; Cys_Ser_trypsin.  
DR InterPro; IPR000001; Kringle.  
DR InterPro; IPR003014; PAN.  
DR InterPro; IPR003609; Pan app.  
DR InterPro; IPR001254; Peptidase S1.  
DR InterPro; IPR001314; Peptidase S1A.  
DR InterPro; IPR003966; Peptidase_S1A_pr.  
DR Pfam; PF0051; kringle; 5.  
DR Pfam; PF00024; PAN; 1.  
DR Pfam; PF00089; trypsin; 1.  
DR PRINTS; PR00722; CHYMOTRYPSIN.  
DR PRINTS; PR00018; KRINGLE.  
DR PRINTS; PR01505; PROTHROMBIN.  
DR ProDom; PD000395; Kringle; 5.  
DR SMART; SM00130; KR; 5.  
DR SMART; SM00473; PAN_AF; 1.  
DR SMART; SM00020; TRYD_SPC; 1.  
DR PROSITE; PS00021; KRINGLE 1; 5.  
DR PROSITE; PS50070; KRINGLE 2; 5.  
DR PROSITE; PS50240; TRYPSIN_DOM; 1.  
DR PROSITE; PS00134; TRYPSIN_HIS; 1.  
DR PROSITE; PS00135; TRYPSIN_SER; 1.  
KW Glycoprotein; Hydrolase; Kringle; Protease; Serine protease; Signal.  
FT SIGNAL 1 19 POTENTIAL.
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FT CHAIN 20 810 PLASMINOGEN.  
SQ SEQUENCE 810 AA; 90555 MW; B05C7D4B0D020B3C CRC64;  
  
Query Match 26.4%; Score 146.5; DB 4; Length 810;  
Best Local Similarity 37.4%; Pred. No. 1.5e-08;  
Matches 37; Conservative 13; Mismatches 32; Indels 17; Gaps 7;  
  
Qy 3 CYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHR---SDALQGLGKHNYCRNP 59  
Db 377 CYHGDSQSYRGTSSTTTGKQCSWSS-----MTPRHQKTPENYNPAGL--TNYCRNPD 430  
  
Qy 60 NRERPWCYQVGLKPLV--QECNVHDCADGKKPS--SP 94  
Db 431 ADKGPWCFT---TDPVRWEYCNLKKS--GTEASVWAPP 465  
  
RESULT 42  
Q9BRB6 PRELIMINARY; PRT; 393 AA.  
AC Q9BRB6;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Similar to receptor tyrosine kinase-like orphan receptor 1.  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC Tissue=Muscle;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.  
DR EMBL; BC006374; AAH06374.1; --  
DR HSP; P00747; ICEA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0016301; F:kinase activity; IEA.  
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.  
DR GO; GO:0007275; P:development; IEA.  
DR InterPro; IPR000024; Fz domain.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig_c2.  
DR InterPro; IPR000001; Kringle.  
DR Pfam; PF01392; Fz; 1.  
DR Pfam; PF00047; Ig; 1.  
DR Pfam; PF00051; kringle; 1.  
DR PRINTS; PR00018; KRINGLE.  
DR ProDom; PD000395; Kringle; 1.  
DR SMART; SM00408; IGc2; 1.  
DR SMART; SM00330; KR; 1.  
DR PROSITE; PS50038; Fz; 1.  
DR PROSITE; PS50835; IG_LIKE; 1.  
DR PROSITE; PS00021; KRINGLE 1; 1.  
DR PROSITE; PS50070; KRINGLE 2; 1.  
KW Glycoprotein; Immunoglobulin domain; Kinase; Kringle; Receptor.  
SQ SEQUENCE 393 AA; 43925 MW; 1F93DCBBB8F53955 CRC64;  
  
Query Match 26.4%; Score 146; DB 4; Length 393;  
Best Local Similarity 44.1%; Pred. No. 7.5e-09;  
Matches 30; Conservative 5; Mismatches 25; Indels 8; Gaps 3;  
  
Qy 3 CYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQGLGKHNYCRNP 60  
Db 313 CYNSTGVDYRGTVSVTKSGRQCQFPWNS-----QVPHHTTFTALRFPFELNGHSYCRNPG 367  
  
Qy 61 RRR-PWCY 67  
Db 368 QKEAPWCF 375  
  
RESULT 43  
Q8BNP9
```



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ID Q8BNP9 PRELIMINARY; PRT; 937 AA.
AC Q8BNP9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor tyrosine kinase-like orphan receptor 1.
GN ROR1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK080896; BAC38068.1; -.
DR MGD; MGI:1347520; Ror1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD0000395; Kringle; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_TYR; 1.
SQ SEQUENCE 937 AA; 104118 MW; CB440323CA66EC28 CRC64;

Query Match 26.4%; Score 146; DB 11; Length 937;
Best Local Similarity 44.1%; Pred. No. 2e-08;
Matches 30; Conservative 5; Mismatches 25; Indels 8; Gaps 3;

Qy 3 CYEGNGHFYRGKASDTWGRPCLPWN SATVLQQTTHAHRSDALQLG--LGKHNYCNP DN 60
Db 313 CYNSTGVYRGTVSVTKSGRCQCPWNS-----QYPHTHSFTALRFPPLNGHGHSCYCNPN 367

Qy 61 RRR-PWCY 67
Db 368 QKEAPWCF 375

RESULT 44
```

```

Q8BG10 PRELIMINARY; PRT; 937 AA.
ID Q8BG10
AC Q8BG10;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Receptor tyrosine kinase-like orphan receptor 1.
GN ROR1
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Adipose tissue;
RX MEDLINE=22354683; PubMed=12466851;
RA The PANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK046699; BAC32840.1; -.
DR MGD; MGI:1347520; Ror1.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR008266; Tyr_kinase_AS.
DR Pfam; PF01392; Fz; 1.
DR Pfam; PF00047; Ig; 1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD0000395; Kringle; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00408; IGC2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS50038; FZ; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_TYR; 1.
SQ SEQUENCE 937 AA; 104088 MW; D6FD84B67D03C69 CRC64;

Query Match 26.4%; Score 146; DB 11; Length 937;
Best Local Similarity 44.1%; Pred. No. 2e-08;
Matches 30; Conservative 5; Mismatches 25; Indels 8; Gaps 3;

Qy 3 CYEGNGHFYRGKASDTWGRPCLPWN SATVLQQTTHAHRSDALQLG--LGKHNYCNP DN 60
Db 313 CYNSTGVYRGTVSVTKSGRCQCPWNS-----QYPHTHSFTALRFPPLNGHGHSCYCNPN 367

Qy 61 RRR-PWCY 67
Db 368 QKEAPWCF 375
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QY 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRR 62

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Db 328 CYVNSGTQYEGTVAQTSSGKQCAPWIDST--SRDFNVHRFPPEL---MNSKNYCRNPGGKK 382
Qy 63 -RPWCYVQVGLKPLVOE--CWVHDCADGKKP 90
Db 383 SRWCY-----SKPMGQEEYCDVPQCPSPDMYP 409

RESULT 47
Q9BLYL1
ID Q9BLYL1 PRELIMINARY; PRT; 928 AA.
AC Q9BLYL1
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Receptor tyrosine kinase (C. elegans Cam-1 protein) (corresponding
sequence C01G6.8a)
DE C01G6.8 OR KIN-8 OR CAM-1.
GN Caenorhabditis elegans.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodirinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N2;
RA Koga M., Take-uchi M., Tameishi T., Ohshima Y.;
RT "Control of DAF-7 TGF expression and neuronal process development by a
RT receptor tyrosine kinase KIN-8 in C. elegans.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bekas M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
RN [4]
RP SEQUENCE FROM N.A.
RA Mortimore B.J.;
RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
DR EMBL; AJ132946; CAC29084.1; -.
DR EMBL; Z35595; CAD36478.1; -.
DR EMBL; Z47808; CAD36478.1; JOINED.
DR EMBL; Z47808; CAD36487.1; -.
DR EMBL; Z35595; CAD36487.1; JOINED.
DR HSSP; P11362; IFGK.
DR WormPep; C01G6.8a; CE32563.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0004713; P:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0004888; P:transmembrane receptor activity; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR GO; GO:0007275; P:development; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR000024; Fz_domain.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR008266; Tyr_pkinase_AS.
DR Pfam; PF00047; Ig_1.
DR Pfam; PF00051; kringle; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRINTS; PR00109; TYRKINASE.
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DR ProDom; PD000395; Kringle; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00408; IGc2; 1.
DR SMART; SM00130; KR; 1.
DR SMART; SM00219; TyxKc; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; 1.
DR PROSITE; PS50038; Fz; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00021; KRINGLE_1; 1.
DR PROSITE; PS00070; KRINGLE_2; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
KW ATP-binding; immunoglobulin domain; Kinase; Kringle; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 928 AA; 103864 MW; F13B8C9BCAB30D20 CRC64;

Query Match 26.2%; Score 145; DB 5; Length 928;
Best Local Similarity 35.2%; Pred. No. 2.6e-08;
Matches 32; Conservative 12; Mismatches 35; Indels 12; Gaps 5;

Qy 3 CYEGNGHFYRGKASTDTMGRLPCLPWSNATVQQTYHAHRSDALQGLGKNYCRNPNRR 62
Db 354 CYVNSGTQYEGTVAQTSSGKQCAPWIDST--SRDFNVHRFPPEL---MNSKNYCRNPGGKK 408

Qy 63 -RPWCYVQVGLKPLVOE--CWVHDCADGKKP 90
Db 409 SRWCY-----SKPMGQEEYCDVPQCPSPDMYP 435

RESULT 48
Q90ZNG6
ID Q90ZNG6 PRELIMINARY; PRT; 709 AA.
AC Q90ZNG6;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hepatocyte growth factor-like 1.
GN MST1 OR HGFL1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Bassett D.I., Wilson S.W.;
RT "Early expression of zebrafish Hepatocyte Growth Factor-Like 1
RT suggests a conserved role in vertebrate neural induction.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -1- SIMILARITY: CONTAINS 4 KRINGLE DOMAINS.
DR EMBL; AF370035; AAK54207.1; -.
DR HSSP; P00761; 1AN1.
DR ZFIN; ZDB-GENE-020806-3; mst1.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0008233; F:peptidase activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR009003; Cys_Ser_trypsin.
DR InterPro; IPR000001; Kringle.
DR InterPro; IPR003014; PAN.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR001254; Peptidase_S1.
DR InterPro; IPR001314; Peptidase_S1A.
DR Pfam; PF00051; kringle; 4.
DR Pfam; PF00024; PAN; 1.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00018; KRINGLE.
DR ProDom; PD000395; Kringle; 4.
DR SMART; SM00130; KR; 4.
DR SMART; SM00473; PAN_AP; 1.
```

Search completed: May 25, 2004, 14:57:19
Job time : 16.9018 secs

XX WO200197752-A2.
 XX 27-DEC-2001.
 XX 13-JUN-2001; 2001WO-US018976.
 XX 20-JUN-2000; 2000US-0212874P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Cines DB, Higazi AA;
 XX WPI; 2002-122240/16.
 XX N-PSDB; AAD27083.
 XX Composition for modulating muscle cell and tissue contractility for
 XX treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 XX comprising domains from urokinase-type plasminogen activator.
 XX Claim 25; Fig 11; 117pp; English.
 XX The invention relates to a composition comprising one or more domains of
 XX urokinase-type plasminogen activator (uPA). The composition is used to
 XX modulate the contractility and angiogenic activity of a mammalian muscle,
 XX endothelial cell or tissue. The composition is used for treating stroke,
 XX hypertension, atherosclerosis, heart attack, microvascular
 XX occlusions, thrombotic microangiopathies, surgically induced thrombotic
 XX disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 XX invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
 XX diabetic retinopathy, wound healing, clotting disorder, uterine
 XX contraction disorder, male impotence, respiratory disease or condition
 XX such as asthma, adult respiratory distress syndrome, primary pulmonary
 XX hypertension, microvascular thrombotic occlusion, and a disorder
 XX associated with chronic intrapulmonary fibrin formation. The present
 XX sequence is human urokinase-type plasminogen activator (uPA) kringle and
 XX connecting peptide
 XX Sequence 96 AA;
 XX Query Match 100.0%; Score 554; DB 5; Length 96;
 XX Best Local Similarity 100.0%; Pred. No. 5.1e-45;
 XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 KTCYEGNGHFGYRGKASTDTMGRLPWNATVLTQYTHAHRSDALQLGLGKHYCRNPDN 60
 XX 1 KTCYEGNGHFGYRGKASTDTMGRLPWNATVLTQYTHAHRSDALQLGLGKHYCRNPDN 60
 XX 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
 XX 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
 XX RESULT 2
 XX AAE16549
 XX ID AAE16549 standard; protein; 143 AA.
 XX AC AAE16549;
 XX DT 09-APR-2002 (first entry)
 XX DE Human uPA amino terminal fragment (ATF) and connecting peptide.
 XX Human; urokinase-type plasminogen activator; uPA; therapy; hypertension;
 XX stroke; hypotension; atherosclerosis; heart attack; thrombotic disorder;
 XX microvascular occlusion; angiogenic disorder; pulmonary fibrosis; asthma;
 XX tumour cell metastasis; glaucoma; diabetic retinopathy; wound healing;
 XX clotting disorder; uterine contraction disorder; respiratory disease;
 XX adult respiratory distress syndrome; amino terminal fragment; ATF;
 XX male impotence.
 XX Homo sapiens.
 XX OS
 XX 28-SEP-2000; 2000WO-US026524.

PN WO200197752-A2.
 PD 27-DEC-2001.
 XX 13-JUN-2001; 2001WO-US018976.
 XX 20-JUN-2000; 2000US-0212874P.
 XX (UYPE-) UNIV PENNSYLVANIA.
 XX Cines DB, Higazi AA;
 XX WPI; 2002-122240/16.
 XX N-PSDB; AAD27082.
 XX Composition for modulating muscle cell and tissue contractility for
 XX treating atherosclerosis, asthma, hypertension, glaucoma, impotence,
 XX comprising domains from urokinase-type plasminogen activator.
 XX Claim 24; Fig 1H; 117pp; English.
 XX The invention relates to a composition comprising one or more domains of
 XX urokinase-type plasminogen activator (uPA). The composition is used to
 XX modulate the contractility and angiogenic activity of a mammalian muscle,
 XX endothelial cell or tissue. The composition is used for treating stroke,
 XX hypertension, atherosclerosis, heart attack, microvascular
 XX occlusions, thrombotic microangiopathies, surgically induced thrombotic
 XX disorders, angiogenic disorders, pulmonary fibrosis, asthma, tumour cell
 XX invasion, tumour cell angiogenesis, tumour cell metastasis, glaucoma,
 XX diabetic retinopathy, wound healing, clotting disorder, uterine
 XX contraction disorder, male impotence, respiratory disease or condition
 XX such as asthma, adult respiratory distress syndrome, primary pulmonary
 XX hypertension, microvascular thrombotic occlusion, and a disorder
 XX associated with chronic intrapulmonary fibrin formation. The present
 XX sequence is human urokinase-type plasminogen activator (uPA) amino
 XX terminal fragment (ATF) and connecting peptide
 XX Sequence 143 AA;
 XX Query Match 100.0%; Score 554; DB 5; Length 143;
 XX Best Local Similarity 100.0%; Pred. No. 7.5e-45;
 XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX 1 KTCYEGNGHFGYRGKASTDTMGRLPWNATVLTQYTHAHRSDALQLGLGKHYCRNPDN 60
 XX 48 KTCYEGNGHFGYRGKASTDTMGRLPWNATVLTQYTHAHRSDALQLGLGKHYCRNPDN 107
 XX 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
 XX 108 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 143
 XX RESULT 3
 XX AAG75492
 XX ID AAG75492 standard; protein; 337 AA.
 XX AC AAG75492;
 XX DT 03-SEP-2001 (first entry)
 XX DE Human colon cancer antigen protein SEQ ID NO:6256.
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 XX colorectal carcinoma; chromosome 10.
 XX Homo sapiens.
 XX OS
 XX WO200122920-A2.
 XX 05-APR-2001.
 XX 28-SEP-2000; 2000WO-US026524.

PR 29-SEP-1999; 99US-0157137P.
XX 03-NOV-1999; 99US-0163280P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
XX N-PSDB; AAH34897.
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 11; Page 7707-7708; 9803pp; English.
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytotoxic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patient's own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAG77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
XX to 1052, 7921 and 7922
XX Sequence 337 AA;
SQ
Query Match 100.0%; Score 554; DB 4; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHYCRNPDN 60
DB 74 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHYCRNPDN 133
QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKPSPPPEE 96
DB 134 RRRPWCYVQVGLKPLVQECWVHDCADGKPSPPPEE 169
RESULT 4
ABP41795
XX ABP41795 standard; protein; 337 AA.
XX
XX ABP41795;
XX
XX 22-AUG-2002 (first entry)
XX Human ovarian antigen HVVCB79, SEQ ID NO:2927.
XX
XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
XX ovarian cancer; breast cancer; tumour; reproductive system disorder;
XX infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
XX PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
XX inflammatory condition; immune disorder; blood disorder;
XX cardiovascular disorder; respiratory disorder; neurological disorder;
XX gastrointestinal disorder; urinary system disorder; drug screening;
XX gene therapy; chromosome mapping; forensic analysis;
XX antibody preparation; cytostatic; immunomodulatory; neuroprotective;
XX antiinflammatory; gynaecological; reproductive; chromosome 10q24.
XX
XX Homo sapiens.
XX
XX WO200200677-A1.
PN

XX 03-JAN-2002.
XX 07-JUN-2001; 2001WO-US018569.
XX 07-JUN-2000; 2000US-0209467P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Birse CE, Rosen CA;
XX WPI; 2002-147878/19.
XX N-PSDB; ABQ54872.
XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
PT cancer), immune disorders, cardiovascular disorders and neurological
PT diseases.
XX Claim 11; SEQ ID NO 2927; 2922pp; English.
XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, coprophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune ophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pot_sequences
XX Sequence 337 AA;
SQ
Query Match 100.0%; Score 554; DB 5; Length 337;
Best Local Similarity 100.0%; Pred. No. 1.7e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHYCRNPDN 60
DB 74 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSDALQLGLGKHYCRNPDN 133
QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKPSPPPEE 96
DB 134 RRRPWCYVQVGLKPLVQECWVHDCADGKPSPPPEE 169
RESULT 5
AAR68854
XX AAR68854 standard; protein; 365 AA.
XX
XX AAR68854;
XX
XX 16-OCT-2003 (revised)
DT

DT 25-MAR-2003 (revised)
 DT 22-NOV-1995 (first entry)
 DE Delta 1-46 urokinase.
 XX Human; des-epidermal growth factor homologous plasminogen activator; uPA;
 KW liver membrane; reduced affinity; EGF homologous; thrombosis;
 KW thrombolytic; increased half-life; urokinase.
 XX Homo sapiens; (engineered).
 XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "amino acids 1-46 of wild-type urokinase have been
 FT deleted"
 FT
 XX US5376547-A.
 XX 27-DEC-1994.
 XX 29-JAN-1988; 88US-00150267.
 XX 30-JAN-1987; 87US-00008795.
 XX (AMH) AMERICAN HOME PROD CORP.
 XX Hung PP, Lee SL, Kalyan NK;
 XX WPI; 1995-043464/06.
 XX New modified plasminogen activator cpds. - having regions removed to
 PT reduce affinity for liver membranes and increase circulation half-life.
 XX Claim 1; Page 2; 26pp; English.
 CC Amino acid residues 1-46 contain the EGF region of human urokinase.
 CC Deletion of this region results in a plasminogen activator with reduced
 CC affinity for liver cell membranes; the mutant protein is not cleared from
 CC the circulation as rapidly as is wild-type tPA. The specification only
 CC gives the sequence around the deletion and not the full-length sequence
 CC of "delta 1-46 urokinase"; the sequence in AAR68854 has been obtained by
 CC amending a previously disclosed wild-type human urokinase sequence (from
 CC W09501427) according to the description given in Example 3. (Updated on
 CC 25-MAR-2003 to correct PF field.) (Updated on 16-OCT-2003 to standardise
 CC OS field)
 XX Sequence 365 AA;
 SQ
 Query Match 100.0%; Score 554; DB 2; Length 365;
 Best Local Similarity 100.0%; Pred. No. 1.8e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KTCYEGNGHFGYRGKASTDTMGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHNCRPN 60
 Db 2 KTCYEGNGHFGYRGKASTDTMGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHNCRPN 61
 Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
 Db 62 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 97
 RESULT 6
 AA013635
 ID AA013635 standard; protein; 378 AA.
 XX AA013635;
 AC
 XX 04-JUN-1997 (first entry)
 DT Human prourokinase variant lacking entire EGF domain.
 DE Human; prourokinase; hPUK; variant; half-life; increase; EGF;
 KW epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.

XX Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Region 1..9
 FT /note= "residues 1-9 of native hPUK"
 FT Region 10..378
 FT /note= "residues 43-411 of native hPUK"
 FT Misc-difference 144
 FT /note= "corresponds to TAC codon"
 XX EP398361-A.
 XX 22-NOV-1990.
 XX 18-MAY-1990; 90EP-00109472.
 XX 18-MAY-1989; 89JP-00126433.
 XX 22-FEB-1990; 90JP-00042020.
 XX (GREG) GREEN CROSS CORP.
 XX Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;
 PI Airmura H;
 XX WPI; 1990-350146/47.
 XX N-PSDB; AAT61672.
 XX Human pro-urokinase variants - deficient in loop regions of epidermal
 PT growth factor, showing long blood half-life, as fibrinolytic agent.
 XX Claim 1; Page; 22pp; English.
 CC New variants of human prourokinase (hPUK) comprise a hPUK deficient in
 CC (i) at least part of the first loop region of the epidermal growth factor
 CC (EGF) domain; (ii) at least part of the first loop and at least part of
 CC the second loop; or (iii) at least part of the third loop. The hPUK
 CC variants show an increased blood half-life comparable to that of the
 CC whole EGF domain-deficient hPUK variant and urokinase while retaining the
 CC same properties as those of hPUK. They have potent thrombolytic activity
 CC and very little tendency to cause spontaneous bleeding. The present
 CC sequence represents a specific variant of hPUK which lacks the entire EGF
 CC domain; the sequence does not appear in the specification and has been
 CC created using the wild-type hPUK sequence and the junction sequence after
 CC deletion, both of which are given (in Fig 1 and in Fig 2(3)),
 CC respectively
 XX Sequence 378 AA;
 SQ
 Query Match 100.0%; Score 554; DB 2; Length 378;
 Best Local Similarity 100.0%; Pred. No. 1.9e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KTCYEGNGHFGYRGKASTDTMGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHNCRPN 60
 Db 15 KTCYEGNGHFGYRGKASTDTMGRPCLPWNSATVLQQTTHAHRSDALQLGLGKHNCRPN 74
 Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
 Db 75 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 110
 RESULT 7
 AAR66266
 ID AAR66266 standard; protein; 386 AA.
 XX AAR66266;
 AC
 XX 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX Bifunctional urokinase variant M33.


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XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KW urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1..365
XX /label= M4
XX /note= "unglycosylated prourokinase(Ser47-Leu411)"
XX
XX Disulfide-bond 4..85
XX Disulfide-bond 25..67
XX Disulfide-bond 56..80
XX Disulfide-bond 102..233
XX Disulfide-bond 143..159
XX Disulfide-bond 151..222
XX Disulfide-bond 247..316
XX Disulfide-bond 279..295
XX Disulfide-bond 306..334
XX Disulfide-bond 365..366
XX Region /label= X1
XX /notes "peptide bond"
XX Region 366..386
XX /label= Y1
XX
XX DE4323754-Cl.
XX
XX 01-DEC-1994.
XX
XX 15-JUL-1993. 93DE-04323754.
XX
XX 15-JUL-1993. 93DE-04323754.
XX
XX (CHEF ) GRUENTHAL GMBH.
XX
XX Steffens GJ. Wndt S, Schneider J, Heinzl-Wieland R;
XX Saunders DJ.
XX
XX WPI; 1995-015191/03.
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 11 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR6244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct PN field.)
XX
XX Sequence 386 AA;
XX
XX Query Match 100.0%; Score 554; DB 2; Length 386;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KTCYEGNGHYRKGASTDTMGRPCLPWNSATVLQOQTYHAHRSALQLGLGKHNYCRNPDN 60
XX 2 KTCYEGNGHYRKGASTDTMGRPCLPWNSATVLQOQTYHAHRSALQLGLGKHNYCRNPDN 61
XX
XX 61 RRRPWCYVQGLKPLVQECMVHDCADGKSPSPPEE 96
XX 62 RRRPWCYVQGLKPLVQECMVHDCADGKSPSPPEE 97
XX
XX RESULT 8
XX AAW13636
XX ID AAW13636 standard; protein; 389 AA.

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XX AAW13636;
XX AC
XX DT 04-JUN-1997 (first entry)
XX DE Human prourokinase variant lacking EGF domain loops 1 and 2.
XX KW Human; prourokinase; hPUK; variant; half-life; increase; EGF;
XX OS epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
XX Synthetic.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Region 1..10
XX /note= "residues 1-10 of native hPUK"
XX Region 11..389
XX /note= "residues 33-411 of native hPUK"
XX Misc-difference 155
XX /note= "corresponds to TAC codon"
XX
XX EP398361-A.
XX
XX 22-NOV-1990.
XX
XX 18-MAY-1990; 90EP-00109472.
XX
XX 18-MAY-1989; 89JP-00126433.
XX 22-FEB-1990; 90JP-00042020.
XX
XX (GREC ) GREEN CROSS CORP.
XX
XX Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;
XX Airmura H;
XX
XX WPI; 1990-350146/47.
XX N-PSDB; AAT61673.
XX
XX Human pro-urokinase variants - deficient in loop regions of epidermal
XX growth factor, showing long blood half-life, as fibrinolytic agent.
XX
XX Claim 6; Page; 22pp; English.
XX
XX New variants of human prourokinase (hPUK) comprise a hPUK deficient in
XX (i) at least part of the first loop region of the epidermal growth factor
XX (EGF) domain, (ii) at least part of the first loop and at least part of
XX the second loop; or (iii) at least part of the third loop. The hPUK
XX variants show an increased blood half-life comparable to that of the
XX whole EGF domain-deficient hPUK variant and urokinase while retaining the
XX same properties as those of hPUK. They have potent thrombolytic activity
XX and very little tendency to cause spontaneous bleeding. The present
XX sequence represents a specific variant of hPUK which lacks loops 1 and 2
XX of the EGF domain; the sequence does not appear in the specification and
XX has been created using the wild-type hPUK sequence and the junction
XX sequence after deletion, both of which are given (in Fig 1 and on page 8,
XX respectively)
XX
XX Sequence 389 AA;
XX
XX Query Match 100.0%; Score 554; DB 2; Length 389;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KTCYEGNGHYRKGASTDTMGRPCLPWNSATVLQOQTYHAHRSALQLGLGKHNYCRNPDN 60
XX 26 KTCYEGNGHYRKGASTDTMGRPCLPWNSATVLQOQTYHAHRSALQLGLGKHNYCRNPDN 85
XX
XX 61 RRRPWCYVQGLKPLVQECMVHDCADGKSPSPPEE 96
XX 86 RRRPWCYVQGLKPLVQECMVHDCADGKSPSPPEE 121
XX
XX RESULT 9

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AAR66245
ID AAR66245 standard; protein; 390 AA.
XX
AC AAR66245;
XX
XX
DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M12.
XX
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KW urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 1. .365
FT /label= M4
FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
FT Disulfide-bond 4. .85
FT Disulfide-bond 25. .67
FT Disulfide-bond 56. .80
FT Disulfide-bond 102. .233
FT Disulfide-bond 143. .159
FT Disulfide-bond 151. .222
FT Disulfide-bond 247. .316
FT Disulfide-bond 279. .295
FT Disulfide-bond 306. .334
FT Disulfide-bond 366. .371
FT Region /label= X1
FT Region /label= Y1
XX
XX DE4323754-C1.
PN
XX
XX 01-DEC-1994.
PD
XX
XX 15-JUL-1993; 93DE-04323754.
PF
XX
XX 15-JUL-1993; 93DE-04323754.
PR
XX
XX (CHEF) GRUENTHAL GMBH.
PA
XX
XX Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX
XX WPI; 1995-015191/03.
DR
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 10 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR66244-R66266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX Sequence 390 AA;

Query Match 100.0%; Score 554; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHYPYRGKASTDTWGRPCLPWNSATVLCQTYHAHRSALQGLGKKNYCRNPDN 60
DB 2 KTCYEGNGHYPYRGKASTDTWGRPCLPWNSATVLCQTYHAHRSALQGLGKKNYCRNPDN 61

QY 61 RRRPWCYVQGLKPLVQECMWHDCADGKPKSPPEE 96
DB 62 RRRPWCYVQGLKPLVQECMWHDCADGKPKSPPEE 97
RESULT 10
AAR66247
ID AAR66247 standard; protein; 390 AA.
XX
XX AAR66247;
XX
XX 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M14.
XX
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KW urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH 1. .365
FT /label= M4
FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
FT Disulfide-bond 4. .85
FT Disulfide-bond 25. .67
FT Disulfide-bond 56. .80
FT Disulfide-bond 102. .233
FT Disulfide-bond 143. .159
FT Disulfide-bond 151. .222
FT Disulfide-bond 247. .316
FT Disulfide-bond 279. .295
FT Disulfide-bond 306. .334
FT Disulfide-bond 366. .371
FT Region /label= X1
FT Region /label= Y1
XX
XX DE4323754-C1.
PN
XX
XX 01-DEC-1994.
PD
XX
XX 15-JUL-1993; 93DE-04323754.
PF
XX
XX 15-JUL-1993; 93DE-04323754.
PR
XX
XX (CHEF) GRUENTHAL GMBH.
PA
XX
XX Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX
XX WPI; 1995-015191/03.
DR
XX
XX New bifunctional urokinase derive and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 10 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR66244-R66266 are specific
CC examples of such derive. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX Sequence 390 AA;

Query Match 100.0%; Score 554; DB 2; Length 390;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDGTGPRCLPWNATVLOQTYHAHRSALQGLGKKNYCRNPDN 60

Db 2 KTCYEGNGHFYRGKASTDGTGPRCLPWNATVLOQTYHAHRSALQGLGKKNYCRNPDN 61

QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 96

Db 62 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 97

RESULT 11

AAR66260

ID AAR66260 standard; protein; 392 AA.

XX AAR66260;

XX 25-MAR-2003 (revised)

DT 17-AUG-1995 (first entry)

XX Bifunctional urokinase variant M27.

XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;

KW urokinase; variant; mutein.

XX Synthetic.

XX Key

FT Location/Qualifiers

FT Region 1..365

FT /label= M4

FT /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85

FT Disulfide-bond 25..67

FT Disulfide-bond 56..80

FT Disulfide-bond 102..233

FT Disulfide-bond 143..159

FT Disulfide-bond 151..222

FT Disulfide-bond 247..316

FT Disulfide-bond 279..295

FT Disulfide-bond 306..334

FT Disulfide-bond 366..371

FT Region

FT /label= X1

FT 372..392

FT /label= Y1

FN DE4323754-Cl.

XX 01-DEC-1994.

XX 15-JUL-1993; 93DE-04323754.

XX 15-JUL-1993; 93DE-04323754.

XX (CHEF) GRUENTHAL GMBH.

XX Steffens GJ, Wnendt S, Schneider J, Heinzl-Wieland R;

PI Saunders DJ;

XX WPI; 1995-015191/03.

XX New bifunctional urokinase derivs and related plasmids - with improved

FT fibrinolytic and thrombin inhibiting activities, for treating cardiac and

PT cerebral infarct, pulmonary embolism, etc.

XX Example 1; Page 11 and Fig 1; 34pp; German.

XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1

CC are claimed (see features table). Sequences AAR66264-R66266 are specific

CC examples of such derivs. which have both improved fibrinolytic and

CC thrombin-inhibiting activities, compared to known plasminogen activators

CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,

CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac

CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003

CC

CC to correct PN field.)

XX

SQ Sequence 392 AA;

Query Match 100.0%; Score 554; DB 2; Length 392;

Best Local Similarity 100.0%; Pred. No. 1.9e-44;

Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDGTGPRCLPWNATVLOQTYHAHRSALQGLGKKNYCRNPDN 60

Db 2 KTCYEGNGHFYRGKASTDGTGPRCLPWNATVLOQTYHAHRSALQGLGKKNYCRNPDN 61

QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 96

Db 62 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 97

RESULT 12

AAR66264

ID AAR66264 standard; protein; 392 AA.

XX AAR66264;

XX 25-MAR-2003 (revised)

DT 17-AUG-1995 (first entry)

XX Bifunctional urokinase variant M31.

XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;

KW urokinase; variant; mutein.

XX Synthetic.

XX Key

FT Location/Qualifiers

FT Region 1..365

FT /label= M4

FT /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85

FT Disulfide-bond 25..67

FT Disulfide-bond 56..80

FT Disulfide-bond 102..233

FT Disulfide-bond 143..159

FT Disulfide-bond 151..222

FT Disulfide-bond 247..316

FT Disulfide-bond 279..295

FT Disulfide-bond 306..334

FT Disulfide-bond 366..371

FT Region

FT /label= X1

FT 372..392

FT /label= Y1

FN DE4323754-Cl.

XX 01-DEC-1994.

XX 15-JUL-1993; 93DE-04323754.

XX 15-JUL-1993; 93DE-04323754.

XX (CHEF) GRUENTHAL GMBH.

XX Steffens GJ, Wnendt S, Schneider J, Heinzl-Wieland R;

PI Saunders DJ;

XX WPI; 1995-015191/03.

XX New bifunctional urokinase derivs and related plasmids - with improved

FT fibrinolytic and thrombin inhibiting activities, for treating cardiac and

PT cerebral infarct, pulmonary embolism, etc.

XX Example 1; Page 11 and Fig 1; 34pp; German.

XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1

CC are claimed (see features table). Sequences AAR66264-R66266 are specific

CC examples of such derivs. which have both improved fibrinolytic and

CC thrombin-inhibiting activities, compared to known plasminogen activators

CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,

CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac

CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003

CC

CC are claimed (see features table). Sequences AAR66244-R66266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 392 AA;

Query Match 100.0%; Score 554; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKKNYCRNPDN 60
DB 2 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKKNYCRNPDN 61
QY 61 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 96
DB 62 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 97

RESULT 13

AAR66255
ID AAR66255 standard; protein; 392 AA.

XX AC AAR66255;

DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)

DE Bifunctional urokinase variant M22.

XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.

OS Synthetic.

PH Key Location/Qualifiers

FT Region 1..365
FT /label= M4
FT /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85

FT Disulfide-bond 25..67

FT Disulfide-bond 56..80

FT Disulfide-bond 102..233

FT Disulfide-bond 143..159

FT Disulfide-bond 151..222

FT Disulfide-bond 247..316

FT Disulfide-bond 279..295

FT Disulfide-bond 306..334

FT Region 366..371

FT /label= X1

FT Region 372..392

FT /label= Y1

XX DB4323754-C1.

XX 01-DEC-1994.

XX 15-JUL-1993; 93DE-04323754.

XX 15-JUL-1993; 93DE-04323754.

XX (CHEF) GRUENTHAL GMBH.

XX Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;

XX Saunders DJ;

XX WPI; 1995-015191/03.

XX New bifunctional urokinase derivs and related plasmids - with improved

PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.

PS Example 1; Page 10 and Fig 1; 34pp; German.

XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR66244-R66266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX

SQ Sequence 392 AA;

Query Match 100.0%; Score 554; DB 2; Length 392;

Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKKNYCRNPDN 60
DB 2 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQLGLGKKNYCRNPDN 61

QY 61 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 96

DB 62 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 97

RESULT 14

AAR66259
ID AAR66259 standard; protein; 392 AA.

XX AC AAR66259;

DT 25-MAR-2003 (revised)

DT 17-AUG-1995 (first entry)

DE Bifunctional urokinase variant M26.

XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.

OS Synthetic.

PH Key Location/Qualifiers

FT Region 1..365

FT /label= M4

FT /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85

FT Disulfide-bond 25..67

FT Disulfide-bond 56..80

FT Disulfide-bond 102..233

FT Disulfide-bond 143..159

FT Disulfide-bond 151..222

FT Disulfide-bond 247..316

FT Disulfide-bond 279..295

FT Disulfide-bond 306..334

FT Region 366..371

FT /label= X1

FT Region 372..392

FT /label= Y1

XX DE4323754-C1.

XX 01-DEC-1994.

XX 15-JUL-1993; 93DE-04323754.

XX 15-JUL-1993; 93DE-04323754.

XX (CHEF) GRUENTHAL GMBH.

```

PI Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX WPI; 1995-015191/03.
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 11 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR66244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct PN field.)
XX
XX Sequence 392 AA;
XX
XX Query Match 100.0%; Score 554; DB 2; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KTCYEGNGHYRGKASTDTMGRCPLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 60
XX |||||
XX DB 2 KTCYEGNGHYRGKASTDTMGRCPLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 61
XX |||||
XX QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
XX |||||
XX DB 62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
XX |||||

RESULT 15
AAR66261
ID AAR66261 standard; protein; 392 AA.
XX
XX AAR66261;
XX
XX 25-MAR-2003 (revised)
XX 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M28.
XX
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1..365
XX /label= M4
XX /note= "unglycosylated prourokinase (Ser47-Leu411)"
XX
XX Disulfide-bond 4..85
XX Disulfide-bond 25..67
XX Disulfide-bond 56..80
XX Disulfide-bond 102..233
XX Disulfide-bond 143..159
XX Disulfide-bond 151..222
XX Disulfide-bond 247..316
XX Disulfide-bond 279..295
XX Disulfide-bond 306..334
XX Region 366..371
XX /label= X1
XX Region 372..392
XX
XX DB4323754-C1.
XX
XX 01-DEC-1994.
XX

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PF 15-JUL-1993; 93DE-04323754.
XX
XX 15-JUL-1993; 93DE-04323754.
XX
XX (CHEF ) GRUENENTHAL GMBH.
XX
XX Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
XX Saunders DJ;
XX
XX WPI; 1995-015191/03.
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 11 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR66244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct PN field.)
XX
XX Sequence 392 AA;
XX
XX Query Match 100.0%; Score 554; DB 2; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KTCYEGNGHYRGKASTDTMGRCPLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 60
XX |||||
XX DB 2 KTCYEGNGHYRGKASTDTMGRCPLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 61
XX |||||
XX QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
XX |||||
XX DB 62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
XX |||||

RESULT 16
AAR66258
ID AAR66258 standard; protein; 392 AA.
XX
XX AAR66258;
XX
XX 25-MAR-2003 (revised)
XX 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M25.
XX
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1..365
XX /label= M4
XX /note= "unglycosylated prourokinase (Ser47-Leu411)"
XX
XX Disulfide-bond 4..85
XX Disulfide-bond 25..67
XX Disulfide-bond 56..80
XX Disulfide-bond 102..233
XX Disulfide-bond 143..159
XX Disulfide-bond 151..222
XX Disulfide-bond 247..316
XX Disulfide-bond 279..295
XX Disulfide-bond 306..334
XX Region 366..371
XX /label= X1
XX Region 372..392
XX

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FT XX /label= Y1
PN DE4323754-C1.
XX
XX
XX 01-DEC-1994.
XX
XX 15-JUL-1993; 93DE-04323754.
XX
XX 15-JUL-1993; 93DE-04323754.
XX
XX (CHEF ) GRUENENTHAL GMBH.
XX
XX Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX
XX WPI; 1995-015191/03.
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 11 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR6244-R66266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX Sequence 392 AA;
XX
XX Query Match 100.0%; Score 554; DB 2; Length 392;
XX Best Local Similarity 100.0%; Pred. NO. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KTCYEGNGHFGKASDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNCRNPDN 60
XX 2 KTCYEGNGHFGKASDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNCRNPDN 61
XX
XX 61 RRRPWCYVQGLKPLVQECMVHDCADGKFPSPPEE 96
XX 62 RRRPWCYVQGLKPLVQECMVHDCADGKFPSPPEE 97
XX
XX RESULT 17
XX AAR6263
XX ID AAR6263 standard; protein; 392 AA.
XX
XX AC AAR6263;
XX
XX 25-MAR-2003 (revised)
XX 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M30.
XX
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1. .365
XX /label= M4
XX /note= "unglycosylated prourokinase(Ser47-Leu411)"
XX
XX Disulfide-bond 4. .85
XX Disulfide-bond 25. .67
XX Disulfide-bond 56. .80
XX Disulfide-bond 102. .233
XX Disulfide-bond 143. .159
XX Disulfide-bond 151. .222

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FT Disulfide-bond 247. .316
FT Disulfide-bond 279. .295
FT Disulfide-bond 306. .334
FT Region 366. .371
FT /label= X1
FT Region 372. .392
FT /label= Y1
XX
XX DE4323754-C1.
XX
XX 01-DEC-1994.
XX
XX 15-JUL-1993; 93DE-04323754.
XX
XX 15-JUL-1993; 93DE-04323754.
XX
XX (CHEF ) GRUENENTHAL GMBH.
XX
XX Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX
XX WPI; 1995-015191/03.
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 11 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR6244-R66266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX Sequence 392 AA;
XX
XX Query Match 100.0%; Score 554; DB 2; Length 392;
XX Best Local Similarity 100.0%; Pred. NO. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 KTCYEGNGHFGKASDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNCRNPDN 60
XX 2 KTCYEGNGHFGKASDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNCRNPDN 61
XX
XX 61 RRRPWCYVQGLKPLVQECMVHDCADGKFPSPPEE 96
XX 62 RRRPWCYVQGLKPLVQECMVHDCADGKFPSPPEE 97
XX
XX RESULT 18
XX AAR6254
XX ID AAR6254 standard; protein; 392 AA.
XX
XX AC AAR6254;
XX
XX 25-MAR-2003 (revised)
XX 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M21.
XX
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Region 1. .365
XX /label= M4
XX /note= "unglycosylated prourokinase(Ser47-Leu411)"
XX
XX Disulfide-bond 4. .85
XX Disulfide-bond 25. .67
XX Disulfide-bond 56. .80
XX Disulfide-bond 102. .233
XX Disulfide-bond 143. .159
XX Disulfide-bond 151. .222

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FT Disulfide-bond 4. .85
FT Disulfide-bond 25. .67
FT Disulfide-bond 56. .80
FT Disulfide-bond 102. .233
FT Disulfide-bond 143. .159
FT Disulfide-bond 151. .222
FT Disulfide-bond 247. .316
FT Disulfide-bond 279. .295
FT Disulfide-bond 306. .334
FT Disulfide-bond 366. .371
FT Region
FT /label= X1
FT Region
FT /label= Y1
XX DE4323754-C1.
XX 01-DEC-1994.
XX 15-JUL-1993; 93DE-04323754.
XX 15-JUL-1993; 93DE-04323754.
XX (CHEP ) GRUENENTHAL GMBH.
XX Steffens GJ, Wnendt S, Schneider J, Heinzl-Wieland R;
XX Saunders DU;
XX WPI; 1995-015191/03.
XX New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX Example 1; Page 10 and Fig 1; 34pp; German.
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR66244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct PN field.)
XX Sequence 392 AA;
XX Query Match 100.0%; Score 554; DB 2; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 2 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 61
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96
DB 62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 97
RESULT 19
AAR66256
ID AAR66256 standard; protein; 392 AA.
XX AAR66256;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 17-AUG-1995 (first entry)
XX DE Bifunctional urokinase variant M23.
XX KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX KW urokinase; variant; mutein.

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OS Synthetic.
XX Key
XX Region
XX Location/Qualifiers
XX 1. .365
XX /label= M4
XX /note= "unglycosylated prourokinase (Ser47-Leu411)"
FT Disulfide-bond 4. .85
FT Disulfide-bond 25. .67
FT Disulfide-bond 56. .80
FT Disulfide-bond 102. .233
FT Disulfide-bond 143. .159
FT Disulfide-bond 151. .222
FT Disulfide-bond 247. .316
FT Disulfide-bond 279. .295
FT Disulfide-bond 306. .334
FT Disulfide-bond 366. .371
FT Region
FT /label= X1
FT Region
FT /label= Y1
XX DE4323754-C1.
XX 01-DEC-1994.
XX 15-JUL-1993; 93DE-04323754.
XX 15-JUL-1993; 93DE-04323754.
XX (CHEP ) GRUENENTHAL GMBH.
XX Steffens GJ, Wnendt S, Schneider J, Heinzl-Wieland R;
XX Saunders DU;
XX WPI; 1995-015191/03.
XX New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX Example 1; Page 10 and Fig 1; 34pp; German.
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR66244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct PN field.)
XX Sequence 392 AA;
XX Query Match 100.0%; Score 554; DB 2; Length 392;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 2 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNYCRNPDN 61
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96
DB 62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 97
RESULT 20
AAR66257
ID AAR66257 standard; protein; 392 AA.
XX AAR66257;
XX AC
XX DT 25-MAR-2003 (revised)
XX DT 17-AUG-1995 (first entry)

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Db 62 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 97

RESULT 22

AAAR66253
ID AAR66253 standard; protein; 393 AA.

XX AC AAR66253;

25-MAR-2003 (revised)

17-AUG-1995 (first entry)

XX DE Bifunctional urokinase variant M20.

XX KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX KW urokinase; variant; mutein.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Region 1..365

FT /label= M4

FT /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85

FT Disulfide-bond 25..67

FT Disulfide-bond 56..80

FT Disulfide-bond 102..233

FT Disulfide-bond 143..159

FT Disulfide-bond 151..222

FT Disulfide-bond 247..316

FT Disulfide-bond 279..295

FT Disulfide-bond 306..334

FT Disulfide-bond 366..372

FT Region /label= X1

FT Region 373..393

FT /label= Y1

XX DE4323754-C1

XX PN

XX XX

XX PD 01-DEC-1994.

XX XX 15-JUL-1993; 93DE-04323754.

XX XX 15-JUL-1993; 93DE-04323754.

XX XX (CHEF) GRUENTHAL GMBH.

XX PA

XX PI Steffens GJ, Wnendt S, Schneider J, Heinzl-Wieland R;

XX PI Saunders DJ;

XX XX WPI; 1995-015191/03.

XX DR

XX XX New bifunctional urokinase derivs and related plasmids - with improved

XX PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and

XX PT cerebral infarct, pulmonary embolism, etc.

XX XX

XX PS Example 1; Page 10 and Fig 1; 34pp; German.

XX XX

XX CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1

XX CC are claimed (see features table). Sequences AAR66244-R66266 are specific

XX CC examples of such derivs. which have both improved fibrinolytic and

XX CC thrombin-inhibiting activities, compared to known plasminogen activators

XX CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,

XX CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac

XX CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003

XX CC to correct PN field.)

XX XX

XX SQ Sequence 393 AA;

XX XX

XX Query Match 100.0%; Score 554; DB 2; Length 393;

XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPCLPWNSATVLOQTYHAHRSDALQGLGKKNYCRNPDN 60
Db 2 KTCYEGNGHFYRGKASTDTMGPCLPWNSATVLOQTYHAHRSDALQGLGKKNYCRNPDN 61
QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 96
Db 62 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 97

RESULT 23

AAAR66249

ID AAR66249 standard; protein; 393 AA.

XX AC AAR66249;

25-MAR-2003 (revised)

17-AUG-1995 (first entry)

XX DE Bifunctional urokinase variant M16.

XX KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX KW urokinase; variant; mutein.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Region 1..365

FT /label= M4

FT /note= "unglycosylated prourokinase (Ser47-Leu411)"

FT Disulfide-bond 4..85

FT Disulfide-bond 25..67

FT Disulfide-bond 56..80

FT Disulfide-bond 102..233

FT Disulfide-bond 143..159

FT Disulfide-bond 151..222

FT Disulfide-bond 247..316

FT Disulfide-bond 279..295

FT Disulfide-bond 306..334

FT Disulfide-bond 366..372

FT Region /label= X1

FT Region 373..393

FT /label= Y1

XX DE4323754-C1.

XX PN

XX PD 01-DEC-1994.

XX XX 15-JUL-1993; 93DE-04323754.

XX XX 15-JUL-1993; 93DE-04323754.

XX XX (CHEF) GRUENTHAL GMBH.

XX PA

XX PI Steffens GJ, Wnendt S, Schneider J, Heinzl-Wieland R;

XX PI Saunders DJ;

XX XX WPI; 1995-015191/03.

XX DR

XX XX New bifunctional urokinase derivs and related plasmids - with improved

XX PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and

XX PT cerebral infarct, pulmonary embolism, etc.

XX XX

XX PS Example 1; Page 10 and Fig 1; 34pp; German.

XX XX

XX CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1

XX CC are claimed (see features table). Sequences AAR66244-R66266 are specific

XX CC examples of such derivs. which have both improved fibrinolytic and

XX CC thrombin-inhibiting activities, compared to known plasminogen activators

XX CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,

XX CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac

XX CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003

XX CC to correct PN field.)

XX Sequence 393 AA;
SQ Query Match 100.0%; Score 554; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOYTHAHRSDALQLGLGKKNYCRNPDN 60
DB 2 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOYTHAHRSDALQLGLGKKNYCRNPDN 61

QY 61 RRPWCYVQVGLKPLVQECWVHDCADGKPKSPPEE 96
DB 62 RRPWCYVQVGLKPLVQECWVHDCADGKPKSPPEE 97

RESULT 24
AAR66252
ID AAR66252 standard; protein; 393 AA.
XX AC AAR66252;
XX DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX DB Bifunctional urokinase variant M19.
XX KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KW urokinase; variant; mutein.
XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Region 1..365
FT /label= M4
FT /notes= "unglycosylated prourokinase (Ser47-Leu411)"
FT Disulfide-bond 4..85
FT Disulfide-bond 25..67
FT Disulfide-bond 56..80
FT Disulfide-bond 102..233
FT Disulfide-bond 143..159
FT Disulfide-bond 151..222
FT Disulfide-bond 247..316
FT Disulfide-bond 279..295
FT Disulfide-bond 306..334
FT Region 366..372
FT /label= X1
FT Region 373..393
FT /label= Y1

PN DB4323754-C1.
XX PD 01-DEC-1994.
XX PF 15-JUL-1993; 93DE-04323754.
XX PR 15-JUL-1993; 93DE-04323754.
XX (CHEP) GRUENTHAL GMBH.
XX PI Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX WPI; 1995-015191/03.
XX DR Example 1; Page 10 and Fig 1; 34pp; German.
XX PS Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX CC are claimed (see features table). Sequences AAR66244-R66286 are specific

XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct PN field.)

SQ Sequence 393 AA;
Query Match 100.0%; Score 554; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOYTHAHRSDALQLGLGKKNYCRNPDN 60
DB 2 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOYTHAHRSDALQLGLGKKNYCRNPDN 61

QY 61 RRPWCYVQVGLKPLVQECWVHDCADGKPKSPPEE 96
DB 62 RRPWCYVQVGLKPLVQECWVHDCADGKPKSPPEE 97

RESULT 25
AAR66244
ID AAR66244 standard; protein; 393 AA.
XX AC AAR66244;
XX DT 25-MAR-2003 (revised)
DT 22-AUG-1995 (first entry)
XX DE Bifunctional urokinase variant M11.
XX KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KW urokinase; variant; mutein.
XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Region 1..365
FT /label= M4
FT /notes= "unglycosylated prourokinase (Ser47-Leu411)"
FT Disulfide-bond 4..85
FT Disulfide-bond 25..67
FT Disulfide-bond 56..80
FT Disulfide-bond 102..233
FT Disulfide-bond 143..159
FT Disulfide-bond 151..222
FT Disulfide-bond 247..316
FT Disulfide-bond 279..295
FT Disulfide-bond 306..334
FT Region 366..374
FT /label= X1
FT Region 375..393
FT /label= Y1

PN DB4323754-C1.
XX PD 01-DEC-1994.
XX PF 15-JUL-1993; 93DE-04323754.
XX PR 15-JUL-1993; 93DE-04323754.
XX (CHEF) GRUENTHAL GMBH.
XX PA Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R;
PI Saunders DJ;
XX WPI; 1995-015191/03.
XX DR New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX PS Example 1; Page 10 and Fig 1; 34pp; German.
XX CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR66244-R66286 are specific

PT cerebral infarct, pulmonary embolism, etc.
XX
PS Example 1; Page 10 and Fig 1; 34pp; German.
XX
CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR66244-R66266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 393 AA;
Query Match 100.0%; Score 554; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 2 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 61
QY 61 RRRPCWYQVGLKPLVQECMVHDCADGKKPSPPEE 96
DB 62 RRRPCWYQVGLKPLVQECMVHDCADGKKPSPPEE 97
RESULT 26
AAR66250
ID AAR66250 standard; protein; 393 AA.
XX
AC AAR66250;
XX
DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX
DE Bifunctional urokinase variant M17.
XX
KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KW urokinase; variant; mutein.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Region 1..365
FT /label= M4
FT /note= "unglycosylated prourokinase (Ser47-Leu411)"
FT
FT Disulfide-bond 4..85
FT Disulfide-bond 25..67
FT Disulfide-bond 56..80
FT Disulfide-bond 102..233
FT Disulfide-bond 143..159
FT Disulfide-bond 151..222
FT Disulfide-bond 247..316
FT Disulfide-bond 279..334
FT Disulfide-bond 306..372
FT Region 366..372
FT /label= X1
FT Region 373..393
FT /label= Y1
XX
DE4323754-Cl.
XX
PD 01-DEC-1994.
XX
PF 15-JUL-1993; 93DE-04323754.
XX
PR 15-JUL-1993; 93DE-04323754.
XX (CHEF) GRUENENTHAL GMBH.
PA Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
PI

PI Saunders DU;
XX
DR WPI; 1995-015191/03.
XX
PT New bifunctional urokinase derivs and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
PS Example 1; Page 10 and Fig 1; 34pp; German.
XX
CC Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR66244-R66266 are specific
CC examples of such derivs. which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 393 AA;
Query Match 100.0%; Score 554; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 1.9e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 2 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 61
QY 61 RRRPCWYQVGLKPLVQECMVHDCADGKKPSPPEE 96
DB 62 RRRPCWYQVGLKPLVQECMVHDCADGKKPSPPEE 97
RESULT 27
AAR99597
ID AAR99597 standard; protein; 393 AA.
XX
AC AAR99597;
XX
DT 05-DEC-1996 (first entry)
DT
DE Chimeric protein M38 encoded by pSE1.
XX
KW Thrombin; inhibition; thrombus; thrombolysis; chimeric protein;
KW plasminogen activating sequence; fibrinolysis; infarction;
KW angina pectoris; deep vein thrombosis.
XX
OS Synthetic.
XX
PN EF714982-A2.
XX
PD 05-JUN-1996.
XX
PF 16-NOV-1995; 95EP-00118050.
XX
PR 30-NOV-1994; 94DE-04442665.
XX
PA (CHEF) GRUENENTHAL GMBH.
XX
PI Wnendt S, Steffens GJ, Janocha E, Heinzel-Wieland R;
XX
DR WPI; 1996-269715/28.
XX
PT Chimeric protein contg. plasminogen activating sequence and thrombin-
PT inhibiting sequence - useful as thrombus-specific thrombolytic agent with
PT rapid action.
XX
PS Example 1; Page 21-22; 37pp; German.
XX
CC Example 1 describes the prodn. of plasmids pSE1 and pSE9 contg. a DNA
CC encoding a chimeric protein with fibrinolytic and thrombin-inhibiting
CC properties. pSE1 encodes the protein given in AAR99597 and pSE9 encodes

CC the protein given in AAR99596
 XX Sequence 393 AA;
 SQ

Query Match 100.0%; Score 554; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.9e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKKNYCRNPDN 60
 |||||
 DB 3 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKKNYCRNPDN 62
 |||||
 QY 61 RRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 96
 |||||
 DB 63 RRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 98
 |||||

RESULT 28

AAR99596
 ID AAR99596 standard; protein; 393 AA.

XX AC AAR99596;
 XX DT 05-DEC-1996 (first entry)
 XX DE Chimeric protein M37 encoded by pSE9.

XX KW Thrombin; inhibition; thrombus; thrombolytic; chimeric protein;
 XX KW plasminogen activating sequence; fibrinolysis; infarction;
 XX KW angina pectoris; deep vein thrombosis.
 XX OS Synthetic.

XX PN EP714982-A2.
 XX PD 05-JUN-1996.

XX PF 16-NOV-1995; 95EP-00118050.
 XX PR 30-NOV-1994; 94DE-04442665.
 XX PA (CHEF) GRUENENTHAL GMBH.

XX PI Wnendt S, Steffens GJ, Janocha E, Heinzel-Wieland R;
 XX DR WPI; 1996-269715/28.

XX PT Chimeric protein contg. plasminogen activating sequence and thrombin-
 inhibiting sequence - useful as thrombus-specific thrombolytic agent with
 rapid action.

XX PS Example 1; Page 19-20; 37pp; German.

XX CC Example 1 describes the prodn. of plasmids pSE1 and pSE9 contg. a DNA
 encoding a chimeric protein with fibrinolytic and thrombin-inhibiting
 properties. pSE1 encodes the protein given in AAR99597 and pSE9 encodes
 the protein given in AAR99596

XX SQ Sequence 393 AA;

Query Match 100.0%; Score 554; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.9e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKKNYCRNPDN 60
 |||||
 DB 3 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKKNYCRNPDN 62
 |||||

QY 61 RRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 96
 |||||
 DB 63 RRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 98
 |||||

RESULT 29

AAR99885
 ID AAR99885 standard; peptide; 393 AA.

XX AC AAR99885;
 XX DT 27-JAN-1997 (first entry)

XX DE M36: fibrinolytic and anticoagulant activity contg. protein.
 XX KW Thrombin; factor Xa; anticoagulant; thrombolytic; plasminogen; urokinase;
 KW activator; streptokinase; staphylokinase; APSAC;
 KW anisolated plasminogen streptokinase activator complex; hirudin;
 KW hirullin; antistatin; pWLT27; pWS1; pSE8; pHS56.

XX OS Synthetic.

XX PN EP712934-A2.

XX PD 22-MAY-1996.

XX PF 03-NOV-1995; 95EP-00117316.
 XX PR 17-NOV-1994; 94DE-04440892.

XX PA (CHEF) GRUENENTHAL GMBH.

XX PI Wnendt S, Heinzel-Wieland R, Steffens GJ;
 XX DR WPI; 1996-240720/25.

XX PT Proteins with fibrinolytic and anticoagulant activity - useful as
 thrombolytic agents.

XX PS Disclosure; Fig 18; 59pp; German.

XX CC New peptides (I) with fibrinolytic and anticoagulant activity comprise a
 plasminogen-activating amino acid sequence (A) fused at the N- and/or C-
 terminus to a thrombin and/or factor Xa inhibiting amino acid sequence
 (B). Excluded from the claims are (i) where (A) is Ser47 to Leu411 of
 unglycosylated urokinase linked at the C-terminus to sequences (i) to
 (iii); T1-RP-T2-GGGNGDFEIPPEYL-T3 (i) T1-RPELRNPNDKYEPFWEDEKNE (ii)
 T1-RPSSEFEFEIDEEK (iii) Where T1= P or V; T2 = L or a bond; T3= Q or
 OH. (A) is pref. (pro)urokinase; tissue plasminogen activator (tPA), bat-
 PA (all opt. modified by deletion, substitution, insertion and/or addn.);
 streptokinase; staphylokinase; and/or APSAC (anisolated plasminogen
 streptokinase activator complex), esp. Prourokinase (411 amino acids) or
 its Ser47 to Leu411 or Ser138 to Leu411 fragments, or t-PA (527 amino
 acids) or its Ser89arg to 527Pro or 174Ser to 527Pro fragments. (B) has
 hirudin or hirulin activities; or is derived from the human thrombin
 receptor, antistatin and/or the tick anticoagulant peptide. Most pref.
 are the 65 amino acid hirudin sequence or one of the six sequences given
 in AAR99879 to AAR99884. Plasmids pWLT27 (M51), pWS1 (M5112), pSE8 (M36)
 and pHS56 (M43) contain the sequences encoding AAR99885 to AAR99888,
 respectively. The products were tested in human citrated plasma (5 microg
 in 200 microl 1:10 diluted plasma). The thrombin time was then 1.2, 3,
 2.8 and 1.2 times greater, respectively, than in the absence of the
 product

XX SQ Sequence 393 AA;

Query Match 100.0%; Score 554; DB 2; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.9e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKKNYCRNPDN 60
 |||||
 DB 3 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLTQTYHAHRSALQGLGKKNYCRNPDN 62
 |||||

QY 61 RRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 96
 |||||
 DB 63 RRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 98
 |||||

RESULT 30
 AAR47902
 ID AAR47902 standard; protein; 395 AA.
 AC
 XX AAR47902;
 DT 13-JUL-1994 (first entry)
 XX
 DT Pro-urokinase derivative.
 DE
 XX Pro-urokinase; half-life; thrombolytic; thrombosis; fibrinolytic; factor.
 KW Homo sapiens.
 OS
 XX JP05336965-A.
 PN
 XX 21-DEC-1993.
 PD
 XX 17-OCT-1991; 91JP-00269615.
 PF
 XX 17-OCT-1991; 91JP-00269615.
 PR
 XX (KYOW) KYOWA HAKKO KOGYO KK.
 XX
 PA WPI; 1994-030907/04.
 DR N-PSDB; AAQ55771.
 XX
 XX Novel human pro-urokinase derivs. having long half-life - with high
 FT thrombolytic activity, useful for treatment of thrombosis.
 PT
 XX Disclosure; Page 14; 29pp; Japanese.
 PS
 XX Sequences (AAQ55771-72) are pro-urokinase derivatives. The products have
 CC an inserted sugar moiety having an amino acid substituted, depleted or
 CC inserted variant around the thrombin cleavage site. They also have a long
 CC half-life allowing them to be used in the treatment of thrombosis
 XX
 XX Sequence 395 AA;
 SQ
 Query Match 100.0%; Score 554; DB 2; Length 395;
 Best Local Similarity 100.0%; Pred. No. 1.9e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDN 60
 DB 32 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDN 91
 QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKPKSPSPPEE 96
 DB 92 RRRPWCYVQVGLKPLVQECWVHDCADGKPKSPSPPEE 127
 RESULT 31
 AAR66265
 ID AAR66265 standard; protein; 395 AA.
 AC AAR66265;
 XX
 XX 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M32.
 XX
 KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT 1..365
 FT Region /label= M4
 FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
 FT

FT Disulfide-bond 4..85
 FT Disulfide-bond 25..57
 FT Disulfide-bond 56..80
 FT Disulfide-bond 102..233
 FT Disulfide-bond 143..159
 FT Disulfide-bond 151..222
 FT Disulfide-bond 247..316
 FT Disulfide-bond 279..295
 FT Disulfide-bond 306..334
 FT Disulfide-bond 366..371
 FT Region /label= X1
 FT Region 372..395
 FT /label= Y1
 XX
 PN DE4323754-C1.
 XX
 PD 01-DEC-1994.
 XX
 PD 15-JUL-1993; 93DE-04323754.
 XX
 PD 15-JUL-1993; 93DE-04323754.
 PR
 XX (CHEF) GRUENENTHAL GMBH.
 PA
 XX Steffens GJ, Wnendt S, Schneider J, Heinzel-Wieland R;
 PI Saunders DJ;
 PI
 XX WPI; 1995-015191/03.
 DR
 XX New bifunctional urokinase derive and related plasmids - with improved
 FT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
 PT cerebral infarct, pulmonary embolism, etc.
 PT
 XX Example 1; Page 11 and Fig 1; 34pp; German.
 PS
 XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
 CC are claimed (see features table). Sequences AAR66244-R66266 are specific
 CC examples of such derivs. which have both improved fibrinolytic and
 CC thrombin-inhibiting activities, compared to known plasminogen activators
 CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
 CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
 CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
 CC to correct PN field.)
 XX
 SQ Sequence 395 AA;
 Query Match 100.0%; Score 554; DB 2; Length 395;
 Best Local Similarity 100.0%; Pred. No. 1.9e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDN 60
 DB 2 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQOTYHAHRSDALQGLGKHNYCRNPDN 61
 QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKPKSPSPPEE 96
 DB 62 RRRPWCYVQVGLKPLVQECWVHDCADGKPKSPSPPEE 97
 RESULT 32
 AAR66262
 ID AAR66262 standard; protein; 395 AA.
 XX
 AC AAR66262;
 XX
 XX 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX
 DE Bifunctional urokinase variant M29.
 XX
 KW fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
 KW urokinase; variant; mutein.
 XX

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OS Synthetic.
XX Key Location/Qualifiers
XX Region 1. .365
XX /label= M4
XX /note= "unglycosylated prourokinase(Ser47-Leu411)"
XX Disulfide-bond 4. .85
XX Disulfide-bond 25. .67
XX Disulfide-bond 56. .80
XX Disulfide-bond 102. .233
XX Disulfide-bond 143. .159
XX Disulfide-bond 151. .222
XX Disulfide-bond 247. .316
XX Disulfide-bond 279. .295
XX Disulfide-bond 306. .334
XX Disulfide-bond 366. .371
XX Region /label= X1
XX Region /label= Y1
XX DE4323754-C1.
XX 01-DEC-1994.
XX 15-JUL-1993; 93DE-04323754.
XX 15-JUL-1993; 93DE-04323754.
XX (CHEP ) GRUENENTHAL GMBH.
XX Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R;
XX Saunders DJ;
XX WPI; 1995-015191/03.
XX New bifunctional urokinase derivs and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX Example 1; Page 11 and Fig 1; 34pp; German.
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR6244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct FN field.)
XX Sequence 395 AA;
XX Query Match 100.0%; Score 554; DB 2; Length 395;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 KTCYEGNGHFYRGKASTDTMGRCPLPWNSTVLTQYTHAHRSDALQLGLGKHNCRNPDN 60
XX 2 KTCYEGNGHFYRGKASTDTMGRCPLPWNSTVLTQYTHAHRSDALQLGLGKHNCRNPDN 61
XX 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
XX 62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
XX RESULT 33
XX AAR66246
XX ID AAR66246 standard; protein; 396 AA.
XX AC AAR66246;
XX 25-MAR-2003 (revised)
XX 17-AUG-1995 (first entry)

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XX Bifunctional urokinase variant M13.
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
XX urokinase; variant; mutein.
XX Synthetic.
XX Key Location/Qualifiers
XX Region 1. .365
XX /label= M4
XX /note= "unglycosylated prourokinase(Ser47-Leu411)"
XX Disulfide-bond 4. .85
XX Disulfide-bond 25. .67
XX Disulfide-bond 56. .80
XX Disulfide-bond 102. .233
XX Disulfide-bond 143. .159
XX Disulfide-bond 151. .222
XX Disulfide-bond 247. .316
XX Disulfide-bond 279. .295
XX Disulfide-bond 306. .334
XX Disulfide-bond 366. .377
XX Region /label= X1
XX Region /label= Y1
XX DE4323754-C1.
XX 01-DEC-1994.
XX 15-JUL-1993; 93DE-04323754.
XX 15-JUL-1993; 93DE-04323754.
XX (CHEP ) GRUENENTHAL GMBH.
XX Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R;
XX Saunders DJ;
XX WPI; 1995-015191/03.
XX New bifunctional urokinase derive and related plasmids - with improved
XX fibrinolytic and thrombin inhibiting activities, for treating cardiac and
XX cerebral infarct, pulmonary embolism, etc.
XX Example 1; Page 10 and Fig 1; 34pp; German.
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
XX are claimed (see features table). Sequences AAR6244-R66266 are specific
XX examples of such derivs. which have both improved fibrinolytic and
XX thrombin-inhibiting activities, compared to known plasminogen activators
XX or thrombin inhibitors. The proteins are useful as thrombolytic agents,
XX e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
XX and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
XX to correct FN field.)
XX Sequence 396 AA;
XX Query Match 100.0%; Score 554; DB 2; Length 396;
XX Best Local Similarity 100.0%; Pred. No. 2e-44;
XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX 1 KTCYEGNGHFYRGKASTDTMGRCPLPWNSTVLTQYTHAHRSDALQLGLGKHNCRNPDN 60
XX 2 KTCYEGNGHFYRGKASTDTMGRCPLPWNSTVLTQYTHAHRSDALQLGLGKHNCRNPDN 61
XX 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
XX 62 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 97
XX RESULT 34
XX AAR66248

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ID AAR66248 standard; protein; 397 AA.
XX
XX AAR66248;
XX
XX 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)
XX
XX Bifunctional urokinase variant M15.
XX
XX fibrinolysis; thrombin inhibition; thrombolytic; anti-thrombotic;
KW urokinase; variant; mutein.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..365
FT /label= M4
FT /note= "unglycosylated prourokinase(Ser47-Leu411)"
FT
FT Disulfide-bond 4..85
FT Disulfide-bond 25..67
FT Disulfide-bond 56..80
FT Disulfide-bond 102..233
FT Disulfide-bond 143..159
FT Disulfide-bond 151..222
FT Disulfide-bond 247..316
FT Disulfide-bond 279..295
FT Disulfide-bond 306..334
FT Disulfide-bond 366..378
FT Region /label= X1
FT Region /label= Y1
XX
XX DE4323754-CL.
XX
XX 01-DEC-1994.
XX
XX 15-JUL-1993. 93DE-04323754.
XX
XX 15-JUL-1993. 93DE-04323754.
XX
XX (CHEF ) GRUENENTHAL GMBH.
XX
XX Steffens GJ, Whendt S, Schneider J, Heinzel-Wieland R,
PI Saunders DJ;
XX
XX WPI; 1995-015191/03.
XX
XX New bifunctional urokinase derivs and related plasmids - with improved
PT fibrinolytic and thrombin inhibiting activities, for treating cardiac and
PT cerebral infarct, pulmonary embolism, etc.
XX
XX Example 1; Page 10 and Fig 1; 34pp; German.
XX
XX Bifunctional urokinase derivatives corresponding to the formula M4-X1-Y1
CC are claimed (see features table). Sequences AAR66244-R66266 are specific
CC examples of such derivs which have both improved fibrinolytic and
CC thrombin-inhibiting activities, compared to known plasminogen activators
CC or thrombin inhibitors. The proteins are useful as thrombolytic agents,
CC e.g. for treatment of arterial occlusions, deep vein thrombosis, cardiac
CC and cerebral infarction and pulmonary embolism. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
XX Sequence 397 AA;
SQ
Query Match 100.0%; Score 554; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFGKASTDTMGSPCLPWN SATVLQOTYHAHRSDALQLGLGKHYCRNPDN 60
DB 2 KTCYEGNGHFGKASTDTMGSPCLPWN SATVLQOTYHAHRSDALQLGLGKHYCRNPDN 61
QY 61 RRRPCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96
|||||
62 RRRPCYVQVGLKPLVQECMVHDCADGKKPSPPEE 97
|||||
RESULT 35
AAW13637
ID AAW13637 standard; protein; 401 AA.
XX
XX AAW13637;
XX
XX 04-JUN-1997 (first entry)
XX
XX Human prourokinase variant lacking EGF domain loop 3.
XX
XX Human prourokinase; hPUK; variant; half-life; increase; EGF;
KW epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Region 1..32
FT /note= "residues 1-32 of native hPUK"
FT Region 33..401
FT /note= "residues 43-411 of native hPUK"
FT Misc-difference 167
FT /note= "corresponds to TAC codon"
XX
XX EP398361-A.
XX
XX 22-NOV-1990.
XX
XX 18-MAY-1990; 90BP-00109472.
XX
XX 18-MAY-1989; 89JP-00126433.
PR 22-FEB-1990; 90JP-00042020.
XX
XX (GREC ) GREEN CROSS CORP.
XX
XX Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;
PI Airmura H;
XX
XX WPI; 1990-350146/47.
DR N-PSDB; AAT61674.
XX
XX Human pro-urokinase variants - deficient in loop regions of epidermal
PT growth factor, showing long blood half-life, as fibrinolytic agent.
XX
XX Claim 11; Page; 22pp; English.
XX
XX New variants of human prourokinase (hPUK) comprise a hPUK deficient in
CC (i) at least part of the first loop region of the epidermal growth factor
CC (EGF) domain; (ii) at least part of the first loop and at least part of
CC the second loop; or (iii) at least part of the third loop. The hPUK
CC variants show an increased blood half-life comparable to that of the
CC whole EGF domain-deficient hPUK variant and urokinase while retaining the
CC same properties as those of hPUK. They have potent thrombolytic activity
CC and very little tendency to cause spontaneous bleeding. The present
CC sequence represents a specific variant of hPUK which lacks EGF domain
CC loop 3; the sequence does not appear in the specification and has been
CC created using the wild-type hPUK sequence and the junction sequence after
CC deletion, both of which are given (in Fig 1 and on page 8, respectively)
XX
XX Sequence 401 AA;
SQ
Query Match 100.0%; Score 554; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFGKASTDTMGSPCLPWN SATVLQOTYHAHRSDALQLGLGKHYCRNPDN 60
DB 38 KTCYEGNGHFGKASTDTMGSPCLPWN SATVLQOTYHAHRSDALQLGLGKHYCRNPDN 97
```

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
 DB 98 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 133

RESULT 36
 AAR23794
 ID AAR23794 standard; protein; 410 AA.

AC AAR23794;
 DT 03-NOV-1992 (first entry)
 DE Prourokinase mutant F157D.
 KW Substitution; animal; plasminogen activator; blood; clot.
 OS Homo sapiens.

XX JP04091792-A.
 XX 25-MAR-1992.
 XX 07-AUG-1990; 90JP-00207659.
 XX 07-AUG-1990; 90JP-00207659.

XX (TOYU) TOSCH CORP.
 XX WPI; 1992-154820/19.

XX Vector contg. pro-urokinase encoding gene - includes mouse-IgG H chain E-
 mu enhancer, enhancer contg. SV40, early phase promoter and SV40
 PT poly:adenylation site.
 XX Claim 3; Page 1; 15pp; Japanese.

XX The sequence is that of mature prourokinase having the substitution
 CC mutation F157D. The sequence per se is not given in the specification, so
 CC the known sequence of prourokinase was used to demonstrate the mutant
 CC protein. The gene encoding prourokinase has been over-expressed by
 CC recombinant DNA technology and provides a method for the rapid, low cost
 CC prodn. of prourokinase, which is a low mol. wt. plasminogen activator
 CC used for dissolving blood clots. See also AAR23795
 XX Sequence 410 AA;

Query Match 100.0%; Score 554; DB 2; Length 410;
 Best Local Similarity 100.0%; Pred. No. 2e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWSATVLCQTYHAHRSALQLGLGKHYCRNPDN 60
 DB 47 KTCYEGNGHFYRGKASTDTMGRPCLPWSATVLCQTYHAHRSALQLGLGKHYCRNPDN 106
 QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
 DB 107 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 142

RESULT 37
 AAR50871
 ID AAR50871 standard; protein; 411 AA.

XX AAR50871;
 XX 30-NOV-1991 (first entry)

XX Sequence encoded by cDNA sequence for human urokinase zymogen (Japanese
 DE Patent Application No.37119/84).
 XX Thrombolytic agent; plasminogen activator activity; fibrin affinity;
 KW enzyme.

XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 50..131
 FT Disulfide-bond 71..113
 FT Disulfide-bond 102..126
 FT Disulfide-bond 148..279
 FT Cleavage-site 158..159
 FT /note= "potential cleavage site which generates the two-
 chain form from the zymogen"

FT Disulfide-bond 189..205
 FT Disulfide-bond 197..268
 FT Disulfide-bond 293..362
 FT Disulfide-bond 325..341
 FT Disulfide-bond 352..380

XX EPI39447-A.

XX 02-MAY-1985.
 XX 07-SEP-1984; 84EP-00306117.
 XX 13-SEP-1983; 83JP-00170354.
 XX 17-OCT-1983; 83JP-00195051.

XX (GREG) GREEN CROSS CORP.
 XX Kasai S, Arimura H, Mori K, Suyama T;
 XX WPI; 1985-106530/18.

XX New urokinase zymogen - useful as thrombolytic agent.
 XX Disclosure; Page 12; 30pp; English.

XX Zymogen AAP50871 is the inactive precursor form of human urokinase.
 CC Urokinase zymogen is cleaved into the two-chain form composed of
 CC characteristic urokinase H (molecular wt. of 30,000) and L (molecular
 CC wt. of 20,000) chains when treated with catalytic amounts of plasmin. The
 CC patentors claim a new urokinase zymogen which has mol. wt. ca. 50,000, a
 CC single chain molecular structure, and selective affinity for fibrin. It
 CC is a thrombolytic agent which manifests its plasminogen activator
 CC activity on cleavage by proteolytic enzymes (e.g. plasmin) and has higher
 CC affinity for fibrin than known forms of urokinase
 XX Sequence 411 AA;

Query Match 100.0%; Score 554; DB 1; Length 411;
 Best Local Similarity 100.0%; Pred. No. 2e-44;
 Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWSATVLCQTYHAHRSALQLGLGKHYCRNPDN 60
 DB 48 KTCYEGNGHFYRGKASTDTMGRPCLPWSATVLCQTYHAHRSALQLGLGKHYCRNPDN 107
 QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
 DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143

RESULT 38
 AAR06244
 ID AAR06244 standard; protein; 411 AA.

XX AAR06244;
 XX 07-DEC-1990 (first entry)

XX Urokinase precursor protein.
 XX Urokinase precursor; fibrinolysis; thrombolytic; cerebral thrombosis;
 KW myocardial infarction.


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XX OS Homo sapiens.
XX PN EP380334-A.
XX PD 01-AUG-1990.
XX PF 25-JAN-1990; 90EP-00300772.
XX PR 27-JAN-1989; 89JP-00016406.
XX PA 17-MAY-1989; 89JP-000121405.
XX (GREC ) GREEN CROSS CORP.
XX Matsuda H, Ueda Y, Tamanouchi K;
XX WPI; 1990-233117/31.
XX Urokinase precursor-lipid composite - used as thrombolytic agent, having
XX prolonged half-life in the blood, enhanced bioavailability and improved
XX activity.
XX Claim 3; Fig 1; 11pp; English.
XX By forming a precursor-lipid composite, the half-life of this
XX thrombolytic agent in the blood may be increased, exhibiting improved
XX activity without abnormal acceleration of fibrinolytic activity. Compound
XX is useful as a thrombolytic agent in treatment of cerebral thrombosis,
XX myocardial infarction etc
XX Sequence 411 AA;
SQ Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFGYKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 60
Db 48 KTCYEGNGHFGYKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 107

QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 96
Db 108 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 143

RESULT 39
AAR07904
ID AAR07904 standard; protein; 411 AA.
XX AC AAR07904;
XX DT 21-FEB-1991 (first entry)
XX DE Human pro-urokinase variant.
XX KW Thrombin; fibrin; bleeding; pHR27.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 10..42
XX FT Region /label= Epidermal growth factor (EGF) domain
XX FT Region 10..19
XX FT Region /label= First loop
XX FT Region 20..31
XX FT Active-site /label= Second loop
XX FT Region 27..29
XX FT Region /label= Modified site
XX FT Region 33..42
XX EP380362-A.
XX PN EP380362-A.

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PD 22-NOV-1990.
XX 18-MAY-1990; 90EP-00109473.
XX 18-MAY-1989; 89JP-00126434.
XX (GREC ) GREEN CROSS CORP.
XX Tarabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;
XX Arimura H;
XX WPI; 1990-350147/47.
XX DR N-PSDB; AAQ06135.
XX Human pro-urokinase variant - produced by recombinant methods, showing
XX increased half life in blood and high affinity for fibrin.
XX Disclosure; Fig 1; 27pp; English.
XX Modified pro-urokinase has a longer half-life in blood, and dissolves
XX thrombin without causing the spontaneous bleeding associated with
XX urokinase. The modification puts an epidermal growth factor domain into
XX the protein, containing the sequence Asn-X-Ser or Asn-X-Thr where X is
XX any residue. Plasmid pHR27 is disclosed as containing the modified
XX sequence
XX Sequence 411 AA;
SQ Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFGYKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 60
Db 48 KTCYEGNGHFGYKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 107

QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 96
Db 108 RRRPWCYVQVGLKPLVQECWVHDCADGKKPSPPEE 143

RESULT 40
AAR07902
ID AAR07902 standard; protein; 411 AA.
XX AC AAR07902;
XX DT 21-FEB-1991 (first entry)
XX DE Human pro-urokinase variant.
XX KW Thrombin; fibrin; bleeding; pHR22.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Domain 10..42
XX FT Region /label= Epidermal growth factor (EGF) domain
XX FT Region 10..19
XX FT Region /label= First loop
XX FT Region 20..31
XX FT Active-site /label= Second loop
XX FT Region 22..24
XX FT Region /label= Modified site
XX FT Region 33..42
XX EP380362-A.
XX PN EP380362-A.
XX PD 22-NOV-1990.
XX 18-MAY-1990; 90EP-00109473.
XX

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PR 18-MAY-1989; 89JP-00126434.
XX (GREC) GREEN CROSS CORP.
PA
XX
XX Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;
PI Arimura H;
XX
XX WPI; 1990-350147/47.
DR N-PSDB; AAQ06133.
XX
XX Human pro-urokinase variant - produced by recombinant methods, showing
PT increased half life in blood and high affinity for fibrin.
XX
XX Disclosure; Fig 1; 27pp; English.
XX
XX Modified pro-urokinase has a longer half-life in blood, and dissolves
CC thrombin without causing the spontaneous bleeding associated with
CC urokinase. The modification puts an epidermal growth factor domain into
CC the protein, containing the sequence Asn-X-Ser or Asn-X-Thr where X is
CC any residue. Plasmid pHR22 is disclosed as containing the modified
CC sequence
XX
SQ Sequence 411 AA;
Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPND 60
DB 48 KTCYEGNGHFYRGKASTDTMGRCPLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPND 107
QY 61 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 96
DB 108 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 143
RESULT 41
AAR07903
ID AAR07903 standard; protein; 411 AA.
XX
AC AAR07903;
XX
XX 21-FEB-1991 (first entry)
DT
XX Human pro-urokinase variant.
DE
XX Thrombin; fibrin; bleeding; pHR24.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 10..42 /label= Epidermal growth factor (EGF) domain
FT Region 10..19 /label= First loop
FT Region 20..31 /label= Second loop
FT Active-site 24..26 /label= Modified site
FT Region 33..42 /label= Third loop
XX
XX EP398362-A.
XX
XX 22-NOV-1990.
FD
XX 18-MAY-1990; 90EP-00109473.
PF
XX 18-MAY-1989; 89JP-00126434.
XX
XX (GREC) GREEN CROSS CORP.
PA
XX

PI Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;
PI Arimura H;
XX
XX WPI; 1990-350147/47.
DR N-PSDB; AAQ06133.
XX
XX Human pro-urokinase variant - produced by recombinant methods, showing
PT increased half life in blood and high affinity for fibrin.
XX
XX Disclosure; Fig 1; 27pp; English.
XX
XX Modified pro-urokinase has a longer half-life in blood, and dissolves
CC thrombin without causing the spontaneous bleeding associated with
CC urokinase. The modification puts an epidermal growth factor domain into
CC the protein, containing the sequence Asn-X-Ser or Asn-X-Thr where X is
CC any residue. Plasmid pHR24 is disclosed as containing the modified
CC sequence
XX
SQ Sequence 411 AA;
Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPND 60
DB 48 KTCYEGNGHFYRGKASTDTMGRCPLPWN SATVLQOTYHAHRSDALQLGLGKKNYCRNPND 107
QY 61 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 96
DB 108 RRRPWCYVQGLKPLVQECMVHDCADGKPSPPPEE 143
RESULT 42
AAR05117
ID AAR05117 standard; protein; 411 AA.
XX
AC AAR05117;
XX
XX 25-MAR-2003 (revised)
DT 04-OCT-1990 (first entry)
DT
XX UK-S3 as encoded by PUKS3.
DE
XX Urokinase; glycosylation.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Misc-difference 153 /label= synthetic mutation
FT /note= "old seq (Leu)"
FT Misc-difference 155 /label= synthetic mutation
FT /note= "old seq (Pro)"
XX
XX EP370205-A.
XX
XX 30-MAY-1990.
PD
XX 28-SEP-1989; 89EP-00117981.
PF
XX 29-SEP-1988; 88JP-00245705.
PR
XX (KYOW) KYOWA HAKKO KOGYO KK.
PA
XX Sasaki K, Nishi T, Yasumura S, Sato M, Itoh S;
PI
XX WPI; 1990-165029/22.
DR N-PSDB; AAQ04486.
XX
XX Polypeptide(s) with added carbohydrate chains - formed by modification of
PT aminoacid sequence, used to improve physio:chemical properties and/or

PT activities.

XX Disclosure; Page ?; 30pp; English.

XX The polypeptide is a deriv. of mature urokinase, designated UK-S3 which

CC has 2 amino acid substns. which result in an N-linked glycosylation site

CC giving the new protein improved stability and activity. See also AAR05113

CC -17. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-

CC 2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 411 AA;

XX Query Match 100.0%; Score 554; DB 2; Length 411;

XX Best Local Similarity 100.0%; Pred. No. 2e-44;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSALQLGLGKHNYCRNPDN 60

DB 48 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSALQLGLGKHNYCRNPDN 107

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96

DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 143

RESULT 43

AAW13634

ID AAW13634 standard; protein; 411 AA.

XX AC AAW13634;

XX 04-JUN-1997 (first entry)

XX Human native prourokinase.

XX Human; prourokinase; hPUK; variant; half-life; increase; EGF;

XX epidermal growth factor domain; deletion; thrombolysis; fibrinolysis.

XX Homo sapiens

XX Key Location/Qualifiers

XX Domain 10..42

XX /label= EGF domain

XX /note= "in claimed variants, at least part of the EGF

XX domain is deleted (see comments)"

XX Region 10..19

XX /label= first_loop

XX Region 20..31

XX /label= second_loop

XX Region 33..42

XX /label= third_loop

XX EP398361-A.

XX 22-NOV-1990.

XX 18-MAY-1990; 90EP-00109472.

XX 18-MAY-1989; 89JP-00126433.

XX 22-FEB-1990; 90JP-00042020.

XX (GREC) GREEN CROSS CORP.

XX Tanabe T, Amatsuji Y, Kasai S, Hirose M, Morita M, Kawabe H;

XX Airmura H;

XX WPI; 1990-350146/47.

XX N-PSDB; AAT61671.

XX Human prourokinase variants - deficient in loop regions of epidermal

XX growth factor, showing long blood half-life, as fibrinolytic agent.

XX Disclosure; Fig 1; 22pp; English.

XX Query Match 100.0%; Score 554; DB 2; Length 411;

XX Best Local Similarity 100.0%; Pred. No. 2e-44;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX New variants of human prourokinase (hPUK) comprise a hPUK deficient in

CC (i) at least part of the first loop region of the epidermal growth factor

CC (EGF) domain; (ii) at least part of the first loop and at least part of

CC the second loop; or (iii) at least part of the third loop. The hPUK

CC variants show an increased blood half-life comparable to that of the

CC whole EGF domain-deficient hPUK variant and urokinase while retaining the

CC same properties as those of hPUK. They have potent thrombolytic activity

CC and very little tendency to cause spontaneous bleeding. The present

CC sequence is that of the wild-type hPUK protein, including the EGF domain

XX Sequence 411 AA;

XX Query Match 100.0%; Score 554; DB 2; Length 411;

XX Best Local Similarity 100.0%; Pred. No. 2e-44;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSALQLGLGKHNYCRNPDN 60

DB 48 KTCYEGNGHFYRGKASTDTMGPRCLPWNATVLOQTYHAHRSALQLGLGKHNYCRNPDN 107

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96

DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 143

RESULT 44

AAW10057

ID AAR10057 standard; protein; 411 AA.

XX AC AAR10057;

XX 18-MAR-1991 (first entry)

XX Pro-urokinase derivative UK-T4 with Ser(153) and Thr(155).

XX pro-urokinase; UK-T4; plasminogen activator; myocardial infarction;

XX cerebral thrombosis.

XX Homo sapiens.

XX EP405285-A.

XX 02-JAN-1991.

XX 18-JUN-1990; 90EP-00111471.

XX 19-JUN-1989; 89JP-00156302.

XX (KYOW) KYOWA HAKKO KOGYO KK.

XX Yasamura S, Nishi T, Ito S;

XX WPI; 1991-008678/02.

XX N-PSDB; AAQ10169.

XX New plasminogen activator almost identical to natural prourokinase - is

XX thrombin resistant and used for prophylaxis-treatment of cerebral

XX thrombosis or myocardial infarction.

XX Disclosure; Page 8; 84pp; English.

XX UK-T4 is one example of a plasminogen activator which differs from

XX natural human prourokinase at positions 153 and 155 (Ileu substituted by

XX Ser; Pro substituted by Thr, respectively). The derivative has decreased

XX susceptibility to thrombin compared to natural type pro-UK and higher

XX specific activity. See also AAQ10168 and AAQ10170

XX Sequence 411 AA;

XX Query Match 100.0%; Score 554; DB 2; Length 411;

XX Best Local Similarity 100.0%; Pred. No. 2e-44;

XX Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOTYHAHRSDALQGLGKHNCRPN 60
DB 48 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOTYHAHRSDALQGLGKHNCRPN 107
QY 61 RRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96
DB 108 RRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 143

RESULT 45
AAR10058
ID AAR10058 standard; protein; 411 AA.
XX
AC AAR10058;
XX
DT 18-MAR-1991 (first entry)
XX
DE Pro-urokinase derivative UK-S3 with Asn(153) and Thr(155).
XX
KW pro-urokinase; UK-S3; plasminogen activator; myocardial infarction;
KW cerebral thrombosis.
XX
OS Homo sapiens.
XX
PN EP405285-A.
XX
PD 02-JAN-1991.
XX
PF 18-JUN-1990; 90EP-00111471.
XX
PR 19-JUN-1989; 89JP-00156302.
XX
PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
PI Yasamura S, Nishi T, Ito S;
XX
DR WPI; 1991-008678/02.
DR N-PSDB; AAQ10170.
XX
PT New plasminogen activator almost identical to natural pro-urokinase - is
PT thrombin resistant and used for prophylaxis-treatment of cerebral
PT thrombosis or myocardial infarction.
XX
PS Disclosure; Page 9; 84pp; English.
XX
CC UK-S3 is one example of a plasminogen activator which differs from
CC natural human pro-urokinase at positions 153 and 155. (Leu substituted by
CC Asn; Pro substituted by Thr, respectively). The derivative has decreased
CC susceptibility to thrombin compared to natural type pro-UK and higher
CC specific activity. See also AAQ10168 and AAQ10169
XX
SQ Sequence 411 AA;

Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOTYHAHRSDALQGLGKHNCRPN 60
DB 48 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOTYHAHRSDALQGLGKHNCRPN 107
QY 61 RRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96
DB 108 RRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 143

RESULT 46
AAR47956
ID AAR47956 standard; protein; 411 AA.
XX
AC AAR47956;
XX
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```
DT 10-FEB-1994 (first entry)
XX
DE PUK G16A G17A.
XX
KW Pre-urokinase; thrombolytic; blood; plasmid; mutant; PUK.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Domain 10..49
FT /label= EGF
FT Region 10..19
FT /label= Loop_1
FT Region 20..31
FT /label= Loop_2
FT Region 33..42
FT /label= Loop_3
XX
PN JP05192142-A.
XX
PD 03-AUG-1993.
XX
PF 20-JAN-1992; 92JP-00030178.
XX
PR 20-JAN-1992; 92JP-00030178.
XX
PA (GREC ) GREEN CROSS CORP.
XX
DR WPI; 1993-277461/35.
XX
PT Mutant human pre-urokinase - by replacing specified aminoacid(s) in N-
PT terminal for providing longer half-life in blood and higher thrombolytic
PT ability.
XX
PS Disclosure; Page 3; 26pp; Japanese.
XX
CC Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or
CC Tyr in the region ranging from residue 10 to 60 in the N-terminal of the
CC human PUK by Thr, Pro or Ala. These mutants have a longer half-life in
CC the blood and a higher thrombolytic ability. For examples see (AAR47956-
CC R47960)
XX
SQ Sequence 411 AA;

Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOTYHAHRSDALQGLGKHNCRPN 60
DB 48 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLQOTYHAHRSDALQGLGKHNCRPN 107
QY 61 RRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 96
DB 108 RRPWCYVQVGLKPLVQECMVHDCADGKKPSPPEE 143

RESULT 47
AAR47966
ID AAR47966 standard; protein; 411 AA.
XX
AC AAR47966;
XX
DT 10-FEB-1994 (first entry)
XX
DE PUK G16A.
XX
KW Pre-urokinase; thrombolytic; blood; plasmid; mutant; PUK.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Domain 10..49
```

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FT      Region      /label= EGF
FT      10..19
FT      /label= Loop_1
FT      20..31
FT      /label= Loop_2
FT      33..42
FT      /label= Loop_3
FT      XX
PN      JP05192142-A
XX
PD      03-AUG-1993
XX
XX      20-JAN-1992; 92JP-00030178.
XX
XX      20-JAN-1992; 92JP-00030178.
XX
XX      (GREC ) GREEN CROSS CORP.
XX
XX      WPI; 1993-277461/35.
XX
XX      Mutant human pre-urokinase - by replacing specified aminoacid(s) in N-
PT      terminal for providing longer half-life in blood and higher thrombolytic
PT      ability.
XX
XX      Disclosure; Page 3; 26pp; Japanese.
XX
XX      Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or
CC      Tyr in the region ranging from residue 10 to 60 in the N-terminal of the
CC      human PUK by Thr, Pro or Ala. These mutants have a longer half-life in
CC      the blood and a higher thrombolytic ability. For examples see (AAR47956-
CC      R47960)
XX
XX      Sequence 411 AA;
XX
XX      Query Match      100.0%; Score 554; DB 2; Length 411;
XX      Best Local Similarity 100.0%; Pred. No. 2e-44;
XX      Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      1 KTCYEGNGHFGYRGKASTDTMGRCPLPWSATVLCQTYHAHRSDALQLGLGKHNYCRNPDN 60
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DB      108 RRRPWCYVQGLKPLVQECWVHDCADGKKPSPPEE 143
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XX      AAR47962
XX      ID AAR47962 standard; protein; 411 AA.
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XX      AC AAR47962;
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XX      DT 10-FEB-1994 (first entry)
XX
XX      DE PUK G38A G39A.
XX
XX      KW Pre-urokinase; thrombolytic; blood; plasmid; mutant; PUK.
XX
XX      OS Homo sapiens.
XX
XX      FH Key      Location/Qualifiers
XX      FT Region 10..60
XX      FT /note= "Ser, Asn, Pro, Gly, or Tyr in the region 10 to 60
XX      FT in the N-terminal of the human PUK can be replaced by
XX      FT Thr, Pro or Ala"
XX      FT 10..49
XX      FT /label= EGF
XX      FT 10..19
XX      FT /label= Loop_1
XX      FT 20..31
XX      FT /label= Loop_2
XX      FT 33..42
XX      FT /label= Loop_3
XX      FT Misc-difference 64
XX      FT /note= "Thr encoded by AGT (sic)"
XX      FT Misc-difference 177
XX      FT /note= "Thr encoded by TAC (sic)"
XX
XX      PN JP05192142-A.
XX
XX      PD 03-AUG-1993.
XX

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PF 20-JAN-1992; 92JP-00030178.
XX PR 20-JAN-1992; 92JP-00030178.
XX PA (GREC) GREEN; CROSS CORP.
XX DR WPI; 1993-277461/35.
XX DR N-PSDB; AAQ48228.
XX PT Mutant human pre:urokinase - by replacing specified aminoacid(s) in N-
PT terminal for providing longer half-life in blood and higher thrombolytic
PT ability.
XX PS Claim 1; Page 14-16; 26pp; Japanese.
XX CC Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or
CC Tyr in the region ranging from residue 10 to 60 in the N-terminal of the
CC human PUK by Thr, Pro or Ala. These mutants have a longer half-life in
CC the blood and a higher thrombolytic ability. For examples see (AAR47956-
CC R47960)
XX SQ Sequence 411 AA;
Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. NO. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX AC AAR47965;
XX DT 10-FEB-1994 (first entry)
XX DE PUK N32P G38K G39K.
XX KW Pre-urokinase; thrombolytic; blood; plasmid; mutant; PUK.
XX OS Homo sapiens
XX FH Key
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XX FT 10..49
XX FT /label= EGF
XX FT Region
XX FT 10..19
XX FT /label= Loop_1
XX FT Region
XX FT 20..31
XX FT /label= Loop_2
XX FT Region
XX FT 33..42
XX FT /label= Loop_3
XX JP05192142-A.
XX PN 03-AUG-1993.
XX PD 20-JAN-1992; 92JP-00030178.
XX PF 20-JAN-1992; 92JP-00030178.
XX PR (GREC) GREEN; CROSS CORP.
XX PA WPI; 1993-277461/35.
XX DR Mutant human pre:urokinase - by replacing specified aminoacid(s) in N-
XX PT terminal for providing longer half-life in blood and higher thrombolytic
XX PT ability.

PT terminal for providing longer half-life in blood and higher thrombolytic
PT ability.
XX PS Disclosure; Page 3; 26pp; Japanese.
XX CC Human pre-urokinase can be modified by replacing: Ser, Asn, Pro, Gly, or
CC Tyr in the region ranging from residue 10 to 60 in the N-terminal of the
CC human PUK by Thr, Pro or Ala. These mutants have a longer half-life in
CC the blood and a higher thrombolytic ability. For examples see (AAR47956-
CC R47960)
XX SQ Sequence 411 AA;
Query Match 100.0%; Score 554; DB 2; Length 411;
Best Local Similarity 100.0%; Pred. NO. 2e-44;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 48 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQQTTHAHRSDALQGLGKHNCRNPDN 107
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Db 108 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 143
Search completed: May 25, 2004, 14:53:02
Job time : 24.4741 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2004, 14:53:05 ; Search time 17.5004 Seconds
(without alignments)
1530.046 Million cell updates/sec

Title: US-09-880-503-9

Perfect score: 554

Sequence: 1 KTCYEGNGHFYRGKASTDTM.....QECMVHDCADGKKRSPPEE 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying Chosen parameters: 1149313

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	554	100.0	143	9	US-09-880-503-8
3	554	100.0	337	14	US-10-106-698-6366
4	554	100.0	337	15	US-10-264-049-2927
5	554	100.0	411	9	US-09-880-503-3
6	554	100.0	431	9	US-09-264-4688-1
7	554	100.0	431	12	US-10-411-037-34
8	554	100.0	431	12	US-10-411-028-34
9	554	100.0	431	13	US-10-076-421-2
10	554	100.0	431	14	US-10-171-311-184
11	554	100.0	431	14	US-10-193-656-4
12	554	100.0	431	14	US-10-301-822-161
13	554	100.0	431	14	US-10-131-985-21
14	554	100.0	431	15	US-10-295-027-414
15	554	100.0	431	15	US-10-295-027-1275

16	554	100.0	431	16	US-10-410-962-34	Sequence 34, Appl
17	554	100.0	431	16	US-10-411-049-34	Sequence 34, Appl
18	554	100.0	437	12	US-10-087-192-594	Sequence 594, App
19	552	99.6	431	14	US-10-247-671-149	Sequence 149, App
20	545	98.4	431	12	US-10-282-174-562	Sequence 562, App
21	544	98.2	411	15	US-10-407-821-2	Sequence 2, Appl
22	543	98.0	445	15	US-10-360-101-266	Sequence 266, App
23	510	92.1	88	9	US-09-880-503-1	Sequence 1, Appl
24	510	92.1	135	9	US-09-880-503-4	Sequence 4, Appl
25	510	92.1	138	9	US-09-984-186-12	Sequence 12, Appl
26	510	92.1	138	14	US-10-237-667-12	Sequence 12, Appl
27	510	92.1	138	14	US-10-237-708-12	Sequence 12, Appl
28	510	92.1	138	14	US-10-237-866-12	Sequence 12, Appl
29	510	92.1	138	14	US-10-237-871-12	Sequence 12, Appl
30	510	92.1	138	14	US-10-237-624-12	Sequence 12, Appl
31	510	92.1	138	16	US-10-702-536-12	Sequence 12, Appl
32	510	92.1	138	16	US-10-702-636-12	Sequence 12, Appl
33	510	92.1	403	9	US-09-880-503-6	Sequence 6, Appl
34	504	91.0	322	12	US-10-424-999-21	Sequence 21, Appl
35	504	91.0	322	12	US-10-425-000-41	Sequence 41, Appl
36	504	91.0	322	15	US-10-233-675A-21	Sequence 21, Appl
37	500	90.3	687	12	US-10-424-999-17	Sequence 17, Appl
38	500	90.3	687	12	US-10-425-000-37	Sequence 37, Appl
39	500	90.3	687	13	US-10-233-675A-17	Sequence 17, Appl
40	499	90.1	86	12	US-10-424-999-5	Sequence 5, Appl
41	499	90.1	86	12	US-10-424-999-62	Sequence 62, Appl
42	499	90.1	86	12	US-10-425-000-97	Sequence 97, Appl
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45	499	90.1	87	12	US-10-424-999-9	Sequence 9, Appl
46	499	90.1	87	12	US-10-425-000-29	Sequence 29, Appl
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48	499	90.1	91	12	US-10-424-999-37	Sequence 37, Appl
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50	494	89.2	86	15	US-10-424-999-1	Sequence 1, Appl
51	494	89.2	86	15	US-10-233-675A-1	Sequence 1, Appl
52	494	89.2	87	12	US-10-424-999-10	Sequence 10, Appl
53	494	89.2	87	12	US-10-425-000-30	Sequence 30, Appl
54	494	89.2	87	15	US-10-233-675A-10	Sequence 10, Appl
55	494	89.2	91	12	US-10-424-999-35	Sequence 35, Appl
56	494	89.2	221	12	US-10-424-999-34	Sequence 34, Appl
57	494	89.2	322	12	US-10-424-999-20	Sequence 20, Appl
58	494	89.2	322	12	US-10-425-000-40	Sequence 40, Appl
59	494	89.2	322	15	US-10-233-675A-20	Sequence 20, Appl
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65	494	89.2	674	15	US-10-233-675A-14	Sequence 14, Appl
66	494	89.2	688	12	US-10-424-999-18	Sequence 18, Appl
67	494	89.2	688	12	US-10-425-000-38	Sequence 38, Appl
68	494	89.2	688	15	US-10-233-675A-18	Sequence 18, Appl
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ALIGNMENTS

RESULT 1
US-09-880-503-9
; Sequence 9, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Root
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND

; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-9

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Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2

US-09-880-503-8
; Sequence 8, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-8

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Best Local Similarity 100.0%; Pred. No. 2.1e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 143

RESULT 3

US-10-106-698-6266
; Sequence 6266, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA00591
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524

; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
; SEQ ID NO 6266
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-698-6266

Query Match 100.0%; Score 554; DB 14; Length 337;
Best Local Similarity 100.0%; Pred. No. 5.5e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-10-264-049-2927
; Sequence 2927, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2927
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-049-2927

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Best Local Similarity 100.0%; Pred. No. 5.5e-56;
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DB 74 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNCRNPDN 133
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
DB 134 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 169

RESULT 5

US-09-880-503-3
; Sequence 3, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13


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; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-3

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QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSPPEE 96
DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSPPEE 143

RESULT 6
US-09-264-468B-1
; Sequence 1, Application US/09264458B
; Patent No. US20020106778A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Jieyi
; APPLICANT: Nienaber, Vicki L.
; APPLICANT: Henkin, Jack
; APPLICANT: Smith, Richard A.
; APPLICANT: Walter, Karl A.
; APPLICANT: Severin, Jean M.
; APPLICANT: Edalji, Robinon
; APPLICANT: Johnson Jr., Robert W.
; APPLICANT: Holzman, Thomas F.
; TITLE OF INVENTION: HIGHLY CRYSTALLINE UROKINASE
; FILE REFERENCE: 6310.US.P1
; CURRENT APPLICATION NUMBER: US/09/264,468B
; PRIOR FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: US 09/036,361
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
; OTHER INFORMATION: Leader sequence
; NAME/KEY: VARIANT
; LOCATION: (279)...(279)
; OTHER INFORMATION: Xaa = any amino acid
; NAME/KEY: VARIANT
; LOCATION: (302)...(302)
; OTHER INFORMATION: Xaa = any amino acid
US-09-264-468B-1

Query Match          100.0%; Score 554; DB 9; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
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RESULT 7
US-10-411-037-34
; Sequence 34, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
; FILE REFERENCE: 040853-01-5082
; CURRENT APPLICATION NUMBER: US/10/411,037
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-037-34

Query Match          100.0%; Score 554; DB 12; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWN SATVLQQTYYAHRS DALQLGLGKHNYCRNPDN 60
DB 68 KTCYEGNGHFYRGKASTDTMGRCPLPWN SATVLQQTYYAHRS DALQLGLGKHNYCRNPDN 127

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSPPEE 163

RESULT 8
US-10-411-026-34
; Sequence 34, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
; FILE REFERENCE: 040853-01-5053
; CURRENT APPLICATION NUMBER: US/10/411,026
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
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; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-026-34

Query Match      100.0%; Score 554; DB 12; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOYVHAHRS DALQLGLGKHNYCNP DN 60
DB 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOYVHAHRS DALQLGLGKHNYCNP DN 127

QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKSPSPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECWVHDCADGKSPSPPEE 163

RESULT 9
US-10-076-421-2
; Sequence 2, Application US/10076421
; Publication No. US20020193304A1
; GENERAL INFORMATION:
; APPLICANT: WADA, MANABU
; APPLICANT: WADA, NAOKO
; TITLE OF INVENTION: ANTI-HIV AGENTS
; FILE REFERENCE: HAYAK-9
; CURRENT APPLICATION NUMBER: US/10/076,421
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: JP 2001-42655
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: JP 2001-184284
; PRIOR FILING DATE: 2001-06-19
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-076-421-2

Query Match      100.0%; Score 554; DB 13; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOYVHAHRS DALQLGLGKHNYCNP DN 60
DB 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOYVHAHRS DALQLGLGKHNYCNP DN 127

QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKSPSPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECWVHDCADGKSPSPPEE 163

RESULT 10
US-10-171-311-184
; Sequence 184, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
```

```
; APPLICANT: Chen, Yan
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171,311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-184

Query Match      100.0%; Score 554; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOYVHAHRS DALQLGLGKHNYCNP DN 60
DB 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOYVHAHRS DALQLGLGKHNYCNP DN 127

QY 61 RRRPWCYVQVGLKPLVQECWVHDCADGKSPSPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECWVHDCADGKSPSPPEE 163

RESULT 11
US-10-193-656-4
; Sequence 4, Application US/10193656
; Publication No. US20030096733A1
; GENERAL INFORMATION:
; APPLICANT: NY, Tor
; APPLICANT: HOLMDAHL, Rikard
; APPLICANT: LI, Jinan
; TITLE OF INVENTION: NOVEL DRUG TARGETS FOR ARTHRITIS
; FILE REFERENCE: 3810/1J577-US3
; CURRENT APPLICATION NUMBER: US/10/193,656
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/304,461
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/304,490
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,182
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: GenBank / P00749
; DATABASE ENTRY DATE: 1986-07-21
; RELEVANT RESIDUES: (1)..(431)
US-10-193-656-4

Query Match      100.0%; Score 554; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNCRNPDN 60
Db 68 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNCRNPDN 127
Qy 61 RRRPWCYVQGLKPLVQECMVHDCADGKKPSSPPEE 96
Db 128 RRRPWCYVQGLKPLVQECMVHDCADGKKPSSPPEE 163

RESULT 12
US-10-301-822-161
; Sequence 151, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: BURGART, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-161

Query Match 100.0%; Score 554; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNCRNPDN 60
Db 68 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNCRNPDN 127
Qy 61 RRRPWCYVQGLKPLVQECMVHDCADGKKPSSPPEE 96
Db 128 RRRPWCYVQGLKPLVQECMVHDCADGKKPSSPPEE 163

RESULT 13
US-10-131-985-21
; Sequence 21, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-21

Query Match 100.0%; Score 554; DB 14; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNCRNPDN 60
Db 68 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQLGLGKHNCRNPDN 127
Qy 61 RRRPWCYVQGLKPLVQECMVHDCADGKKPSSPPEE 96
Db 128 RRRPWCYVQGLKPLVQECMVHDCADGKKPSSPPEE 163

RESULT 14
US-10-295-027-414
; Sequence 414, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 414
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-414

Query Match 100.0%; Score 554; DB 15; Length 431;
US-10-295-027-414

Best Local Similarity 100.0%; Pred. No. 7.2e-56; Indels 0; Gaps 0;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHFGKASTDTMGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRNPDN 60
Db 68 KTCYEGNGHFGKASTDTMGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRNPDN 127
Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 128 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 163

RESULT 15
US-10-295-027-1275
; Sequence 1275, Application US/10295027
; Publication No. US2003023350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevez, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 1275 :
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1275

Query Match 100.0%; Score 554; DB 15; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHFGKASTDTMGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRNPDN 60
Db 68 KTCYEGNGHFGKASTDTMGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRNPDN 127
Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 128 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 163

RESULT 16
US-10-410-962-34
; Sequence 34, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
; TITLE OF INVENTION: GLYCOCONJUGATION OF G-CSF
; FILE REFERENCE: 040853-01-5054
; CURRENT APPLICATION NUMBER: US/10/410,962
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 34 :
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-962-34
Query Match 100.0%; Score 554; DB 16; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHFGKASTDTMGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRNPDN 60
Db 68 KTCYEGNGHFGKASTDTMGRPCLPWNSATVLQOYTHAHRSDALQGLGKHNYCRNPDN 127
Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 128 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 163

RESULT 17
US-10-411-049-34
; Sequence 34, Application US/10411049
; Publication No. US20040082026A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David
; APPLICANT: Chen, Xi
; APPLICANT: Bove, Caryn
; TITLE OF INVENTION: INTERPERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERPERON
; TITLE OF INVENTION: ALPHA
; FILE REFERENCE: 040853-01-5055
; CURRENT APPLICATION NUMBER: US/10/411,049
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/328,523
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/344,692

```
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/387,292
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: US 60/391,777
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/396,594
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US 60/404,249
; PRIOR FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 60/407,527
; PRIOR FILING DATE: 2002-08-28
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 34
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-411-049-34

Query Match      100.0%; Score 554; DB 16; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.2e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQGLGKKNYCRNPDN 60
Db 68 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQGLGKKNYCRNPDN 127

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKFPSSPPEE 96
Db 128 RRRPWCYVQVGLKPLVQECMVHDCADGKFPSSPPEE 163

RESULT 18
US-10-087-192-594
; Sequence 594, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 594
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-087-192-594

Query Match      100.0%; Score 554; DB 12; Length 437;
Best Local Similarity 100.0%; Pred. No. 7.3e-56;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQGLGKKNYCRNPDN 60
Db 74 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQGLGKKNYCRNPDN 133

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKFPSSPPEE 96
Db 134 RRRPWCYVQVGLKPLVQECMVHDCADGKFPSSPPEE 169

RESULT 19
US-10-247-671-149
; Sequence 149, Application US/10247671
; Publication No. US20030194721A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 149
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1453334CD1
US-10-247-671-149

Query Match      99.6%; Score 552; DB 14; Length 431;
Best Local Similarity 99.0%; Pred. No. 1.2e-55;
Matches 95; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQGLGKKNYCRNPDN 60
Db 68 KTCYEGNGHYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQGLGKKNYCRNPDN 127

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKFPSSPPEE 96
Db 128 RRRPWCYVQVGLKPLVQECMVHDCADGKFPSSPPEE 163

RESULT 20
US-10-282-174-562
; Sequence 562, Application US/10282174
; Publication No. US20030224380A1
; GENERAL INFORMATION:
; APPLICANT: Becker, Kenneth David
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Wang, Xin
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Bertram, Lars
; APPLICANT: Saunders, Alistair J.
; APPLICANT: Mullin, Kristina M.
; APPLICANT: Sampson, Andrew Johnson
; APPLICANT: Blacker, Deborah Lyne
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ON CHROMOSOME 10
; TITLE OF INVENTION: ASSOCIATED WITH ALZHEIMER'S DISEASE AND OTHER
; TITLE OF INVENTION: NEURODEGENERATIVE DISEASES
; FILE REFERENCE: 37481-3308
; CURRENT APPLICATION NUMBER: US/10/282,174
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: US 60/339,525
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/338,010
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/336,929
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/338,363
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: US 60/337,052
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/368,919
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 562
; LENGTH: 431
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 15, 58, 141, 214, 231, 274, 366
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-282-174-562

Query Match      98.4%; Score 545; DB 12; Length 431;
Best Local Similarity 99.0%; Pred. No. 8e-55;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPDN 60
DB 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPDN 127
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 163

RESULT 21
US-10-407-821-2
; Sequence 2, Application US/10407821
; Publication No. US20030219386A1
; GENERAL INFORMATION:
; APPLICANT: IDELL, STEVEN
; TITLE OF INVENTION: INTRAPLEURAL SINGLE-CHAIN UROKINASE ALONE OR COMPLEXED
; TITLE OF INVENTION: TO ITS SOLUBLE RECEPTOR PROTECTS AGAINST PLEURAL
; TITLE OF INVENTION: ADHESIONS IN TETRACYCLINE-INDUCED PLEURITIS IN RABBITS
; FILE REFERENCE: UTSN:022US
; CURRENT APPLICATION NUMBER: US/10/407,821
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/414,202
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: 60/370,466
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 411
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-407-821-2

Query Match      98.2%; Score 544; DB 15; Length 411;
Best Local Similarity 99.0%; Pred. No. 9.9e-55;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPDN 60
DB 48 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPDN 107
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143

RESULT 22
US-10-360-101-266
; Sequence 266, Application US/10360101
; Publication No. US20040009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 266
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; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of urokinase
US-10-360-101-266

Query Match      98.0%; Score 543; DB 15; Length 445;
Best Local Similarity 98.0%; Pred. No. 1.4e-54;
Matches 96; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTY--HAHRSALQLGLGKHNCRNP 58
DB 70 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYFTHAHRSDALQLGLGKHNCRNP 129
QY 59 DNRREPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
DB 130 DNRREPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 167

RESULT 23
US-09-880-503-1
; Sequence 1, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-1

Query Match      92.1%; Score 510; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPDN 60
DB 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQLGLGKHNCRNPDN 60
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
DB 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88

RESULT 24
US-09-880-503-4
; Sequence 4, Application US/09880503
; Patent No. US20020131964A1
; GENERAL INFORMATION:
; APPLICANT: CINES, Douglas B
; APPLICANT: HIGAZI, Abd Al-Roof
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
; TITLE OF INVENTION: TISSUE CONTRACTABILITY
; FILE REFERENCE: 9596-331
; CURRENT APPLICATION NUMBER: US/09/880,503
; CURRENT FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/212,847
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 135
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-4

Query Match          92.1%; Score 510; DB 9; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.6e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 60
Db 48 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 107

QY 61 RRPWCYVQVGLKPLVQECWVHDCADGK 88
Db 108 RRPWCYVQVGLKPLVQECWVHDCADGK 135

RESULT 25
US-09-984-186-12
; Sequence 12, Application US/09984186
; Patent No. US20020151011A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/984,186
; FILING DATE: 29-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-984-186-12      92.1%; Score 510; DB 9; Length 138;
Query Match

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-4

Query Match          92.1%; Score 510; DB 9; Length 135;
Best Local Similarity 100.0%; Pred. No. 2.6e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 60
Db 48 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 107

QY 61 RRPWCYVQVGLKPLVQECWVHDCADGK 88
Db 108 RRPWCYVQVGLKPLVQECWVHDCADGK 135

RESULT 26
US-10-237-667-12
; Sequence 12, Application US/10237667
; Publication No. US20030022306A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,667
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-667-12      92.1%; Score 510; DB 14; Length 138;
Query Match

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-4

Query Match          92.1%; Score 510; DB 9; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 60
Db 51 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 110

QY 61 RRPWCYVQVGLKPLVQECWVHDCADGK 88
Db 111 RRPWCYVQVGLKPLVQECWVHDCADGK 138

RESULT 26
US-10-237-667-12
; Sequence 12, Application US/10237667
; Publication No. US20030022306A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,667
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-667-12      92.1%; Score 510; DB 14; Length 138;
Query Match

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-503-4

Query Match          92.1%; Score 510; DB 9; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 60
Db 51 KTCYEGNGHFYRGKASTDTMGRPCLPWN SATVLQOITYHAHRS DALQLGLGKHNYCRNPDN 110

QY 61 RRPWCYVQVGLKPLVQECWVHDCADGK 88
Db 111 RRPWCYVQVGLKPLVQECWVHDCADGK 138

RESULT 26
US-10-237-667-12
; Sequence 12, Application US/10237667
; Publication No. US20030022306A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,667
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-667-12      92.1%; Score 510; DB 14; Length 138;
Query Match
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RESULT 28
US-10-237-866-12
; Sequence 12, Application US/10237866
; Publication No. US20030036171A1
; GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitten, Jean-Dominique
; Jung, Gerard
; Yen, Fatrice
;
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, COMPOSITION
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
;
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/237,866
; FILING DATE: 10-Sep-2002
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: 9-38,619
; REFERENCE/DOCKET NUMBER: SI92006-US
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
;
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
;
US-10-237-866-12
;
; Query Match 92.1%; Score 510; DB 14; Length 138;
; Best Local Similarity 100.0%; Pred. No. 2,7e-51;
; Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
QY 1 KTCYEGNGHYFGKASTDTMGPRCLPWSNATVLCQTYHAHRSALQGLGKHYCRNPDN 60
DB 51 KTCYEGNGHYFGKASTDTMGPRCLPWSNATVLCQTYHAHRSALQGLGKHYCRNPDN 110
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
DB 111 RRRPWCYVQVGLKPLVQECMVHDCADGK 138
;
RESULT 29
US-10-237-871-12
; Sequence 12, Application US/10237871

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Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEROF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (patentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38 619
REFERENCE/DOCKET NUMBER: SF92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-237-624-12
Query Match 92.1%; Score 510; DB 14; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFFYRGKASTDTWGRCLPWNSATVLQOYTHAHRSDALQLGLGKHNYCRNPDN 60
DB 51 KTCYEGNGHFFYRGKASTDTWGRCLPWNSATVLQOYTHAHRSDALQLGLGKHNYCRNPDN 110
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
DB 111 RRRPKCYVQVGLKPLVQECMVHDCADGK 138
RESULT 31
US-10-702-536-12
; Sequence 12, Application US/10702536
; Publication No. US20040086976A1
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guittou, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEROF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES

```

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/702,536
FILING DATE: 07-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-702-536-12
Query Match 92.1%; Score 510; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-702-536-12
QY 1 KTCYEGNGHFYRGKASTDTMGRCLPWN SATVLQOQTYHAHRS DALQLGLGKHN YCRNPDN 60
DB 51 KTCYEGNGHFYRGKASTDTMGRCLPWN SATVLQOQTYHAHRS DALQLGLGKHN YCRNPDN 110
QY 61 RRRPWCYVQGLKPLVQECMVHDCADGK 88
DB 111 RRRPWCYVQGLKPLVQECMVHDCADGK 138
RESULT 32
US-09-880-503-6
Sequence 6, Application US/09880503
Patent No. US20020131964A1
GENERAL INFORMATION:
APPLICANT: CINES, Douglas B
APPLICANT: HIGAZI, Abd Al-Roof
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING MUSCLE CELL AND
TITLE OF INVENTION: TISSUE CONTRACTILITY
FILE REFERENCE: 9596-331
CURRENT APPLICATION NUMBER: US/09/880,503
CURRENT FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/212,847
PRIOR FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 403
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-503-6
Query Match 92.1%; Score 510; DB 9; Length 403;

NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/702,536
FILING DATE: 07-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-702-536-12
Query Match 92.1%; Score 510; DB 16; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
US-10-702-536-12
QY 1 KTCYEGNGHFYRGKASTDTMGRCLPWN SATVLQOQTYHAHRS DALQLGLGKHN YCRNPDN 60
DB 51 KTCYEGNGHFYRGKASTDTMGRCLPWN SATVLQOQTYHAHRS DALQLGLGKHN YCRNPDN 110
QY 61 RRRPWCYVQGLKPLVQECMVHDCADGK 88
DB 111 RRRPWCYVQGLKPLVQECMVHDCADGK 138
RESULT 32
US-10-702-636-12
Sequence 12, Application US/10702636
Publication No. US20040086977A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, COMPOSITION
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville

```
Best Local Similarity 100.0%; Pred. No. 8.7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 60
Db 48 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 107

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
Db 108 RRRPWCYVQVGLKPLVQECMVHDCADGK 135

RESULT 34
US-10-424-999-21
; Sequence 21, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein human abrogen
US-10-424-999-21

Query Match 91.0%; Score 504; DB 12; Length 322;
Best Local Similarity 93.5%; Pred. No. 3.4e-50;
Matches 87; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 60
Db 2 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 61

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSP 93
Db 62 RRRPWCYVQVGLKPLVQECMVHDCADRLPRGP 94

RESULT 35
US-10-425-000-41
; Sequence 41, Application US/10425000
; Publication No. US2004005277A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanchette, Francis
; TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
; TITLE OF INVENTION: Angiogenesis
; FILE REFERENCE: ST01027-B
; CURRENT APPLICATION NUMBER: US/10/425,000
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human derived fusion protein
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US-10-425-000-41

Query Match 91.0%; Score 504; DB 12; Length 322;
Best Local Similarity 93.5%; Pred. No. 3.4e-50;
Matches 87; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 60
Db 2 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 61

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSP 93
Db 62 RRRPWCYVQVGLKPLVQECMVHDCADRLPRGP 94

RESULT 36
US-10-233-675A-21
; Sequence 21, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods fo
; TITLE OF INVENTION: Them To Inhibit Angiogenesis
; FILE REFERENCE: ST01027
; CURRENT APPLICATION NUMBER: US/10/233,675A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 322
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein human abrogen
US-10-233-675A-21

Query Match 91.0%; Score 504; DB 15; Length 322;
Best Local Similarity 93.5%; Pred. No. 3.4e-50;
Matches 87; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 60
Db 2 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRSDALQLGLGKHN YCRNPDN 61

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPKSP 93
Db 62 RRRPWCYVQVGLKPLVQECMVHDCADRLPRGP 94

RESULT 37
US-10-424-999-17
; Sequence 17, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbitt, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanchette, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods fo
; TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 687
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein human abrogen
US-10-424-999-17

Query Match          90.3%; Score 500; DB 12; Length 687;
Best Local Similarity 98.9%; Pred. No. 2.3e-49;
Matches 86; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 60
Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 61
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
Db 62 RRRPWCYVQVGLKPLVQECMVHDCADG 88

RESULT 38
US-10-425-000-37
; Sequence 37, Application US/10425000
; Publication No. US20040052777A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; TITLE OF INVENTION: Krigle Polypeptides and Methods for Using Them to Inhibit
; FILE REFERENCE: ST01027-B
; CURRENT APPLICATION NUMBER: US/10/425,000
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human derived fusion protein
US-10-425-000-37

Query Match          90.3%; Score 500; DB 12; Length 687;
Best Local Similarity 98.9%; Pred. No. 2.3e-49;
Matches 86; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 60
Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 61
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
Db 62 RRRPWCYVQVGLKPLVQECMVHDCADG 88

RESULT 39
US-10-233-675A-17
; Sequence 17, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027
; CURRENT APPLICATION NUMBER: US/10/233,675A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
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```
; SEQ ID NO 17
; LENGTH: 687
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein human abrogen
US-10-233-675A-17

Query Match          90.3%; Score 500; DB 15; Length 687;
Best Local Similarity 98.9%; Pred. No. 2.3e-49;
Matches 86; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 60
Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 61
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
Db 62 RRRPWCYVQVGLKPLVQECMVHDCADG 88

RESULT 40
US-10-424-999-5
; Sequence 5, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human abrogen
US-10-424-999-5

Query Match          90.1%; Score 499; DB 12; Length 86;
Best Local Similarity 100.0%; Pred. No. 3e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 60
Db 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQGLGKHNCRPN 60
QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
Db 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

RESULT 41
US-10-424-999-62
; Sequence 62, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
```

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; CURRENT APPLICATION NUMBER: US/10/233,675A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human derived abrogen
US-10-233-675A-5

Query Match          90.1%; Score 499; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 3e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCVEGNHGYRGKASDTTNGRCLPWN SATVLQQTVAHRS DALQLGLGKHNYCRNPDN 60
DB 1 KTCVEGNHGYRGKASDTTNGRCLPWN SATVLQQTVAHRS DALQLGLGKHNYCRNPDN 60

QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
DB 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

RESULT 44
US-10-233-675A-22
; Sequence 22, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Them To Inhibit Angiogenesis
; FILE REFERENCE: ST01027
; CURRENT APPLICATION NUMBER: US/10/233,675A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of human urokinase plasminogen activator
US-10-233-675A-22

Query Match          90.1%; Score 499; DB 15; Length 86;
Best Local Similarity 100.0%; Pred. No. 3e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCVEGNHGYRGKASDTTNGRCLPWN SATVLQQTVAHRS DALQLGLGKHNYCRNPDN 60
DB 1 KTCVEGNHGYRGKASDTTNGRCLPWN SATVLQQTVAHRS DALQLGLGKHNYCRNPDN 60

QY 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
DB 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86

RESULT 45
US-10-424-999-9
; Sequence 9, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis

```

```
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; PRIOR FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human abrogen as secreted from pME063 (abrogen D43)
US-10-424-999-9

Query Match          90.1%; Score 499; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.1e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 60
Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 61

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
Db 62 RRRPWCYVQVGLKPLVQECMVHDCAD 87

RESULT 46
US-10-425-000-29
; Sequence 29, Application US/10425000
; Publication No. US20040052777A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Kringle Polypeptides and Methods for Using Them to Inhibit
; FILE OF INVENTION: Angiogenesis
; FILE REFERENCE: ST01027-B
; CURRENT APPLICATION NUMBER: US/10/425,000
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 105
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human abrogen (D43)
US-10-425-000-29

Query Match          90.1%; Score 499; DB 12; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.1e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 60
Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 61

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
Db 62 RRRPWCYVQVGLKPLVQECMVHDCAD 87

RESULT 47
US-10-233-675A-9
; Sequence 9, Application US/10233675A
; Publication No. US20030228298A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Nesbit, Mark
; APPLICANT: Fong, Timothy
; APPLICANT: Brockstedt, Dirk
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027
; CURRENT APPLICATION NUMBER: US/10/233,675A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/316,300
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human derived fusion protein
US-10-233-675A-9

Query Match          90.1%; Score 499; DB 15; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.1e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 60
Db 2 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 61

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
Db 62 RRRPWCYVQVGLKPLVQECMVHDCAD 87

RESULT 48
US-10-424-999-37
; Sequence 37, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Nesbit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; FILE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 37
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Abrogen D43
US-10-424-999-37

Query Match          90.1%; Score 499; DB 12; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.2e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 60
Db 6 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOTYHAHRS DALQLGLGKHNYCRNP DN 65

Qy 61 RRRPWCYVQVGLKPLVQECMVHDCAD 86
Db 66 RRRPWCYVQVGLKPLVQECMVHDCAD 91

RESULT 49
US-10-424-999-36
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Search completed: May 25, 2004, 15:03:49
Job time : 18.5004 secs

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; Sequence 36, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Neebit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 36
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: TrxA-Abrogen D43 fusion protein
US-10-424-999-36

Query Match          90.1%; Score 499; DB 12; Length 221;
Best Local Similarity 100.0%; Pred. No. 8.6e-50;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNCRNPDN 60
Db 136 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNCRNPDN 195

QY 61 RRPWCYVQVGLKPLVQECWVHDCAD 86
Db 196 RRPWCYVQVGLKPLVQECWVHDCAD 221

RESULT 50
US-10-424-999-1
; Sequence 1, Application US/10424999
; Publication No. US20040052810A1
; GENERAL INFORMATION:
; APPLICANT: Neebit, Mark
; APPLICANT: Cameron, Beatrice
; APPLICANT: Blanche, Francis
; TITLE OF INVENTION: Abrogen Polypeptides, Nucleic Acids Encoding Them and Methods for
; TITLE OF INVENTION: Using Them to Inhibit Angiogenesis
; FILE REFERENCE: ST01027-A
; CURRENT APPLICATION NUMBER: US/10/424,999
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: 10/233,675
; PRIOR FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Human abrogen N43
US-10-424-999-1

Query Match          89.2%; Score 494; DB 12; Length 86;
Best Local Similarity 98.8%; Pred. No. 1.1e-49;
Matches 85; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Db 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLQOTYHAHRSDALQLGLGKHNCRNPDN 60

QY 61 RRPWCYVQVGLKPLVQECWVHDCAD 86
Db 61 RRPWCYVQVGLKPLVQECWVHDCAD 86
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 25, 2004, 14:48:05 ; Search time 6.6468 Seconds
(without alignments)
745.636 Million cell updates/sec

Title: US-09-880-503-9

Perfect score: 554

Sequence: 1 KTCVGNHGFYRGKASTDTM.....QECMVHDCADGKFPSPPEE 96

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/iaa/6A_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	100.0	200	4	US-09-101-272G-73
2	554	100.0	208	4	US-09-101-272G-98
3	554	100.0	365	1	US-08-093-741-83
4	554	100.0	365	1	US-08-720-012-83
5	554	100.0	393	2	US-08-560-098A-44
6	554	100.0	393	3	US-08-367-024C-24
7	554	100.0	393	3	US-08-967-024C-25
8	554	100.0	411	1	US-08-087-163-1
9	554	100.0	411	1	US-08-286-748B-18
10	554	100.0	411	1	US-08-453-799-18
11	554	100.0	411	1	US-09-403-736-2
12	554	100.0	430	1	US-07-942-157A-3
13	554	100.0	431	4	US-09-101-272G-1
14	554	100.0	431	6	5188829-1
15	554	100.0	432	2	US-08-560-098A-47
16	544	98.2	411	3	US-09-181-816-1
17	543	98.0	411	2	US-08-560-098A-48
18	538.5	97.2	430	6	5219569-2
19	530	95.7	157	3	US-08-142-590B-25
20	510	92.1	138	2	US-08-787-689-12
21	510	92.1	138	4	US-09-984-186-12
22	505	91.2	194	4	US-09-101-272G-80
23	505	91.2	201	4	US-09-101-272G-96
24	489	88.3	87	4	US-09-101-272G-62
25	241	43.5	477	2	US-08-560-098A-51
26	226	40.8	527	1	US-07-609-510B-16
27	226	40.8	527	2	US-08-811-949-39

ALIGNMENTS

RESULT 1
US-09-101-272G-73
; Sequence 73, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101.272G
; CURRENT FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

28	226	40.8	527	5	PCT-US91-01025A-2	Sequence 2, Appli
29	226	40.8	527	6	5185259-8	Patent No. 5185259
30	226	40.8	527	6	5520913-1	Patent No. 5520913
31	226	40.8	546	6	5200340-6	Patent No. 5200340
32	226	40.8	562	2	US-08-811-949-43	Sequence 43, Appl
33	226	40.8	562	2	US-08-560-098A-50	Sequence 50, Appl
34	226	40.8	562	2	US-08-883-795A-38	Sequence 38, Appl
35	226	40.8	562	4	US-09-703-695A-4	Sequence 4, Appli
36	226	40.8	562	6	5185259-3	Patent No. 5185259
37	226	40.8	562	6	5200340-2	Patent No. 5200340
38	226	40.8	562	6	5344773-2	Patent No. 5344773
39	221.5	40.0	356	1	US-08-427-640-8	Sequence 8, Appli
40	221	39.9	437	2	US-08-811-949-49	Sequence 49, Appl
41	221	39.9	437	2	US-08-811-949-51	Sequence 51, Appl
42	221	39.9	437	2	US-08-811-949-55	Sequence 55, Appl
43	221	39.9	437	2	US-08-811-949-57	Sequence 57, Appl
44	220.5	39.8	378	4	US-09-553-498-10	Sequence 10, Appl
45	220.5	39.8	378	4	US-09-618-869-10	Sequence 10, Appl
46	219.5	39.6	389	2	US-08-811-949-67	Sequence 67, Appl
47	218.5	39.4	386	4	US-09-111-977-3	Sequence 3, Appli
48	218.5	39.4	355	1	US-08-137-116-1	Sequence 1, Appli
49	218.5	39.4	355	1	US-08-217-618-1	Sequence 1, Appli
50	218.5	39.4	355	1	US-08-427-640-2	Sequence 2, Appli
51	218.5	39.4	355	1	US-08-217-617A-1	Sequence 1, Appli
52	218.5	39.4	355	1	US-08-217-616-1	Sequence 1, Appli
53	218.5	39.4	355	2	US-08-811-949-45	Sequence 45, Appl
54	218.5	39.4	355	2	US-08-811-949-47	Sequence 47, Appl
55	218.5	39.4	355	2	US-08-811-949-53	Sequence 53, Appl
56	218.5	39.4	355	3	US-08-811-949-51	Sequence 51, Appl
57	218.5	39.4	355	6	5223256-1	Patent No. 5223256
58	218.5	39.4	389	2	US-08-811-949-65	Sequence 65, Appl
59	218.5	39.4	472	2	US-08-811-949-63	Sequence 63, Appl
60	218.5	39.4	562	6	524676-5	Patent No. 524676
61	216.5	39.1	354	2	US-08-811-949-61	Sequence 61, Appl
62	215	38.8	347	2	US-08-811-949-59	Sequence 59, Appl
63	215	38.8	355	2	US-08-811-949-59	Sequence 59, Appl
64	213.5	38.5	355	1	US-08-427-640-6	Sequence 6, Appli
65	213	38.4	83	2	US-08-811-949-2	Sequence 2, Appli
66	204	36.8	356	1	US-08-427-640-4	Sequence 4, Appli
67	194.5	35.1	655	1	US-08-148-910-12	Sequence 12, Appl
68	194.5	35.1	655	1	US-08-448-337A-12	Sequence 12, Appl
69	154	27.8	458	3	US-09-039-609-2	Sequence 2, Appli
70	152	27.4	812	4	US-08-991-761A-7	Sequence 7, Appli
71	149	26.9	810	4	US-08-991-761A-11	Sequence 11, Appl
72	148.5	26.8	711	1	US-08-184-012C-8	Sequence 8, Appli
73	148.5	26.8	711	1	US-08-334-177-2	Sequence 2, Appli
74	148.5	26.8	711	2	US-08-666-082B-1	Sequence 1, Appli
75	148.5	26.8	711	2	US-08-786-382-2	Sequence 2, Appli

; OTHER INFORMATION: ATP domain of uPA
US-09-101-272G-73

Query Match 100.0%; Score 554; DB 4; Length 200;
Best Local Similarity 100.0%; Pred. No. 3e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHYRGKASTDTMGRCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDN 60
Db 68 KTCYEGNGHYRGKASTDTMGRCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDN 127
Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 128 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 163

RESULT 2
US-09-101-272G-98
; Sequence 98, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101.272G
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 98
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ATFHI-ML chimeric protein
US-09-101-272G-98

Query Match 100.0%; Score 554; DB 4; Length 208;
Best Local Similarity 100.0%; Pred. No. 3.2e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHYRGKASTDTMGRCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDN 60
Db 49 KTCYEGNGHYRGKASTDTMGRCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDN 108
Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 109 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 144

RESULT 3
US-08-093-741-83
; Sequence 83, Application US/08093741
; Patent No. 5681721
; GENERAL INFORMATION:
; APPLICANT: STEFFENS, GERD J.
; APPLICANT: WENDET, STEPHAN
; APPLICANT: SCHNEIDER, JOHANNES
; APPLICANT: HEINZEL-WIELAND, REGINA
; APPLICANT: SAUNDERS, DEREK J.
; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
; TITLE OF INVENTION: INHIBITING EFFECT
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N. W. Suite 700
; CITY: Washington, D.C.
; COUNTRY: U.S.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093.741
; FILING DATE: 20-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P43 23 754.1
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/41345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)628-8800
; TELEFAX: (202)628-8844
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-093-741-83

Query Match 100.0%; Score 554; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 6.2e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 62 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 97

RESULT 4
US-08-720-012-83
; Sequence 83, Application US/08720012
; Patent No. 5747291
; GENERAL INFORMATION:
; APPLICANT: STEFFENS, GERD J.
; APPLICANT: WENDET, STEPHAN
; APPLICANT: SCHNEIDER, JOHANNES
; APPLICANT: HEINZEL-WIELAND, REGINA
; APPLICANT: SAUNDERS, DEREK J.
; TITLE OF INVENTION: BIFUNCTIONAL UROKINASE VARIANTS WITH
; TITLE OF INVENTION: IMPROVED FIBRINOLYTIC CHARACTERISTICS AND THROMBIN
; TITLE OF INVENTION: INHIBITING EFFECT
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N. W. Suite 700
; CITY: Washington, D.C.
; COUNTRY: U.S.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/720.012
; FILING DATE: 27-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093.741
; FILING DATE: 20-JUL-1993
; APPLICATION NUMBER: DE P43 23 754.1
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.

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;
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/41345
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)628-8800
; TELEFAX: (202)628-8844
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-720-012-83
;
Query Match 100.0%; Score 554; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 6.2e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 60
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Db 2 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 61
;
QY 61 RRRPWCYVQVGLKPLVQECMWHDCADGKKPSSPPEE 96
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Db 62 RRRPWCYVQVGLKPLVQECMWHDCADGKKPSSPPEE 97
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RESULT 5
US-08-560-098A-44
; Sequence 44, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WENNDT, Stephan
; APPLICANT: STEFFENS, Gerd Josef
; APPLICANT: HEINZEL-WIELAND, Regina
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE: 17-NOV-1995
; APPLICATION NUMBER: US/08/560,098A
; PRIORITY DATE: 17-NOV-1995
; APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-560-098A-44
;
Query Match 100.0%; Score 554; DB 2; Length 393;
Best Local Similarity 100.0%; Pred. No. 6.8e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 3 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 62
;
QY 61 RRRPWCYVQVGLKPLVQECMWHDCADGKKPSSPPEE 96
;
Db 63 RRRPWCYVQVGLKPLVQECMWHDCADGKKPSSPPEE 98
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;
RESULT 6
US-08-967-024C-24
; Sequence 24, Application US/08967024C
; Patent No. 6133011
; GENERAL INFORMATION:
; APPLICANT: WENNDT, Stephan
; APPLICANT: STEFFENS, Gerd Josef
; APPLICANT: JANOCHA, Elke
; APPLICANT: HEINZEL-WIELAND, Regina
; TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: P 44 42 665.8
; FILING DATE: 30-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42444
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 393 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-967-024C-24
;
Query Match 100.0%; Score 554; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 6.8e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 60
;
Db 3 KTCYEGNGHFYRGKASTDTMGPRCLPWN SATVLQOQTYHAHRS DALQLGLGKHNYCRNPDN 62
;
QY 61 RRRPWCYVQVGLKPLVQECMWHDCADGKKPSSPPEE 96
;
Db 63 RRRPWCYVQVGLKPLVQECMWHDCADGKKPSSPPEE 98
;
;
RESULT 7
US-08-967-024C-25
; Sequence 25, Application US/08967024C
; Patent No. 6133011
; GENERAL INFORMATION:
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APPLICANT: WENEDT, Stephan
APPLICANT: STEFFENS, Gerd Josef
APPLICANT: JANOSCH, Elke
APPLICANT: HEINZEL-WIELAND, Regina
TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Stevenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,024C
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 42 565.8
FILING DATE: 30-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42444
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-967-024C-25

Query Match 100.0%; Score 554; DB 3; Length 393;
Best Local Similarity 100.0%; Pred. No. 6.8e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHYRGKASTDTWGRCLPWNSTVLOQTYHAHRSDALQGLGKHNCRNPDN 60
Db 3 KTCYEGNGHYRGKASTDTWGRCLPWNSTVLOQTYHAHRSDALQGLGKHNCRNPDN 62
Qy 61 RRRPWCYVQGLKPLVQECMVHDCADGKXSSPPEE 96
Db 63 RRRPWCYVQGLKPLVQECMVHDCADGKXSSPPEE 98

RESULT 8
US-08-087-163-1
Sequence 1, Application US/08087163
Patent No. 5472692
GENERAL INFORMATION:
APPLICANT: Liu, Jian-Ning
APPLICANT: Gurewicz, Victor
TITLE OF INVENTION: PRO-UKINASE MUTANTS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,163
FILING DATE: 07/02/93
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04353/003001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 411
TYPE: amino acid
STRANDEDNESS: N/A
TOPOLOGY: N/A
US-08-087-163-1

Query Match 100.0%; Score 554; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 7.2e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KTCYEGNGHYRGKASTDTWGRCLPWNSTVLOQTYHAHRSDALQGLGKHNCRNPDN 60
Db 48 KTCYEGNGHYRGKASTDTWGRCLPWNSTVLOQTYHAHRSDALQGLGKHNCRNPDN 107
Qy 61 RRRPWCYVQGLKPLVQECMVHDCADGKXSSPPEE 96
Db 108 RRRPWCYVQGLKPLVQECMVHDCADGKXSSPPEE 143

RESULT 9
US-08-286-748B-18
Sequence 18, Application US/08286748B
Patent No. 5759542
GENERAL INFORMATION:
APPLICANT: Victor Gurewicz
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DELIVERY
TITLE OF INVENTION: OF DRUGS BY PLATELETS FOR THE TREATMENT OF
TITLE OF INVENTION: CARDIOVASCULAR AND OTHER DISEASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,748B
FILING DATE: August 5, 1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J. Peter Fasse
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04547/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

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;
;
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; US-08-286-748B-18
;
; Query Match 100.0%; Score 554; DB 1; Length 411;
; Best Local Similarity 100.0%; Pred. No. 7.2e-58;
; Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 60
; DB 48 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 107
;
; QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
; DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
;
; RESULT 10
; US-08-153-799-18
; Sequence 18, Application US/08153799
; Patent No. 5765883
; GENERAL INFORMATION:
; APPLICANT: Ballance, David J
; APPLICANT: Goodey, Andrew R
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: R Hain Swope, BOC Health Care Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,799
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847975
; FILING DATE: 06-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8909916.2
; FILING DATE: 29-APR-1989
; PRIOR APPLICATION DATA: PCT/GB90/00650
; FILING DATE: 26-APR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/775952
; FILING DATE: 29-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Swope, R Hain
; REGISTRATION NUMBER: 24864
; REFERENCE/DOCKET NUMBER: 92H832
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 665 2400
; TELEFAX: (908) 771 6159
; TELEX: 219484
;
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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US-08-153-799-18
Query Match 100.0%; Score 554; DB 1; Length 411;
Best Local Similarity 100.0%; Pred. No. 7.2e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 60
DB 48 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 107
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
RESULT 11
US-09-403-736-2
Sequence 2, Application US/09403736
Patent No. 6638502
GENERAL INFORMATION:
APPLICANT: Aventis S.A.
APPLICANT: Li, Hong
APPLICANT: LU, He
APPLICANT: GRISCELLI, Frank
APPLICANT: OPOLON, Paule
APPLICANT: SORIA, Claudine
APPLICANT: RAGOT, Thierry
APPLICANT: LAGRANDE, Yves
APPLICANT: SORIA, Jeanette
APPLICANT: MABILAT, Christelle
APPLICANT: PERRICAUDET, Michel
APPLICANT: YEH, Patrice
TITLE OF INVENTION: Adenovirus-Mediated Intratumoral Delivery Of An Angiogenesis Ant
TITLE OF INVENTION: For The Treatment Of Tumors
FILE REFERENCE: A2778A-US
CURRENT APPLICATION NUMBER: US/09/403,736
CURRENT FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/EP98/02491
PRIOR FILING DATE: 1998-11-05
PRIOR APPLICATION NUMBER: 60/044,980
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patent in version 3.0
SEQ ID NO 2
LENGTH: 411
TYPE: PRT
ORGANISM: humanurokinase
US-09-403-736-2
Query Match 100.0%; Score 554; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 7.2e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 60
DB 48 KTCYEGNGHFYRGKASTDTMGRCPLPWSATVLOQTYHAHRSDALQGLGKHNYCRNPDN 107
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 96
DB 108 RRRPWCYVQVGLKPLVQECMVHDCADGKKPSSPPEE 143
RESULT 12
US-07-942-157A-3
Sequence 3, Application US/07942157A
Patent No. 5648253
GENERAL INFORMATION:
APPLICANT: Wei, Cha-Mer
TITLE OF INVENTION: Inhibitor-Resistant Urokinase
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street Suite 2800
```

CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/942.157A
FILING DATE: 19920908
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/631673
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: TS1108Cont.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)815-6508
TELEFAX: (404)815-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..19
OTHER INFORMATION: /label= peptide
OTHER INFORMATION: /note= "WAP signal"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 198..203
OTHER INFORMATION: /label= modified
OTHER INFORMATION: /note= "six amino acids deleted in mutant"
US-07-942-157A-3
Query Match 100.0%; Score 554; DB 1; Length 430;
Best Local Similarity 100.0%; Pred. No. 7.6e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 67 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 126
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 96
DB 127 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 162
RESULT 13
US-09-101-272G-1
Sequence 1, Application US/09101272G
Patent No. 6509445
GENERAL INFORMATION:
APPLICANT: Nissin Food Products Co., Ltd.
TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
FILE REFERENCE: Q50979
CURRENT APPLICATION NUMBER: US/09/101.272G
CURRENT FILING DATE: 1998-07-08
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patent in version 3.1
SEQ ID NO 1
LENGTH: 431
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: mat_peptide
LOCATION: (21)..()
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (20)..()
OTHER INFORMATION: Urokinase-type plasminogen activator (uPA)
US-09-101-272G-1
Query Match 100.0%; Score 554; DB 4; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.6e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 127
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 163
RESULT 14
5188829-1
Patent No. 5188829
APPLICANT: KOBAYASHI, YO-ICHI-OMORI, MUNAKI, YAMADA, CHIKAKO
TITLE OF INVENTION: RAPIDLY ACTING PROTEINASE
NUMBER OF SEQUENCES: 23
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/340.007
FILING DATE: 18-AUG-1988
SEQ ID NO: 1
LENGTH: 431
5188829-1
Query Match 100.0%; Score 554; DB 6; Length 431;
Best Local Similarity 100.0%; Pred. No. 7.6e-58;
Matches 96; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 60
DB 68 KTCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSDALQLGLGKHNYCRNPDN 127
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 96
DB 128 RRRPWCYVQVGLKPLVQECMVHDCADGKPSPPPEE 163
RESULT 15
US-08-560-098A-47
Sequence 47, Application US/08560098A
Patent No. 5976841
GENERAL INFORMATION:
APPLICANT: WENDEL, Stephan
APPLICANT: HEINZEL-WISLAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1300 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560.098A

;; FILING DATE: 17-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: P 44 40 892.7
;; FILING DATE: 17-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D.
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 148/42448
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 47:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 432 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-560-098A-47:

Query Match 100.0%; Score 554; DB 2; Length 432;
Best Local Similarity 100.0%; Pred. No. 7.6e-58;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 60
Db 69 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 128

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 129 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 164

RESULT 16
US-09-181-816-1
;; Sequence 1, Application US/09181816
;; Patent No. 6277818
;; GENERAL INFORMATION:
;; APPLICANT: MAZAR, Andrew P.
;; APPLICANT: JONES, Terence R.
;; TITLE OF INVENTION: CYCLIC PEPTIDE LIGANDS THAT TARGET UROKINASE
;; FILE REFERENCE: 329042000300 SIDN 1-7
;; CURRENT APPLICATION NUMBER: US/09/181,816
;; CURRENT FILING DATE: 1998-10-29
;; NUMBER OF SEQ ID NOS: 7
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 1
;; LENGTH: 411
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-09-181-816-1

Query Match 98.2%; Score 544; DB 3; Length 411;
Best Local Similarity 99.0%; Pred. No. 1.1e-56;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 60
Db 48 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 107

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 108 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 143

RESULT 17
US-08-560-098A-48
;; Sequence 48, Application US/08560098A
;; Patent No. 5976841
;; GENERAL INFORMATION:
;; APPLICANT: WENNDT, Stephan
;; APPLICANT: HEINZEL-WIELAND, Regina

Query Match 97.2%; Score 538.5; DB 6; Length 430;
Best Local Similarity 99.0%; Pred. No. 5.3e-56;
Matches 95; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 60

;; APPLICANT: STEFFENS, Gerd Josef
;; TITLE OF INVENTION: Proteins Having Fibrinolytic and
;; APPLICATION: Coagulation-inhibiting Properties
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
;; STREET: 1200 G Street, N.W., Suite 700
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/560,098A
;; FILING DATE: 17-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: P 44 40 892.7
;; FILING DATE: 17-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D.
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 148/42448
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 48:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 411 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-560-098A-48

Query Match 98.0%; Score 543; DB 2; Length 411;
Best Local Similarity 99.0%; Pred. No. 1.5e-56;
Matches 95; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 60
Db 48 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 107

QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 96
Db 108 RRRPWCYVQVGLKPLVQECMVHDCADGKSPSPPEE 143

RESULT 18
5219569-2
;; Patent No. 5219569
;; APPLICANT: BLABER, MICHAEL; HEYNEKER, HERBERT L.; VEHAR,
;; GORDON A.
;; TITLE OF INVENTION: PROTEASE RESISTANT UROKINASE
;; NUMBER OF SEQUENCES: 6
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/766,858
;; FILING DATE: 16-AUG-1985
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 725,468
;; FILING DATE: 22-APR-1985
;; SEQ ID NO: 2
;; LENGTH: 430
;; 5219569-2

Query Match 97.2%; Score 538.5; DB 6; Length 430;
Best Local Similarity 99.0%; Pred. No. 5.3e-56;
Matches 95; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 KTCYEGNGHYRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHYCRNPDN 60

Db 68 KTCYEGNGHFRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHNCRPN 127
Qy 61 RRRPWCYVQVGLKPLVQECMWHDCADGKXPSPPEE 96
Db 128 RRRPWCYVQVGLKPLVQECMWHDCADG-KPSPPEE 162

RESULT 19
US-08-142-590B-25
; Sequence 25, Application US/08142590B
; Patent No. 6120765
; GENERAL INFORMATION:
; APPLICANT: HIBINO, Taahiko, TAKAHASHI, Tadahito; HORII, Izumi; and GORTINCK,
; TITLE OF INVENTION: UROKINASE PLASMINOGEN ACTIVATOR FRAGMENTS
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,590B
; FILING DATE: 25-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/042,318
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Paul L.
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: MGP-009CP
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 157 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-142-590B-25

Query Match 95.78; Score 530; DB 3; Length 157;
Best Local Similarity 95.8; Pred. No. 1.6e-55;
Matches 92; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHNCRPN 60
Db 48 KTCYEGNGHFRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHNCRPN 107

Qy 61 RRRPWCYVQVGLKPLVQECMWHDCADGKXPSPPEE 96
Db 108 RRRPWCYVQVGLKPLVQECMWHDCADGKXPSPPEE 143

RESULT 20
US-08-797-689-12
; Sequence 12, Application US/08797689
; Patent No. 5878969
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; APPLICANT: Fournier, Alain
; APPLICANT: Guitton, Jean-Dominique
; APPLICANT: Jung, Gerard
; APPLICANT: Yeh, Patrice

; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; TITLE OF INVENTION: PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/797,689
; FILING DATE: 31-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,927
; FILING DATE: 28-JUL-1994
; APPLICATION NUMBER: FR 92/01064
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR93/00085
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith Ph.D., Julie K.
; REGISTRATION NUMBER: P-38,619
; REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3839
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 138 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-797-689-12

Query Match 92.1; Score 510; DB 2; Length 138;
Best Local Similarity 100.0; Pred. No. 3.4e-53;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTCYEGNGHFRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHNCRPN 60
Db 51 KTCYEGNGHFRGKASTDTMGRCLPWN SATVLQQTTHAHRSDALQLGLGKHNCRPN 110

Qy 61 RRRPWCYVQVGLKPLVQECMWHDCADGK 88
Db 111 RRRPWCYVQVGLKPLVQECMWHDCADGK 138

RESULT 21
US-09-984-186-12
; Sequence 12, Application US/09984186
; Patent No. 6686179
; GENERAL INFORMATION:
; APPLICANT: Fleer, Reinhard
; Fournier, Alain
; Guitton, Jean-Dominique
; Jung, Gerard
; Yeh, Patrice
; TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
; PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
; CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43

```

; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: System 7.1
; SOFTWARE: Word 5.1 (Patentin)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/984,186
;   FILING DATE: 29-Oct-2001
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/797,689
;   FILING DATE: 31-JAN-1997
;   APPLICATION NUMBER: US 08/256,927
;   FILING DATE: 28-JUL-1994
;   APPLICATION NUMBER: FR 92/01064
;   FILING DATE: 31-JAN-1992
;   APPLICATION NUMBER: PCT/FR93/00085
;   FILING DATE: 28-JAN-1993
;   NAME: Smith Ph.D., Julie K.
;   REGISTRATION NUMBER: P-38,619
;   REFERENCE/DOCKET NUMBER: ST92006-US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (610) 454-3839
;   TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 12:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 138 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-984-186-12

Query Match          92.1%; Score 510; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 3.4e-53;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYYAHRSDALQLGLGKHNYCRNPDN 60
Db 51 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYYAHRSDALQLGLGKHNYCRNPDN 110
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADGK 88
Db 111 RRRPWCYVQVGLKPLVQECMVHDCADGK 138

RESULT 22
US-09-101-272G-80
; Sequence 80, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
US-09-101-272G-80

Query Match          91.2%; Score 505; DB 4; Length 194;
Best Local Similarity 100.0%; Pred. No. 2e-52;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYYAHRSDALQLGLGKHNYCRNPDN 60
Db 49 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYYAHRSDALQLGLGKHNYCRNPDN 108
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
Db 109 RRRPWCYVQVGLKPLVQECMVHDCADG 135

RESULT 23
US-09-101-272G-96
; Sequence 96, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 96
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ATFHI-CL chimeric protein
US-09-101-272G-96

Query Match          91.2%; Score 505; DB 4; Length 201;
Best Local Similarity 100.0%; Pred. No. 2.1e-52;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYYAHRSDALQLGLGKHNYCRNPDN 60
Db 49 KTCYEGNGHYRGKASTDTMGRPCLPWNSATVLQQTYYAHRSDALQLGLGKHNYCRNPDN 108
QY 61 RRRPWCYVQVGLKPLVQECMVHDCADG 87
Db 109 RRRPWCYVQVGLKPLVQECMVHDCADG 135

RESULT 24
US-09-101-272G-62
; Sequence 62, Application US/09101272G
; Patent No. 6509445
; GENERAL INFORMATION:
; APPLICANT: Nissin Food Products Co., Ltd.
; TITLE OF INVENTION: CANCEROUS METASTASIS INHIBITOR
; FILE REFERENCE: Q50979
; CURRENT APPLICATION NUMBER: US/09/101,272G
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: JP 1059/1996
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 62
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: residues 43-131 of the ATF domain of uPA
US-09-101-272G-62

Query Match          88.3%; Score 489; DB 4; Length 89;
Best Local Similarity 100.0%; Pred. No. 6.3e-51;
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Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLOQTYHAHRSALQLGLGKHNCRPN 60
Db 6 KTCYEGNGHYRGKASTDTMGRCPLPNSATVLOQTYHAHRSALQLGLGKHNCRPN 65
QY 61 RRRPWCYVQVGLKPLVQECMVHDC 84
Db 66 RRRPWCYVQVGLKPLVQECMVHDC 89

RESULT 25
US-08-560-098A-51
; Sequence 51, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WENDT, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEPFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-560-098A-51

Query Match 43.5%; Score 241; DB 2; Length 477;
Best Local Similarity 50.0%; Pred. No. 1.7e-20;
Matches 42; Conservative 12; Mismatches 30; Indels 0; Gaps 0;
QY 2 TCYEGNGHYRGKASTDTMGRCPLPNSATVLOQTYHAHRSALQLGLGKHNCRPN 61
Db 127 TCYEQGVYRGTWSTESGACINWNSNLLTRTYNGRRSDAITLGLGHNCRPN 186
QY 62 RRPWCYVQVGLKPLVQECMVHDC 85
Db 187 SKPWCYVIKASKFILEFCSPVCS 210

RESULT 26
US-07-609-510B-16
; Sequence 16, Application US/07609510B
; Patent No. 5326700
```

```
; GENERAL INFORMATION:
; APPLICANT: Berg et al.
; TITLE OF INVENTION: Method for Altering Post-Translational Processing of Tissue PI
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: U.S.A.
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
; COMPUTER: Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/609,510B
; FILING DATE: 19901106
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-609-510B-16

Query Match 40.8%; Score 226; DB 1; Length 527;
Best Local Similarity 47.7%; Pred. No. 1.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
QY 2 TCYEGNGHYRGKASTDTMGRCPLPNSATVLOQTYHAHRSALQLGLGKHNCRPN 61
Db 91 TCYEDQGISYRGTWSTAESGAECTNWNSSALAQKPYSGRRPDAIRLGLGHNCRPN 150
QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
Db 151 SKPWCYVFKACKYSSEFCSTPACSEG 176

RESULT 27
US-08-811-949-39
; Sequence 39, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-966-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-811-949-39

Query Match 40.8%; Score 226; DB 2; Length 527;
Best Local Similarity 47.7%; Pred. No. 1.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDR 61
DB 91 TCYEDQGISYRGTWSTAESGAECTWNSSALAKPKYSGRPDALRLGLGNHNYCRNPDR 150

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
DB 151 SKPWCYVFKAGKYSSEFCSTPACSEG 176

RESULT 29
5185259-8
; Patent No. 5185259
; APPLICANT: GOEDDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
; VEEAR, GORDON A.
; TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
; ACTIVATOR
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/489,855
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 12,694
; FILING DATE: 09-FEB-1987
; APPLICATION NUMBER: 483,052
; FILING DATE: 07-APR-1983
; APPLICATION NUMBER: 398,003
; FILING DATE: 14-JUL-1982
; APPLICATION NUMBER: 374,860
; FILING DATE: 05-MAY-1982
; SEQ ID NO: 8:
; LENGTH: 527
5185259-8

Query Match 40.8%; Score 226; DB 6; Length 527;
Best Local Similarity 47.7%; Pred. No. 1.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDR 61
DB 91 TCYEDQGISYRGTWSTAESGAECTWNSSALAKPKYSGRPDALRLGLGNHNYCRNPDR 150

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
DB 151 SKPWCYVFKAGKYSSEFCSTPACSEG 176

RESULT 30
5520913-1
; Patent No. 5520913
; APPLICANT: ANDERSON, STEPHEN; BENNETT, WILLIAM F.; BOTSTEIN,
; DAVID; HIGGINS, DEBORAH L.; PAONI, NICHOLAS F.; ZOLLER, MARK J.
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR HAVING
; ZMOGENIC PROPERTIES
; NUMBER OF SEQUENCES: 35
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/88,451
; FILING DATE: 06-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 770,510
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: 384,608
; FILING DATE: 24-JUL-1989
; APPLICATION NUMBER: 240,856
; FILING DATE: 02-SEP-1988
; SEQ ID NO: 1:
; LENGTH: 527
5520913-1

Query Match 40.8%; Score 226; DB 6; Length 527;
Best Local Similarity 47.7%; Pred. No. 1.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDR 61
DB 91 TCYEDQGISYRGTWSTAESGAECTWNSSALAKPKYSGRPDALRLGLGNHNYCRNPDR 150

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
DB 151 SKPWCYVFKAGKYSSEFCSTPACSEG 176

RESULT 30
5520913-1
; Patent No. 5520913
; APPLICANT: ANDERSON, STEPHEN; BENNETT, WILLIAM F.; BOTSTEIN,
; DAVID; HIGGINS, DEBORAH L.; PAONI, NICHOLAS F.; ZOLLER, MARK J.
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR HAVING
; ZMOGENIC PROPERTIES
; NUMBER OF SEQUENCES: 35
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/88,451
; FILING DATE: 06-JUL-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 770,510
; FILING DATE: 03-OCT-1991
; APPLICATION NUMBER: 384,608
; FILING DATE: 24-JUL-1989
; APPLICATION NUMBER: 240,856
; FILING DATE: 02-SEP-1988
; SEQ ID NO: 1:
; LENGTH: 527
5520913-1

Query Match 40.8%; Score 226; DB 5; Length 527;
Best Local Similarity 47.7%; Pred. No. 1.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

PCT-US91-01025A-2
; Sequence 2, Application PC/TUS9101025A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin
; CLONING INFORMATION: Specific Properties
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01025A
; FILING DATE: 19910214
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/486,657
; FILING DATE: 1 March 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 454P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; PCT-US91-01025A-2

Query Match 40.8%; Score 226; DB 5; Length 527;
Best Local Similarity 47.7%; Pred. No. 1.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLOQTYHAHRSALQGLGKHNYCRNPDR 61
DB 91 TCYEDQGISYRGTWSTAESGAECTWNSSALAKPKYSGRPDALRLGLGNHNYCRNPDR 150

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
DB 151 SKPWCYVFKAGKYSSEFCSTPACSEG 176

RESULT 28
PCT-US91-01025A-2
; Sequence 2, Application PC/TUS9101025A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Tissue Plasminogen Activator Having Fibrin
; CLONING INFORMATION: Specific Properties
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01025A
; FILING DATE: 19910214
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/486,657
; FILING DATE: 1 March 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 454P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 527 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; PCT-US91-01025A-2

Query Match 40.8%; Score 226; DB 5; Length 527;
Best Local Similarity 47.7%; Pred. No. 1.1e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
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Db 91 TCYEDQGISYRGWTSAESGAECTNNSSALAQPKYSGRPPDAIRLGLGNHNYCRNPDNR 150
QY 62 RRPWCYVQVGLKPLVQECVHDCADG 87
Db 151 SKPCWCVFKAGKYSSEFCSTPACSEG 176

RESULT 31
US-08-811-949-43
Patent No. 5200340
APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINGJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
ACTIVATORS
NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/53,412
FILING DATE: 22-MAY-1987
SEQ ID NO: 6:
LENGTH: 546
5200340-6

Query Match 40.8%; Score 226; DB 6; Length 546;
Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLTQTYHAHRSDALQGLGKHNYCRNPDNR 61
Db 126 TCYEDQGISYRGWTSAESGAECTNNSSALAQPKYSGRPPDAIRLGLGNHNYCRNPDNR 185
QY 62 RRPWCYVQVGLKPLVQECVHDCADG 87
Db 186 SKPCWCVFKAGKYSSEFCSTPACSEG 211

RESULT 32
US-08-811-949-43
Sequence 43, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-43

Query Match 40.8%; Score 226; DB 2; Length 562;
Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLTQTYHAHRSDALQGLGKHNYCRNPDNR 61
Db 126 TCYEDQGISYRGWTSAESGAECTNNSSALAQPKYSGRPPDAIRLGLGNHNYCRNPDNR 185
QY 62 RRPWCYVQVGLKPLVQECVHDCADG 87
Db 186 SKPCWCVFKAGKYSSEFCSTPACSEG 211

RESULT 33
US-08-560-098A-50
Sequence 50, Application US/08560098A
Patent No. 5576841
GENERAL INFORMATION:
APPLICANT: WENDT, Stephan
APPLICANT: HEINZEL-WIELAND, Regina
APPLICANT: STEFFENS, Gerd Josef
TITLE OF INVENTION: Proteins having Fibrinolytic and
Coagulation-inhibiting Properties
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/560,098A
FILING DATE: 17-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: P 44 40 892.7
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D.
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 148/42448
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 562 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-560-098A-50

Query Match 40.8%; Score 226; DB 2; Length 562;
Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLTQTYHAHRSDALQGLGKHNYCRNPDNR 61
Db 126 TCYEDQGISYRGWTSAESGAECTNNSSALAQPKYSGRPPDAIRLGLGNHNYCRNPDNR 185

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QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
:|||||:
DB 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 34
US-08-883-795A-38
; Sequence 38, Application US/08883795A
; Patent No. 5985607
; GENERAL INFORMATION:
; APPLICANT: Delcuve, Genevieve
; APPLICANT: Awang, Gregor
; TITLE OF INVENTION: Recombinant DNA Molecules and Expression
; TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BERSKIN & PARR
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3Y2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/883,795A
; FILING DATE: 27-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 7841-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 562 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein (tpa)
US-08-883-795A-38

Query Match 40.8%; Score 226; DB 2; Length 562;
Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQQLGLGKHNYCRNPDNR 61
:|||||:
DB 126 TCYEDQGISYRGWTSTAESGAECTNNSSALAKPYSGRRPDAIRLGLGNHNYCRNPDNR 185

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
:|||||:
DB 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 35
US-09-703-695A-4
; Sequence 4, Application US/09703695A
; Patent No. 6593097
; GENERAL INFORMATION:
; APPLICANT: Xu, Yuan
; TITLE OF INVENTION: REVERSE-PHASE HPLC ASSAY FOR PLASMINOGEN ACTIVATORS
; FILE REFERENCE: P1798R1
; CURRENT APPLICATION NUMBER: US/09/703,695A
; CURRENT FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: US 60/163,607
; PRIOR FILING DATE: 1999-11-04

Query Match 40.8%; Score 226; DB 6; Length 562;
Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQQLGLGKHNYCRNPDNR 61
:|||||:
DB 126 TCYEDQGISYRGWTSTAESGAECTNNSSALAKPYSGRRPDAIRLGLGNHNYCRNPDNR 185

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
:|||||:
DB 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 36
US-08-883-795A-38
; Patent No. 5185259
; APPLICANT: GOEDDEL, DAVID V.; KOHR, WILLIAM J.; PENNICA, DIANE;
; VEHAR, GORDON A.
; TITLE OF INVENTION: TRUNCATED HUMAN TISSUE PLASMINOGEN
; ACTIVATOR
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/489,855
; FILING DATE: 02-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 12,694
; FILING DATE: 09-FEB-1987
; APPLICATION NUMBER: 483,052
; FILING DATE: 07-APR-1983
; APPLICATION NUMBER: 398,003
; FILING DATE: 14-JUL-1982
; APPLICATION NUMBER: 374,860
; FILING DATE: 05-MAY-1982
; SEQ ID NO: 3:
; LENGTH: 562
5185259-3

Query Match 40.8%; Score 226; DB 6; Length 562;
Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQOQTYHAHRSDALQQLGLGKHNYCRNPDNR 61
:|||||:
DB 126 TCYEDQGISYRGWTSTAESGAECTNNSSALAKPYSGRRPDAIRLGLGNHNYCRNPDNR 185

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
:|||||:
DB 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 37
US-09-703-695A-4
; Patent No. 5200340
; APPLICANT: FOSTER, DONALD C.; MULVIHILL, EILEEN R.; O'HARA,
; PATRICK J.; PINGEL, KURT; YOSHITAKE, SHINJI
; TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
; ACTIVATORS
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/53,412
; FILING DATE: 22-MAY-1987
; SEQ ID NO: 2:
; LENGTH: 562
5200340-2

Query Match 40.8%; Score 226; DB 6; Length 562;
```

Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGPCLPWNSATVLOOTYHAHRSALQGLGKHNYCRNPDR 61
DB 126 TCYEDQGISYRGTWSTAESGAECTNWNSSALQPKYSGRRPDAIRLGLGNHNYCRNPDRD 185

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
DB 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 38
5344773-2
Patent No. 5344773
APPLICANT: WEI, CHA-MER; HSIUNG, NANCY; REDDY, VERMURI B.;
LEMONTT, JEFFREY P.; DACKOWSKI, WILLIAM; DOUGLAS, RICHARD;
COLE, EDWARD S.; PURCELL JR., RICHARD D.; LAU, DAVID TAI-YUI
TITLE OF INVENTION: HUMAN UTERINE TISSUE PLASMINOGEN
ACTIVATOR PRODUCED BY RECOMBIANT DNA
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/782,686
FILING DATE: 01-OCT-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 656,770
FILING DATE: 01-OCT-1984
SEQ ID NO: 2:
LENGTH: 562
5344773-2

Query Match 40.8%; Score 226; DB 6; Length 562;
Best Local Similarity 47.7%; Pred. No. 1.2e-18;
Matches 41; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 2 TCYEGNGHFYRGKASTDTMGPCLPWNSATVLOOTYHAHRSALQGLGKHNYCRNPDR 61
DB 126 TCYEDQGISYRGTWSTAESGAECTNWNSSALQPKYSGRRPDAIRLGLGNHNYCRNPDRD 185

QY 62 RRPWCYVQVGLKPLVQECMVHDCADG 87
DB 186 SKPCYVFKAGKYSSEFCSTPACSEG 211

RESULT 39
US-08-427-640-8
Sequence 8, Application US/08427640
Patent No. 5659788
GENERAL INFORMATION:
APPLICANT: Berg et al.
TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
CITY: Indianapolis
STATE: IN.
COUNTRY: U.S.A.
ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,640
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/689,410
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 356 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-427-640-8

Query Match 40.0%; Score 221.5; DB 1; Length 356;
Best Local Similarity 44.2%; Pred. No. 2.4e-18;
Matches 42; Conservative 12; Mismatches 40; Indels 1; Gaps 1;

QY 2 TCYEGNGHFYRGKASTDTMGPCLPWNSATVLOOTYHAHRSALQGLGKHNYCRNPDR 61
DB 8 TCYEDQGISYRGTWSTAESGAECTNWNSSALQPKYSGRRPDAIRLGLGNHNYCRNPDRD 67

QY 62 RRPWCYVQVGLKPLVQECMVHDCAD-GKKPSSPPE 95
DB 68 AKPWCHLVKNNRLTWEYCDVPCSCSTCGLRQVYSQPO 102

RESULT 40
US-08-811-949-49
Sequence 49, Application US/08811949
Patent No. 5840533
GENERAL INFORMATION:
APPLICANT: NIWA, MINEO
APPLICANT: SAITO, YOSHIMASA
APPLICANT: SASAKI, HITOSHI
APPLICANT: HAYASHI, MASAKO
APPLICANT: NOTANI, JOUJI
APPLICANT: KOBAYASHI, MASAKAZU
TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-811-949-49

Query Match 39.9%; Score 221; DB 2; Length 437;
Best Local Similarity 47.1%; Pred. No. 3.6e-18;
Matches 40; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGPCLPWNSATVLOOTYHAHRSALQGLGKHNYCRNPDR 62
DB 2 CYEDQGISYRGTWSTAESGAECTNWNSSALQPKYSGRRPDAIRLGLGNHNYCRNPDRS 61

QY 63 RRPWCYVQVGLKPLVQECMVHDCADG 87

Db 62 KPWCYVFKAGKYSFCSFPCACSEG 86

RESULT 41

US-08-811-949-51

Sequence 51, Application US/08811949

Patent No. 5840533

GENERAL INFORMATION:

APPLICANT: NIWA, MINEO

APPLICANT: SAITO, YOSHIMASA

APPLICANT: SASAKI, HITOSHI

APPLICANT: HAYASHI, MASAKO

APPLICANT: NOTANI, JOUJI

APPLICANT: KOBAYASHI, MASAKAZU

TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/811,949

FILING DATE: 05-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 18-966-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-811-949-51

Query Match 39.9%; Score 221; DB 2; Length 437;

Best Local Similarity 47.1%; Pred. No. 3.6e-18;

Matches 40; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGPRCLPWN SATVLQQTYYHAHRS DALQLGLGKHN YCRNPDRR 62

Db 2 CYEDQGISYRGTWSTAESGAECTNWNSSALAKPYSGRPRDAIRLGLGNHNYCNPDRDS 61

QY 63 RPWCYVQVGLKPLVQECMVHDCADG 87

Db 62 KPWCYVFKAGKYSFCSFPCACSEG 86

RESULT 42

US-08-811-949-55

Sequence 55, Application US/08811949

Patent No. 5840533

GENERAL INFORMATION:

APPLICANT: NIWA, MINEO

APPLICANT: SAITO, YOSHIMASA

APPLICANT: SASAKI, HITOSHI

APPLICANT: HAYASHI, MASAKO

APPLICANT: NOTANI, JOUJI

APPLICANT: KOBAYASHI, MASAKAZU

TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/811,949

FILING DATE: 05-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 18-966-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-811-949-51

Query Match 39.9%; Score 221; DB 2; Length 437;

Best Local Similarity 47.1%; Pred. No. 3.6e-18;

Matches 40; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGPRCLPWN SATVLQQTYYHAHRS DALQLGLGKHN YCRNPDRR 62

Db 2 CYEDQGISYRGTWSTAESGAECTNWNSSALAKPYSGRPRDAIRLGLGNHNYCNPDRDS 61

QY 63 RPWCYVQVGLKPLVQECMVHDCADG 87

Db 62 KPWCYVFKAGKYSFCSFPCACSEG 86

RESULT 43

US-08-811-949-57

Sequence 57, Application US/08811949

Patent No. 5840533

GENERAL INFORMATION:

APPLICANT: NIWA, MINEO

APPLICANT: SAITO, YOSHIMASA

APPLICANT: SASAKI, HITOSHI

APPLICANT: HAYASHI, MASAKO

APPLICANT: NOTANI, JOUJI

APPLICANT: KOBAYASHI, MASAKAZU

TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/811,949

FILING DATE: 05-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 18-966-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-811-949-55

Query Match 39.9%; Score 221; DB 2; Length 437;

Best Local Similarity 47.1%; Pred. No. 3.6e-18;

Matches 40; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGPRCLPWN SATVLQQTYYHAHRS DALQLGLGKHN YCRNPDRR 62

Db 2 CYEDQGISYRGTWSTAESGAECTNWNSSALAKPYSGRPRDAIRLGLGNHNYCNPDRDS 61

QY 63 RPWCYVQVGLKPLVQECMVHDCADG 87

Db 62 KPWCYVFKAGKYSFCSFPCACSEG 86

RESULT 44

US-08-811-949-59

Sequence 59, Application US/08811949

Patent No. 5840533

GENERAL INFORMATION:

APPLICANT: NIWA, MINEO

APPLICANT: SAITO, YOSHIMASA

APPLICANT: SASAKI, HITOSHI

APPLICANT: HAYASHI, MASAKO

APPLICANT: NOTANI, JOUJI

APPLICANT: KOBAYASHI, MASAKAZU

TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/811,949

FILING DATE: 05-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 18-966-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 437 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-811-949-51

Query Match 39.9%; Score 221; DB 2; Length 437;

Best Local Similarity 47.1%; Pred. No. 3.6e-18;

Matches 40; Conservative 9; Mismatches 36; Indels 0; Gaps 0;

QY 3 CYEGNGHFYRGKASTDTMGPRCLPWN SATVLQQTYYHAHRS DALQLGLGKHN YCRNPDRR 62

Db 2 CYEDQGISYRGTWSTAESGAECTNWNSSALAKPYSGRPRDAIRLGLGNHNYCNPDRDS 61

QY 63 RPWCYVQVGLKPLVQECMVHDCADG 87

Db 62 KPWCYVFKAGKYSFCSFPCACSEG 86

RESULT 45

US-08-811-949-61

Sequence 61, Application US/08811949

Patent No. 5840533

GENERAL INFORMATION:

APPLICANT: NIWA, MINEO

APPLICANT: SAITO, YOSHIMASA

APPLICANT: SASAKI, HITOSHI

APPLICANT: HAYASHI, MASAKO

APPLICANT: NOTANI, JOUJI

APPLICANT: KOBAYASHI, MASAKAZU

TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/811,949

FILING DATE: 05-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 18-966-0

<

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/811.949
;; FILING DATE: 05-MAR-1997
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: OBLON, NORMAN F.
;; REGISTRATION NUMBER: 24,618
;; REFERENCE/DOCKET NUMBER: 18-966-0
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-413-3000
;; TELEFAX: 703-413-2220
;; INFORMATION FOR SEQ ID NO: 57:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 437 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: Protein
US-08-811-949-57

Query Match 39.9%; Score 221; DB 2; Length 437;
Best Local Similarity 47.1%; Pred. No. 3.5e-18;
Matches 40; Conservative 9; Mismatches 36; Indels 0; Gaps 0;
Qy 3 CYEGNGHYRGKASTDTMGRCPLPWSATVLQOQTYHAHRSDALQLGLGKHYCRNPDR 62
Db 2 CYEDGHSYRGTSAGTWSALAQKPYSGRRPDAIRLGLGNHNYCRNPDRDS 61
Qy 63 RWCYVQVGLKPLVQECMVHDCADG 87
Db 62 KPCVYFKAGKYSSEFCSTPACSEG 86

RESULT 44
US-09-553-498-10
; Sequence 10, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwarz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553.498
; CURRENT FILING DATE: 2000-04-20
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 10
; LENGTH: 378
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-10

Query Match 39.8%; Score 220.5; DB 4; Length 378;
Best Local Similarity 44.7%; Pred. No. 3.5e-18;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;
Qy 3 CYEGNGHYRGKASTDTMGRCPLPWSATVLQOQTYHAHRSDALQLGLGKHYCRNPDR 62
Db 31 CYFNGSAYRGTHSLTESGASCLPWSMILIGKVYTAQNPSAQLGLGKHYCRNPDR 90
Qy 63 RWCYVQVGLKPLVQECMVHDCADG-GKXPSPPE 95
Db 91 KPWCVLTNRRLTWECYCDVPCSTCGLRQYSQPQ 124

RESULT 45
US-09-618-869-10
; Sequence 10, Application US/09618869
; Patent No. 645279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee

;; APPLICANT: Rudolph, Rainer
;; APPLICANT: Schaeffner, Joerg
;; APPLICANT: Schwarz, Elisabeth
;; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
;; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
;; TITLE OF INVENTION: CHAPERONES
;; FILE REFERENCE: 20381
;; CURRENT APPLICATION NUMBER: US/09/618.869
;; CURRENT FILING DATE: 2000-07-19
;; PRIOR APPLICATION NUMBER: EP99114811.5
;; PRIOR FILING DATE: 1999-07-29
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 10
;; LENGTH: 378
;; TYPE: PRT
;; ORGANISM: Escherichia coli
US-09-618-869-10

Query Match 39.8%; Score 220.5; DB 4; Length 378;
Best Local Similarity 44.7%; Pred. No. 3.5e-18;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;
Qy 3 CYEGNGHYRGKASTDTMGRCPLPWSATVLQOQTYHAHRSDALQLGLGKHYCRNPDR 62
Db 31 CYFNGSAYRGTHSLTESGASCLPWSMILIGKVYTAQNPSAQLGLGKHYCRNPDR 90
Qy 63 RWCYVQVGLKPLVQECMVHDCADG-GKXPSPPE 95
Db 91 KPWCVLTNRRLTWECYCDVPCSTCGLRQYSQPQ 124

RESULT 46
US-08-811-949-67
; Sequence 67, Application US/08811949
; Patent No. 5840533
; GENERAL INFORMATION:
; APPLICANT: NIWA, MINEO
; APPLICANT: SAITO, YOSHIMASA
; APPLICANT: SASAKI, HITOSHI
; APPLICANT: HAYASHI, MASAKO
; APPLICANT: NOTANI, JOUJI
; APPLICANT: KOBAYASHI, MASAKAZU
; TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.C. SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811.949
; FILING DATE: 05-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 18-966-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 389 amino acids
; TYPE: amino acid

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811.949
FILING DATE: 05-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-966-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-311-949-67

Query Match 39.6%; Score 219.5; DB 2; Length 389;
Best Local Similarity 44.7%; Pred. No. 4,7e-18;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;

Qy 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLCQTYHAHRSDALQLGLGKHNCRPNRR 62
Db 42 CYFGNSAYRGTHSLTESGASCLPWNMILICKVYTAQNPSAQLGLGKHNCRPNR 101

Qy 63 RWCYVQVGLKPLVQECMVDCA-DGKFPSSPPE 95
Db 102 KPCHVLKRRLTWEYCDVPSCTGLRQYSQP 135

RESULT 47

US-09-411-977-3

; Sequence 3, Application US/09411977
; Patent No. 6372473
; GENERAL INFORMATION:
; APPLICANT: Moore, Paul A.
; APPLICANT: Ruben, Steven M.
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Tissue Plasminogen Activator-Like Protease
; FILE REFERENCE: PF378P1
; CURRENT APPLICATION NUMBER: US/09/411,977
; EARLIER FILING DATE: 1999-10-04
; EARLIER APPLICATION NUMBER: 09/084,491
; EARLIER FILING DATE: 1998-05-27
; EARLIER APPLICATION NUMBER: 60/048,000
; EARLIER FILING DATE: 1997-05-28
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-977-3

Query Match 39.4%; Score 218.5; DB 4; Length 326;
Best Local Similarity 44.7%; Pred. No. 5e-18;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;

Qy 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLCQTYHAHRSDALQLGLGKHNCRPNRR 62
Db 25 CYFGNSAYRGTHSLTESGASCLPWNMILICKVYTAQNPSAQLGLGKHNCRPNR 84

Qy 63 RWCYVQVGLKPLVQECMVDCA-DGKFPSSPPE 95
Db 85 KPCHVLKRRLTWEYCDVPSCTGLRQYSQP 118

RESULT 48

US-08-137-116-1

; Sequence 1, Application US/08137116
; Patent No. 5500411
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich
; APPLICANT: Koshig, Reinhard
; TITLE OF INVENTION: METHOD FOR TREATING THROMBOEMBOLIC
; TITLE OF INVENTION: CONDITIONS BY INHIBITING REOCCCLUSION
; TITLE OF INVENTION: VIA THE USE OF MULTIPLE BOLUS
; TITLE OF INVENTION: ADMINISTRATION OF THROMBOLYTICALLY
; TITLE OF INVENTION: ACTIVE PROTEINS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA

; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/137,116
; FILING DATE: June 30, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP92/00851
; FILING DATE: 15 April 1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 41 12 398
; FILING DATE: 16 April 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 41 23 845
; FILING DATE: 18 July 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5500411man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: ROER 1026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
US-08-137-116-1

Query Match 39.4%; Score 218.5; DB 1; Length 355;
Best Local Similarity 44.7%; Pred. No. 5.6e-18;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;

Qy 3 CYEGNGHFYRGKASTDTMGRPCLPWNSATVLCQTYHAHRSDALQLGLGKHNCRPNRR 62
Db 8 CYFGNSAYRGTHSLTESGASCLPWNMILICKVYTAQNPSAQLGLGKHNCRPNR 67

Qy 63 RWCYVQVGLKPLVQECMVDCA-DGKFPSSPPE 95
Db 68 KPCHVLKRRLTWEYCDVPSCTGLRQYSQP 101

RESULT 49

US-08-217-618-1

; Sequence 1, Application US/08217618
; Patent No. 5510330
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich
; APPLICANT: Fischer, Stephan
; TITLE OF INVENTION: COMBINATIONS OF THROMBOLYTICALLY ACTIVE
; TITLE OF INVENTION: PROTEINS AND NON-HEPARIN ANTICOAGULANTS, AND USES THEREOF
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/217,618
; FILING DATE: 25-MARCH-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:

Search completed: May 25, 2004, 15:00:09
Job time : 7.6468 secs

NAME: Hanson, No. 5510330man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: BOER 1032
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 688-3884
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acids
TOPOLOGY: linear
US-08-217-618-1

Query Match 39.4%; Score 218.5; DB 1; Length 355;
Best Local Similarity 44.7%; Pred. No. 5.6e-18;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;
Qy 3 CYEGNGHYGKASTDTMGRCPLPWSATVLOQTYHAHRS DALQLGLGKHNYCRNPDR 62
Db 8 CYFGNGSAYRTHSLTESGASCLPWSNMLIGKYYTAQNPSAQLGLGKHNYCRNP 67
Qy 63 RPMCVOVGLKPLVOECMWHDCAD-GKKPSSPPE 95
Db 68 KPCHVLKRRRLTWECYDVPSCSTCGLRQYSQPQ 101

RESULT 50
US-08-427-640-2
; Sequence 2, Application US/08427640
; Patent No. 5658788
; GENERAL INFORMATION:
; APPLICANT: Berg et al.
; TITLE OF INVENTION: Compounds and Methods for Treatment of Thromboembolic Disor
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: IN
; COUNTRY: U.S.A.
; ZIP: 46285

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 Mb storage
COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/427,640
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/689,410
FILING DATE: 22 APRIL 1991
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-08-427-640-2

Query Match 39.4%; Score 218.5; DB 1; Length 355;
Best Local Similarity 44.7%; Pred. No. 5.6e-18;
Matches 42; Conservative 10; Mismatches 41; Indels 1; Gaps 1;
Qy 3 CYEGNGHYGKASTDTMGRCPLPWSATVLOQTYHAHRS DALQLGLGKHNYCRNPDR 62
Db 8 CYFGNGSAYRTHSLTESGASCLPWSNMLIGKYYTAQNPSAQLGLGKHNYCRNP 67
Qy 63 RPMCVOVGLKPLVOECMWHDCAD-GKKPSSPPE 95
Db 68 KPCHVLKRRRLTWECYDVPSCSTCGLRQYSQPQ 101